

2) INFORMATION FOR SEQ ID NO: 158

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

20	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGC	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ATACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
25	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ACTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
30	ACGAAGGCCG	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTGGAGAT	750
35	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

40 2) INFORMATION FOR SEQ ID NO: 159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *Choleraesuis*
 (B) STRAIN: ATCC 7001

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGYCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
60	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200

	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGTGACGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
5	CGCGGTATCA	TCAAAGTGGG	YGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGTTGG	500
	ACGAAGGCCG	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
10	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCAATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

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2) INFORMATION FOR SEQ ID NO: 160

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 807 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*

(B) STRAIN: ATCC 43973

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACC	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCGGT	ACATTATCGT	GTTCTTGAAC	100
35	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACGCCAA	200
	TCGTTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
	GCGAAAATCA	TCGAAGTGGC	TGGCTTCCTG	GATTCTTACA	TCCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
40	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAARCTGCTG	GACGAAGGCC	500
	GTGCWGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
45	CAAGTTCGAA	TCTGAAGTGT	ATATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACCACT	700
	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTGGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACGG					807

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2) INFORMATION FOR SEQ ID NO: 161

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Heidelberg
 (B) STRAIN: ATCC 8326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

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10  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
    ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
15  GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACCTGCTGG      500
20  ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
    GCGGCCGTCA YACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACTACTG ACGTGACTGG CACCATCGAA TTGCCGGAAG GCGTAGAGAT      750
25  GGTAATGCCG GCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA TC                      832
  
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30 2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*
 (B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

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45  CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA      50
    TCCTGCTGGG TCGTCAGGTA GCGTTCCGT ACATCATCGT GTTCCTGAAC      100
    AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA      150
    AGTTCGTGAA CTTCTGTCTC AGTACGATTT CCCGGGCGAC GACACGCCGA      200
50  TCGTGCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAATGGGAA      250
    GCGAAAATCA TCGAACTGGC TGGCTACCTG GATTCTTACA TCCCAGGAACC      300
    AGAGCGTGCG ATTGACAAAC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
    CTATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC      400
    ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA      450
55  GTCGACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC      500
    GTGCTGGCGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA      550
    ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC      600
    CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGCCGTC      650
    ATRACTCGTT CTTCAAAGGC TACCGTCCGC AATTCTACTT CCGTACGACT      700
60  GACGTGACTG GCACCATCGA ACTGCCGGAA GCGGTGGAGA TGGTAATGCC      750
  
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GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807

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2) INFORMATION FOR SEQ ID NO: 163

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*
(B) STRAIN: ATCC 43976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

CGCGATCCTG GTTGTGCTG CGACTGACGG CCCGATGCCG CAGACCCGTG 50
AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTT 100
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
25 AATGGAAGTT CGTGAACCTC TGTCTCAGTA CGACTTCCCG GGTGACGACA 200
CGCCGATCGT GCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG 250
TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATTCC 300
GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG 350
TATTCTCCAT CTCCGGTCGT GGTACYGTTG TTACCGGTCG TGTAGAGCGC 400
30 GGTATCATCA AAGTGGGCGA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC 450
TCAGAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
AAGGCCGTGC CCGTGAGAAC GTAGGTGTTC TGCTGCGTGG TATCAAACGT 550
GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCA CCATCAAGCC 600
GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GATGAAGGCG 650
35 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT 700
ACTACTGACG TGA CTGGCAC CATCGA ACTG CCGGAAGGCG TAGAGATGGT 750
AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CATCCGATCG 800
CRATGGACGA CCGTCTGCGT TTCGCAA 827

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2) INFORMATION FOR SEQ ID NO: 164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
(B) STRAIN: ATCC 43972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GCGTTCCGT ACATCATCGT GTTCCTGAAC 100
60 AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACCTG TAGAAATGGA 150

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AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACGCCGA 200
TCGTGCGTGG TTCCGCTCTG AAAGCGCTGG AAGGCGAMGC TGAGTGGGAA 250
GMGAAAATCA TCGAACTGGC TGGCTWCCTG GATTCTTACA TTCCGGAACC 300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
5 CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC 400
ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
GTGCCGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
10 CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGCCGTC 650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACCACT 700
GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTGGAGA TGGTAATGCC 750
GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807
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2) INFORMATION FOR SEQ ID NO: 165

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 832 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Salmonella choleraesuis subsp. choleraesuis
30 serotype Typhi
    (B) STRAIN: ATCC 10749

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

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35 CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
ACACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
40 GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGGTGG 500
45 ACGAAGGCCG TGCNNGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACY AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
50 GGTAATGCCG GGCACACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCAATGGA CGACGGTCTG CGTTTCGCAA TC 832

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55 2) INFORMATION FOR SEQ ID NO: 166

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    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 817 bases
    (B) TYPE: Nucleic acid
60 (C) STRANDEDNESS: Double

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(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia fonticola*

(B) STRAIN: DSM 4576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

10
 CGGCGCTATC CTGGTTGTAG CTGCGACTGA CGGCCCTATG CCTCAGACTC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTA 100
 TTCATGAACA AATGCGACAT GGTTGATGAT GAAGAGCTGC TGGAAGTGGT 150
 AGAAATGGAA GTTCGTGAAC TTCTGTCTGC TTATGACTTC CCTGGTGATG 200
 15 ACCTGCCGGT TGTTCTGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAAGCT 250
 GAGTGGGAAG CTAAAATCAT CGAGCTGGCC GGTCACCTGG ATTCCTACAT 300
 CCCAGAACCA GAGCGTGCTA TCGATCAGCC GTTCCTGCTG CCAATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TAGTTACCGG TCGTGTGAG 400
 CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 20 CACCGTTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGG 500
 ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG 550
 CGTGAAGACA TCGAACGTGG TCAGGTACTG GCTAAACCAG GTTCCATCAA 600
 GCCGCACACT CAGTTCGATT CAGAAGTGTA TATCCTGAGC AAAGAAGAAG 650
 GTGGTCGTCA TACTCCATTG TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
 25 CGTACAACCTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
 GGTAATGCCA GGCGATAACG TGAACATGGT TGTTACCCTG ATCCACCCAA 800
 TCGCTATGGA CCAAGGC 817

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2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia liquefaciens*

(B) STRAIN: ATCC 27592

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

GCTGCGACTG ACGGCCCAAT GCCTCAGACC CGTGAGCACA TCCTGCTGGG 50
 TCGTCAGGTT GGCGTTCCTT TCATCATCGT ATTCATGAAC AAATGCGACA 100
 TGGTTGATGA TGAAGAGCTG CTGGAAGTGG TAGAAATGGA AGTTCGTGAA 150
 50 CTTCTGTCTG CTTACGACTT CCCTGGTGAT GACCTGCCGG TTGTTCTGTG 200
 TTCAGCGCTG AAAGCACTGG AAGGCGAAGC TGAGTGGGAA GCTAAAATCA 250
 TCGAGCTGGC CGGTTACCTG GATTCTTACA TCCCAGAACC AGAGCGTGCT 300
 ATCGACAAGC CGTTCCTGCT GCCAATCGAA GACGTCTTCT CCATCTCCGG 350
 TCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGTATC GTTAAAGTTG 400
 55 GCGAAGAAGT TGAAATCGTT GGTATCAAAG ACACCGTTAA GTCTACCTGT 450
 ACTGGCGTTG AAATGTTCCG CAAAGTCTG GACGAAGGCC GTGCTGGTGA 500
 GAACGTTGGT GTTCTGCTGC GTGGTATCAA GCGTGAAGAC ATCGAACGTG 550
 GTCAGGTACT GGCTAAACCA GGTTCAATCA AGCCACACAC CAAGTTCGAC 600
 TCAGAAGTGT ACATCCTGAG CAAAGAAGAA GGTGGTCGTC ATACTCCATT 650
 60 CTTCAAAGGC TACCGTCCAC AGTTCTACTT CCGTACAAC GACGTGACCG 700

GTACCATCGA ACTGCCAGAA GCGTTGAAA TGGTAATGCC AGGTGACAAC 750
 GTGAACATGG TTGTTACCCT GATCCACCCA ATCGCGA 787

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2) INFORMATION FOR SEQ ID NO: 168

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 745 bases
 10 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Serratia marcescens*
 (B) STRAIN: ATCC 13880

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

GCCTCAGACT CGTGAGCACA TCCTGCTGGG TCGTCAGGTT GCGTTTCCTT 50
 TCATCATCGT ATTCATGAAC AAATGCGACA TGGTTGATGA TGAAGAGCTG 100
 YTGGAACTGG TAGAAATGGA AGTTCGCGAA CTGCTGTCCG CTTACGACTT 150
 25 CCCTGGCGAC GACCTGCCGG TAATCCGCGG TTCCGCGCTG AAAGCGCTGG 200
 AAGGCGAAGC TGAGTGGGAA GCGAAAATCA TCGAACTGGC CGAAGCCCTG 250
 GACAGCTACA TCCCAGAGCC AGAGCGTGCT ATCGACAAGC CGTTCCTGCT 300
 GCCAATCGAA GACGTATTCT CCATCTCCGG TCGTGGTACC GTTGTTACCG 350
 GTCGTGTTGA GCGCGGCATC ATCAAAGTTG GCGAAGAAGT TGAAATCGTT 400
 30 GGTATCAAAG ACACCGTTAA GTCTACCTGT ACTGGCGTTG AAATGTTCCG 450
 CAAACTGCTG GACGAAGGCC GTGCTGGTGA GAACGTAGGT GTTCTGCTGC 500
 GTGGTATCAA ACGTGAAGAA ATCGAACGTG GTCAGGTA CT GGCTAAGCCA 550
 GGCTCCATCA AGCCGCACAC CCAGTTCGAA TCTGAAGTGT ACATCCTGAG 600
 CAAAGATGAA GGTGGTCGTC ACACKCCATT CTTCAAAGGC TACCGTCCAC 650
 35 AGTTCTACTT CCGTACCACT GACGTGACCG GTACCATCGA ACTGCCAGAA 700
 GCGGTAGAGA TGGTAATGCC AGGCGACAAC GTGAACATGG TTGTA 745

40 2) INFORMATION FOR SEQ ID NO: 169

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 50 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Serratia odorifera*
 (B) STRAIN: ATCC 33077

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

GGCGCAATCC TGGTTGTTGC TGCGACTGAC GGCCCTATGC CTCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GCCAGGTTGG CGTTCCTTTC ATCATCGTGT 100
 TCATGAACAA ATGTGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA 150
 GAAATGGAAG TTCGCGAGCT GCTGTCTGCT TACGATTTCC CTGGCGACGA 200
 60 CCTGCCAGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GCGAAGCAG 250

	AGTGGGAAGC	TAAGATTGTA	GAAGTGGCTG	AAGCGCTGGA	TTCTTACATC	300
	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCTTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
5	ACCGTTAAGT	CTACCTGTAC	CGGTGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCTATCAAG	600
	CCGCACACCA	AATTCGACTC	AGAAGTGTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACGCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
10	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTTACCCTGA	TTCACCCAAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTCGCAA			829

15

2) INFORMATION FOR SEQ ID NO: 170

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 830 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Serratia plymuthica</i>
(B)	STRAIN: DSM 4540

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

	CGGCGCAATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	GCGTTCCTTT	CATCATCGTA	100
	TTCATGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
35	AGAAATGGAA	GTTCGTGAAC	TTCTGTCTGC	TTACGACTTC	CCTGGTGATG	200
	ACCTGCCGGT	TGTTTCGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAACCA	250
	GAGTGGGAAG	CTAAAATCAT	CGAGCTGGCT	GGTTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCTA	TCGACAAGCC	GTTTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
40	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACCGTTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTGGGTG	TTCTGCTGCG	TGGTATCAAG	550
	CGCGAAGATA	TCGAACGTGG	TCAGGTCCTG	GCTAAACCAG	GTTCAATCAA	600
	GCCACACACC	AAGTTTGACT	CAGAAGTGTA	CATCCTGAGC	AAAGAAGAAG	650
45	GTGGTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGACAACG	TGAACATGGT	TGTAACCCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGCCTG	CGTTTCGCAA			830

50

2) INFORMATION FOR SEQ ID NO: 171

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 829 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia rubidaea*

(B) STRAIN: ATCC 27593

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

	GGCGCAATCC	TGGTAGTAGC	AGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGCC	GCCAGGTAGG	CGTACCTTAC	ATCATCGTAT	100
10	TCATGAACAA	ATGCGACATG	GTAGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCTGCT	TACGACTTCC	CAGGCGACGA	200
	CCTGCCGGTA	ATCCGTGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	GAAAATCGTT	GAGCTGGCAG	AAGCGCTGGA	CAGCTACATC	300
	CCAGAGCCAG	AGCGTGCTGT	AGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
15	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTAG	AAATCGTAGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CGAAGCCAGG	TTCAATCAAG	600
20	CCGCACACCC	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGACAACGT	GAACATGAAA	GTTACTCTGA	TTCACCCAAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTCGCAA			829

25

2) INFORMATION FOR SEQ ID NO: 172

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Shigella boydii*

40

(B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

	CGGCGCGATC	YTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
45	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GTTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCCT	GGAAGTGGCT	GGCTTCCTGG	ATTCTTACAT	300
50	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
55	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
60	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 173

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

20	TGGTAGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAAATGGAAG	150
	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	200
	GTTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
25	GAAAATCCTG	GAAGTGGCTG	GCTTCCTGGA	TTCYTAYATT	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGAC	GCGGTATCAT	400
	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACYCAGAAGT	450
	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
30	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CGAAGCCRGG	CACCATCAAG	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	650
	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
35	GCGACAACAT	CAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	800
	GACGGTCTGC	GTTTCGCA				818

40 2) INFORMATION FOR SEQ ID NO: 174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
 (B) STRAIN: ATCC 12022

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

55

	CCTGGTAGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TTGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACTCCGA	200
60	TCGTTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250

	GCGAAAATCC	TGGAAGTGGC	TGGCTTCCTG	GATTCTTACA	TTCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	ACGCGGTATC	400
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
5	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
	GTGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGMCCTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
10	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACG					806

15

2) INFORMATION FOR SEQ ID NO: 175

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 832 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Shigella sonnei</i>
(B)	STRAIN: ATCC 29930

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

	CGGCGCGATC	CTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
35	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCCT	GGAAGTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
40	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
45	GCGGYCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

50

2) INFORMATION FOR SEQ ID NO: 176

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 716 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: ATCC 13301

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

	TCTGCTGCTG	ACGGTCCAAT	GCCACAAACT	CGTGAACACA	TTCTTTTATC	50
	ACGTAACGTT	GGTGTACCAG	CATTAGTAGT	ATTCTTAAAC	AAAGTTGACA	100
10	TGGTTGACGA	TGAAGAATTA	TTAGAATTAG	TAGAAATGGA	AGTTCGTGAC	150
	TTATTAAGCG	AATATGACTT	CCCAGGTGAC	GATGTACCTG	TAATCGCTGG	200
	TTCAGCATT	AAAGCTTTAG	AAGGCGATGC	TCAATACGAA	GAAAAAATCT	250
	TAGAATTAAT	GGAAGCTGTA	GATACTTACA	TTCCAACCTC	AGAACGTGAT	300
	TCTGACAAAC	CATTCATGAT	GCCAGTTGAG	GACGTATTCT	CAATCACTGG	350
15	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	ATCAAAGTTG	400
	GTGAAGAAGT	TGAAATCATC	GGTTTACATG	ACACATCTAA	AACAACGTGT	450
	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	AAGCTGGTGA	500
	CAACATTGGT	GCATTATTAC	GTGGTGTTCG	TCGTGAAGAC	GTACAACGTG	550
	GTCAAGTATT	AGCTGCTCCT	GGTTCAATTA	CACCACATAC	TGAATTCAAA	600
20	GCAGAAGTAT	ACGTATTATC	AAAAGACGAA	GGTGGACGTC	ACACTCCATT	650
	CTTCTCAAAC	TATCGTCCAC	AATTCTATTT	CCGTACTACT	GACGTAACCTG	700
	GTGTTGTTCA	CTTACC				716

25

2) INFORMATION FOR SEQ ID NO: 177

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 719 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: ATCC 29247

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

	TTCTTTTATC	ACGTAACGTT	GGTGTACCAG	CATTAGTAGT	ATTCTTAAAC	50
	AAAGTTGACA	TGGTTGACGA	TGAAGAATTA	TTAGAATTAG	TAGAAATGGA	100
	AGTTCGTGAC	TTATTAAGCG	AATATGACTT	CCCAGGTGAC	GATGTACCTG	150
45	TAATCGCTGG	TTCAGCATT	AAAGCTTTAG	AAGGCGATGC	TCAATACGAA	200
	GAAAAAATCT	TAGAATTAAT	GGAAGCTGTA	GATACTTACA	TTCCAACCTC	250
	AGAACGTGAT	TCTGACAAAC	CATTCATGAT	GCCAGTTGAG	GACGTATTCT	300
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	350
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCATC	GGTTTACATG	ACACATCTAA	400
50	AACAACGTGT	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	450
	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTCG	TCGTGAAGAC	500
	GTACAACGTG	GTCAAGTATT	AGCTGCTCCT	GGTTCAATTA	CACCACATAC	550
	TGAATTCAAA	GCAGAAGTAT	ACGTATTATC	AAAAGACGAA	GGTGGACGTC	600
	ACACTCCATT	CTTCTCAAAC	TATCGTCCAC	AATTCTATTT	CCGTACTACT	650
55	GACGTAACCTG	GTGTTGTTCA	CTTACCAGAA	GGTMCTGAAA	TGGTAATGCC	700
	TGGTGATAAC	GTTGAAATG				719

60 2) INFORMATION FOR SEQ ID NO: 178

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 625 bases
- (B) TYPE: Nucleic acid
- 5 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 10 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: ATCC 33591

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

15	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	50
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	100
	AGAAATGGAA	GTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	150
	ATGTACCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGATGCT	200
20	CAATACGAAG	AAAAAATCTT	AGAATTAATG	GAAGCTGTAG	ATACTTACAT	250
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	300
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	350
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	400
	CACATCTAAA	ACAACTGTTA	CAGGTGTTGA	AATGTTCCGT	AAATTATTAG	450
25	ACTACGCTGA	AGCTGGTGAC	AACATTGGTG	CATTATTACG	TGGTGTGCT	500
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	550
	ACCACATACT	GAATTCAAAG	CAGAAGTATA	CGTATTATCA	AAAGACGAAG	600
	GTGGACGTCA	CACTCCATTC	TTCTC			625

30

2) INFORMATION FOR SEQ ID NO: 179

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 704 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: ATCC 43300

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

	GTTGGTGTAC	CAGCATTAGT	AGTATTCTTA	AACAAAGTTG	ACATGGTTGA	50
	CGATGAAGAA	TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAA	100
50	GCGAATATGA	CTTCCCAGGT	GACGATGTAC	CTGTAATCGC	TGGTTCAGCA	150
	TTAAAAGCTT	TAGAAGGCGA	TGCTCAATAC	GAAGAAAAAA	TCTTAGAATT	200
	AATGGAAGCT	GTAGATACTT	ACATTCCAAC	TCCAGAACGT	GATTCTGACA	250
	AACCATTTCAT	GATGCCAGTT	GAGGACGTAT	TCTCAATCAC	TGGTCGTGGT	300
	ACTGTTGCTA	CAGGCCGTGT	TGAACGTGGT	CAAATCAAAG	TTGGTGAAGA	350
55	AGTTGAAATC	ATCGGTTTAC	ATGACACATC	TAAAACAAC	GTTACAGGTG	400
	TTGAAATGTT	CCGTAAATTA	TTAGACTACG	CTGAAGCTGG	TGACAACATT	450
	GGTGCAATTAT	TACGTGGTGT	TGCTCGTGAA	GACGTACAAC	GTGGTCAAGT	500
	ATTAGCTGCT	CCTGGTTCAA	TTACACCACA	TACTGAATTC	AAAGCAGAAG	550
	TATACGTATT	ATCAAAAGAC	GAAGGTGGAC	GTCACACTCC	ATTCTTCTCA	600
60	AACTATCGTC	CACAATTCTA	TTTCCGTACT	ACTGACGTAA	CTGGTGTGTT	650

TCACCTTACCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACGTTGAAA 700
TGAC 704

5

2) INFORMATION FOR SEQ ID NO: 180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
(B) STRAIN: ATCC 6538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA 50
TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT 100
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG 150
25 ATGTACCTGT AATCGCTGGT TCAGCATTA AAGCTTTAGA AGGCGATGCT 200
CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT 250
TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 300
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 350
CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 400
30 CACATCTAAA ACAACTGTGA CAGGTGTTGA AATGTTCCGT AAATTATTAG 450
ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTTGCT 500
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 550
ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG 600
GTGGACGTCA CACTCCATTC TTCTCAAAC ATCGTCCACA ATTCTATTTC 650
35 CGTACTACTG ACGTAACTGG TGTGTTTCAC TTACCAGAAG GTACTGAAAT 700
GGTAATGCCT GGTGATAACG TTGAAATGAC 730

40 2) INFORMATION FOR SEQ ID NO: 181

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
(B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

55

CGGTGCGATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAACTC 50
GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
TTCTTAAACA AAGTTGACCA AGTTGACGAC GAAGAATTAT TAGAATTAGT 150
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATACGACTAC CCAGGTGACG 200
60 ATGTACCTGT AATCTCTGGT TCTGCGTTGA AAGCATTAGA AGGCGACAAA 250


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GAATACGAAC AAAAATCTT AGACTTAATG CAACAAGTTG ACGATTACAT 300
TCCAACCTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAAG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACAGG CCGTGTTGAA 400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATGAAAGA 450
5 CGGTTTCAAA AAAACAACAG TTAAGTGGT AGAAATGTTT CGTAAATTAT 500
TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTATT 550
TCACGTGAAG AAGTACAACG TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT 600
TACACCACAC ACTAAATTCA CTGCAGAAGT TTACGTATTA TCTAAAGATG 650
AAGGTGGACG TCACACTCCA TTCTTCTCTA ACTACCGTCC ACAATTCTAT 700
10 TTCCGTACTA CTGACGTAAC AGGTGTTGTT ACTTTACCAG AAGGTACAGA 750
AATGGTAATG CCTGGCGATA ACGTTAAAAT GGAAGTTGAA TTAATTTCTC 800
CAATCGCTAT CGAAGACGGT ACTCGTTTCT CAAT 834

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15

2) INFORMATION FOR SEQ ID NO: 182

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA
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(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus capitis subsp. capitis
(B) STRAIN: ATCC 27840

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

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CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC 50
GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
TTCTTAAACA AAGTTGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
35 TGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGATG 200
ATGTACCTGT AATCGCTGGT TCAGCATTA AAGCTTTAGA AGGCGATGCT 250
CAATACGAAG AAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTACAT 300
TCCAACCTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
40 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTATCCACGA 450
AACTTCTAAA ACAACTGTGA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTTGCT 550
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATCAC 600
ACCAACACACT AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
45 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCACA ATTCTATTTC 700
CGTACTACTG ACGTAACTGG TGTTGTAAAC TTACCAGAAG GTACTGAAAT 750
GGTTATGCCT GGCACAAACG TTGAAATGAC AGTTGAATTA ATCGCTCCTA 800
TCGCTATTGA AGACGGTACT CGTTTCTCAA TCGGA 835

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50

2) INFORMATION FOR SEQ ID NO: 183

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(i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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50 (ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Macrococcus caseolyticus*

(B) STRAIN: ATCC 13548

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

	GTATCTTAGT	AGTATCTGCT	GCTGACGGTC	CAATGCCACA	AACTCGTGAA	50
	CACATCCTTT	TATCACGTAA	CGTTGGTGTA	CCAGCATTAG	TAGTATTCTT	100
10	GAACAAAGTT	GACATGGTTG	ACGATGAAGA	ATTATTAGAA	TTAGTTGAAA	150
	TGGAAGTTCG	TGACTTATTA	TCTGAATATG	ACTTCCCTGG	TGACGATGTA	200
	CCTGTAATCG	CTGGATCTGC	TTTAAAAGCA	TTAGAAGGCG	TTGAAGAATA	250
	CGAAGACAAA	ATCATGGAAT	TAATGGACGC	AGTTGATGAG	TACATCCCAA	300
	CTCCAGAACG	TGATTCTGAC	AAACCATTCA	TGATGCCAGT	TGAGGACGTA	350
15	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCA	ACTGGACGTG	TTGAGCGTGG	400
	ACAAGTTAAA	GTTGGTGAAG	AAGTTGAAAT	CATTGGTTTA	ACTGAAGAAC	450
	CAGCAAAAAC	TACAGTTACA	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAT	500
	TACGCTGAAG	CTGGAGATAA	CATCGGTGCT	TTATTACGTG	GTGTTTCTCG	550
	TGAAGACGTA	CAACGTGGAC	AAGTATTAGC	TAAACCAGGT	TCAATTACTC	600
20	CACATACTAA	ATTCAAAGCT	GAAGTTTACG	TATTATCTAA	AGAAGAAGGT	650
	GGACGTCATA	CTCCATTCTT	CACTAACTAC	CGCCCTCAGT	TCTACTTCCG	700
	TACAACTGAC	GTAAGTGGTG	TAGTTAACTT	ACCAGAAGGT	ACTGAAATGG	750
	TAATGCCTGG	AGATAACATC	GAAATGAACG	TTGAATTAAT	TTCTCCAATC	800
	GCGA					804

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2) INFORMATION FOR SEQ ID NO: 184

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus cohnii*

40 (B) STRAIN: DSM 20260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
45	GTGAACATAT	CCTTTTATCA	CGTAACGTTG	GTGTTCCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCTCTGGT	TCAGCATTAA	AAGCTCTTGA	AGGCGACGCT	250
	GACTATGAGC	AAAAAATCTT	AGACTTAATG	CAAGCTGTTG	ATGACTTCAT	300
50	TCCAACACCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	GCGTGTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATGCAAGA	450
	AGATTCAAGC	AAAACAACGT	TTACTGGTGT	AGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATTG	GTGCGTTATT	ACGTGGTGT	550
55	GCACGTGAAG	ACATCCAACG	TGGTCAAGTT	TTAGCTGCTC	CTGGTTCAAT	600
	TACACCACAC	ACAAACTTTA	AAGCGGAAGT	TTACGTTTTA	TCAAAAGATG	650
	AAGGTGGCCG	TCATACGCCA	TTCTTCAGTA	ACTATCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	AGGTGTTGTT	ACTTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAGAAAT	GGAAGTTGAA	CTAATTTCTC	800
60	CAATCGCTAT	CGAAGACGGT	ACACGTTTCT	CT		832

2) INFORMATION FOR SEQ ID NO: 185

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: CSG 269

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

20 ATCTGCTGCT GACGGTCCAA TGCCACAAAC TCGTGAACAC ATCTTATTAT 50
 CACGTAACGT TGGTGTACCA GCATTAGTTG TATTCTTAAA CAAAGTTGAC 100
 ATGGTAGACG ACGAAGAATT ATTAGAATTA GTTGAAATGG AAGTTCGTGA 150
 CTTATTAAGC GAATATGACT TCCCAGGTGA CGATGTACCT GTAATCGCTG 200
 GTTCTGCATT AAAAGCATTGA GAAGGCGATG CTGAATACGA ACAAAAAATC 250
 25 TTAGACTTAA TGCAAGCAGT TGATGATTAC ATTCCAACCTC CAGAACGTGA 300
 TTCTGACAAA CCATTCATGA TGCCAGTTGA GGACGTATTG TCAATCACTG 350
 GTCGTGGTAC TGTGCTACA GGCCGTGTTG AACGTGGTCA AATCAAAGTT 400
 GGTGAAGAAG TTGAAATCAT CGGTATGCAC GAAACTTCTA AAACAACTGT 450
 TACTGGTGTA GAAATGTTCC GTAAATTATT AGACTACGCT GAAGCTGGTG 500
 30 ACAACATCGG TGCTTTATTA CGTGGTGTG CACGTGAAGA CGTACAACGT 550
 GGTCAAGTAT TAGCTGCTCC TGGTCTATT ACACCACACA CAAAATTCAA 600
 AGCTGAAGTA TACGTATTAT CTAAAGATGA AGGTGGACGT CACACTCCAT 650
 TCTTCACTAA CTATCGCCCA CAATTCTATT TCCGTACTAC TGACGTAAC 699

35

2) INFORMATION FOR SEQ ID NO: 186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC 50
 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA 100
 55 TTCTTAAATA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT 150
 TGAAATGGAA GTACGTGACT TATTATCTGA ATACGACTTC CCAGGTGACG 200
 ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 250
 CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT 300
 TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
 60 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA 400

5 CGTGGGCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATTG ~~GTATCCATTGA~~ 450
 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CATTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATCAC 600
 5 ACCTCACACA AAATTTAAAG CAGACGTATA CGTTTTATCT AAAGACGAAG 650
 GTGGACGTCA CACTCCATTC TTCACAACT ATCGTCCACA ATTCTATTTC 700
 CGTACTACTG ACGTAACTGG TGTTGTTAAC TTACCAGAAG GTACTGAAAT 750
 GGTTATGCCT GCGGACAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCA 829
 10

2) INFORMATION FOR SEQ ID NO: 187

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 705 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus warneri*
 25 (B) STRAIN: CSG 123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

30 CACAACTCG TGAACACATT CTTTTATCAC GTAACGTTGG TGTACCAGCT 50
 TTAGTTGTAT TCTTAAACAA AGTTGATATG GTAGACGACG AAGAATTATT 100
 AGAATTAGTA GAAATGGAAG TTCGTGACTT ATTATCTGAA TATGACTTCC 150
 CAGGTGACGA CGTACCTGTA ATCGCTGGTT CAGCATTAAG AGCTTTAGAA 200
 GCGGACGAAA AATACGAAGA AAAAATCTTA GAATTAATGC AAGCAGTTGA 250
 TGACTACATT CCAACTCCAG AACGTGATTC TGACAAACCA TTCATGATGC 300
 35 CAGTTGAGGA CGTATTCTCA ATCACTGGTC GTGGTACTGT TGCTACAGGC 350
 CGTGTTGAAC GTGGTCAAAT CAAAGTTGGT GAAGAAGTTG AAATCATCGG 400
 TTTACATGAC ACTTCTAAAA CAACTGTTAC TGGTGTAGAA ATGTTCCGTA 450
 AGTTATTAGA CTACGCTGAA GCTGGTGACA ACATCGGTGC TTTATTACGT 500
 GGTGTTGCTC GTGAAGACGT ACAACGTGGT CAAGTATTAG CTGCTCCTGG 550
 40 TTCAATTACA CCACATACAA AATTCAAAGC GGAAGTTTAC GTTTTATCTA 600
 AAGACGAAGG TGGACGTCAC ACTCCATTCT TCAGTAACTA CCGCCACAA 650
 TTCTATTTCC GTACTACTGA CGTAACTGGC GTTGTTCAAT TACCAGAAGG 700
 TACTG 705

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2) INFORMATION FOR SEQ ID NO: 188

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 678 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 55 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: CSG 23
 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188

	TTTTATCACG	TAACGTTGGT	GTACCAGCAT	TAGTAGTATT	CTTAAACAAA	50
	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTTG	AAATGGAAGT	100
5	ACGTGACTTA	TTATCTGAAT	ACGACTTCCC	AGGTGACGAC	GTACCTGTAA	150
	TCGCTGGTTC	AGCTTTAAAA	GCTTTAGAAG	GCGATGCTCA	ATACGAAGAA	200
	AAAATCTTAG	AATTAATGCA	AGCAGTTGAT	GATTACATTC	CAACTCCAGA	250
	ACGTGACTCT	GATAAACCAT	TCATGATGCC	AGTTGAGGAC	GTATTCTCAA	300
	TCACTGGTTC	TGGTACTGTT	GCTACAGGTC	GTGTTGAACG	TGGTCAAATC	350
10	AAAGTTGGTG	AAGAAGTTGA	AATTATTGGT	ATCAAAGAAA	CTTCTAAAAC	400
	AACTGTTACT	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	TACGCTGAAG	450
	CTGGTGACAA	CATCGGTGCT	TTATTACGTG	GTGTTGCTCG	TGAAGATGTA	500
	CAACGTGGTC	AAGTATTAGC	TGCTCCAGGT	TCAATTACAC	CTCACACAAA	550
	ATTCAAAGCA	GACGTATACG	TTTTATCAAA	AGATGAAGGT	GGACGTCATA	600
15	CTCCATTCTT	CACTAACTAT	CGTCCACAAT	TCTATTTCCG	TACTACTGAC	650
	GTAAGTGGTG	TTGTTAACTT	ACCAGAAG			678

20 2) INFORMATION FOR SEQ ID NO: 189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: CSG 33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

35	ACCAGCATTA	GTAGTATTCT	TAAATAAAGT	TGACATGGTT	GACGATGAAG	50
	AATTATTAGA	ATTAGTTGAA	ATGGAAGTAC	GTGACTTATT	ATCTGAATAC	100
	GACTTCCCAG	GTGACGATGT	ACCTGTAATC	GCTGGTTCAG	CATTAAAAGC	150
	TTTAGAAGGC	GATGCTCAAT	ACGAAGAAAA	AATCTTAGAA	TTAATGCAAG	200
40	CAGTTGATGA	CTACATTCCA	ACTCCAGAAC	GTGATTCTGA	CAAACCATTG	250
	ATGATGCCAG	TTGAGGACGT	ATTCTCAATC	ACTGGTCGTG	GTACTGTTGC	300
	TACAGGCCGT	GTTGAACGTG	GTCAAATCAA	AGTTGGTGAA	GAAGTTGAAA	350
	TCATTGGTAT	CCATGACACT	TCTAAAACAA	CTGTTACTGG	TGTAGAAATG	400
	TTCCGTAAAT	TATTAGACTA	CGCTGAAGCT	GGTGACAACA	TCGGTGCAAT	450
45	ATTACGTGGT	GTTGCTCGTG	AAGACGTACA	ACGTGGTCAA	GTATTAGCTG	500
	CTCCAGGTTC	AATCACACCT	CACACAAAAT	TTAAAGCAGA	CGTATACGTT	550
	TTATCTAAAG	ACGAAGGTGG	ACGTCACACT	CCATTCTTCA	CAAACATATCG	600
	TCCACAATTC	TATTTCCGTA	CTACTGACGT	AACTGGTGTT	GTTAACTTAC	650
	CAGAAGGTAC	TGAAATGG				668

50

2) INFORMATION FOR SEQ ID NO: 190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

5 (A) ORGANISM: *Staphylococcus haemolyticus*
(B) STRAIN: CSG 8

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 190

	AAAGTTGACA	TGGTTGACGA	TGAAGAATTA	TTAGAATTAG	TTGAAATGGA	50
10	AGTACGTGAC	TTATTATCTG	AATACGACTT	CCCAGGTGAC	GATGTACCTG	100
	TAATCGCTGG	TTCAGCATTA	AAAGCTTTAG	AAGGCGATGC	TCAATACGAA	150
	GAAAAAATCT	TAGAATTAAT	GCAAGCAGTT	GATGATTACA	TTCCAACCTC	200
	AGAACGTGAT	TCTGACAAAC	CATTCATGAT	GCCAGTTGAG	GACGTATTCT	250
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	300
15	ATCAAAGTTG	GTGAAGAAGT	TGAAATCATT	GGTATCCATG	ACACTTCTAA	350
	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	400
	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTGTC	TCGTGAAGAC	450
	GTACAACGTG	GTCAAGTATT	AGCTGCTCCA	GGTTCAATCA	CACCTCACAC	500
	AAAATTTAAA	GCAGACGTAT	ACGTTTTATC	TAAAGACGAA	GGTGGACGTC	550
20	ACACTCCATT	CTTCACAAAC	TATCGTCCAC	AATTCTATTT	CCG	593

2) INFORMATION FOR SEQ ID NO: 191

25

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
30 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

35 (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
(B) STRAIN: ATCC 27844

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 191

40	CGGCGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGTGACT	TATTATCTGA	ATACGACTTC	CCAGGTGACG	200
	ACGTACCTGT	AATCGCTGGT	TCAGCTTTAA	AAGCTTTAGA	AGGCGATGCT	250
45	CAATACGAAG	AAAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGATTATAT	300
	TCCAACCTCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATTATTG	GTATCAAAGA	450
	AACTTCTAAA	ACAACTGTTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
50	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCT	550
	CGTGAAGATG	TACAACGTGG	TCAAGTATTA	GCTGCTCCAG	GTTCAATTAC	600
	ACCTCACACA	AAATTCAAAG	CAGACGTATA	CGTTTTATCA	AAAGATGAAG	650
	GTGGACGTCA	TACTCCATTC	TTCTCTAACT	ATCGTCCACA	ATTCTATTTC	700
	CGTACTACTG	ACGTAACCTG	TGTTGTTAAC	TTACCAGAAG	GTACTGAAAT	750
55	GGTAATGCCT	GGTGACAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
	TCGCGATTGA	AGACGGTACT	CGTTTCTC			828

60 2) INFORMATION FOR SEQ ID NO: 192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 35982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

15 ATGGTCCAAT GCCACAACT CGTGAACACA TTCTTTTATC ACGTAACGTT 50
 GGTGTACCAG CTTTAGTTGT ATTCTTAAAC AAAGTTGATA TGGTAGACGA 100
 CGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC TTATTATCTG 150
 AATATGACTT CCCAGGTGAC GACGTACCTG TAATCGCTGG TTCAGCATTA 200
 20 AAAGCTTTAG AAGGCGACGA AAAATACGAA GAAAAAATCT TAGAATTAAT 250
 GCAAGCAGTT GATGACTACA TTCCAACCTC AGAACGTGAT TCTGACAAAC 300
 CATTCATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG TCGTGGTACT 350
 GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG GTGAAGAAGT 400
 TGAAATCATC GGTTTACATG ACACTTCTAA ACAAAGTGT ACTGGTGTAG 450
 25 AAATGTTCCG TAAGTTATTA GACTACGCTG AAGCTGGTGA CAACATCGGT 500
 GCTTTATTAC GTGGTGTGTC TCGTGAAGAC GTACAACGTG GTCAAGTATT 550
 AGCTGCTCCT GGTTC AATTA CACCACATAC AAAATTCAA GCGGAAGTTT 600
 ACGTTTTATC TAAAGACGAA 620

30

2) INFORMATION FOR SEQ ID NO: 193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 170

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

CCAGCATTAG TAGTATTCTT AAACAAAGTT GACATGGTTG ACGATGAAGA 50
 ATTATTAGAA TTAGTTGAAA TGGAAGTACG TGACTTATTA TCTGAATACG 100
 50 ACTTCCCAGG TGACGACGTA CCTGTAATCG CTGGTTCAGC TTTAAAAGCT 150
 TTAGAAGGCG ATGCTCAATA CGAAGAAAAA ATCTTAGAAT TAATGCAAGC 200
 AGTTGATGAT TATATTCCAA CTCCAGAACG TGACTCTGAT AAACCATTC A 250
 TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG TACTGTTGCT 300
 ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTTGGTGAAG AAGTTGAAAT 350
 55 TATTGGTATC AAAGAACTT CTAAAACAAC TGTTACTGGT GTAGAAATGT 400
 TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT CCGTGCTTTA 450
 TTACGTGGTG TTGCTCGTGA AGATGTACAA CGTGGTCAAG TATTAGCTGC 500
 TCCAGGTTCA ATTACACCTC ACACAAAATT CAAAGCAGAC GTATACGTTT 550
 TATCAAAAGA TGAAGGTGGA CGTCATACTC CATTCTTCTC TAACTATCGT 600
 60 CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTG TTAACCTACC 650

AGAAGGTACT GAAATGGTAA TGCCTGGTGA CAACGTTGAA AT

5 2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

20 CATTCTTTTA TCACGTAACG TTGGTGTACC AGCATTAGTA GTATTCTTAA 50
 ACAAAGTTGA CATGGTTGAC GATGAAGAAT TATTAGAATT AGTTGAAATG 100
 GAAGTACGTG ACTTATTATC TGAATACGAC TTCCCAGGTG ACGACGTACC 150
 TGTAATCGCT GGTTTCAGCTT TAAAAGCTTT AGAAGGCGAT GCTCAATACG 200
 25 AAGAAAAAAT CTTAGAATTA ATGCAAGCAG TTGATGATTA TATTCCAAC 250
 CCAGAACGTG ACTCTGATAA ACCATTTCATG ATGCCAGTTG AGGACGTATT 300
 CTCAATCACT GGTCGTGGTA CTGTTGCTAC AGGCCGTGTT GAACGTGGTC 350
 AAATCAAAGT TGGTGAAGAA GTTGAAATTA TTGGTATCAA AGAAACTTCT 400
 AAAACAAC 450
 30 TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTGTG GCTCGTGAAG 500
 ATGTACAACG TGGTCAAGTA TTAGCTGCTC CAGGTTCAAT TACACCTCAC 550
 ACAAATTC AAGCAGACGT ATACGTTTTC TCAAAAGATG AAGGTGGACG 600
 TCATACTCCA TTCTTCTCTA ACTATCGTCC ACAATTCTAT TTCCGTACTA 650
 CTGACGTAAC TGGTGTTGTT AACTTACCAG AAGG 684

2) INFORMATION FOR SEQ ID NO: 195

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 50 (B) STRAIN: CSG 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

55 ACCAGCATTG TAGTATTCT TAAACAAAGT TGACATGGTT GACGATGAAG 50
 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC 100
 GACTTCCAG GTGACGACGT ACCTGTAATC GCTGGTTCAG CTTTAAAAGC 150
 TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG 200
 CAGTTGATGA TTACATTCCA ACTCCAGAAC GTGACTCTGA TAAACCATTC 250
 ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC 300
 60 TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA 350

TTATTGGTAT CAAAGAACT TCTAAAACAA CTGTTACTGG TGTAGAAATG 400
 TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCTTT 450
 ATTACGTGGT GTTGCTCGTG AAGATGTACA ACGTGGTCAA GTATTAGCTG 500
 CTCCAGGTTC AATTACACCT CACACAAAAT TCAAAGCAGA CGTATACGTT 550
 5 TTATCAAAAG ATGAAGGTGG ACGTCATACT CCATTCTTCA CTAACATATCG 600
 TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTT GTTAACTTAC 650
 CAGAAGGTAC TGAAATGGTA ATGCCTGGCG ACAAC 685

10

2) INFORMATION FOR SEQ ID NO: 196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 62

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

GACTTATTAT CTGAATACGA CTTCCCAGGT GACGACGTAC CTGTAATCGC 50
 TGGTTCAGCT TTAAAAGCTT TAGAAGGCGA TGCTCAATAC GAAGAAAAAA 100
 TCTTAGAATT AATGCAAGCA GTTGATGATT ACATTCCAAC TCCAGAACGT 150
 30 GACTCTGATA AACCATTTCAT GATGCCAGTT GAGGACGTAT TCTCAATCAC 200
 TGGTCGTGGT ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG 250
 TTGGTGAAGA AGTTGAAATT ATTGGTATCA AAGATACTTC TAAAACAAC 300
 GTTACTGGTG TAGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG 350
 TGACAACATC GGTGCTTTAT TACGTGGTGT TGCTCGTGAA GATGTACAAC 400
 35 GTGGTCAAGT ATTAGCTGCT CCAGGTTCAA TCACACCTCA CACAAAATTC 450
 AAAGCAGACG TATATGTTTT ATCAAAAGAT GAAGGTGGAC GTCATACTCC 500
 ATTCTTCACT AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA 550
 CTGGTGTGTG TAACTTACCA GAAGGTACTG AAATGGTAAT GCCTGGCGAC 600
 AACGTTGAAA T 611

40

2) INFORMATION FOR SEQ ID NO: 197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus lugdunensis*
 55 (B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

CGGCGGTATC TTAGTAGTTT CTGCTGCAGA TGGTCCAATG CCACAACTC 50
 50 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTGCCAGC ATTAGTAGTA 100

	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGATT	TATTAAGTGA	ATATGACTTC	CCAGGTGACG	200
	ATGTGCCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGACGAA	250
	AAATACGAAG	CTAAAATCTT	AGAATTAATG	GATGCAGTTG	ATAACTACAT	300
5	TCCAACCTCA	GAACGTGACT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATTATTG	GTATCCACGA	450
	TACTACTAAA	ACAACGTGTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CGTTATTACG	TGGTGTGCT	550
10	CGTGAAGATG	TACAACGTGG	ACAAGTATTA	GCTGCTCCAG	GTTCAATTAC	600
	ACCTCACACT	AAATTTAAAG	CTGACGTATA	TGTTTTATCT	AAAGATGAAG	650
	GTGGACGTCA	TACACCATTG	TTCTCAAAC	ACCGCCACCA	ATTCTATTTC	700
	CGTACTACAG	ACGTAACTGG	TGTTGTTAAC	TTACCAGAAG	GTACAGAAAT	750
	GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
15	TCGCTATCGA	AGACGGAAC	CGTTTCTC			828

2) INFORMATION FOR SEQ ID NO: 198

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 35552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

35	AGTAGTATCT	GCTGCTGATG	GCCCAATGCC	ACAACTCGT	GAACACATTC	50
	TTTTATCACG	TAACGTTGGT	GTTCCAGCAT	TAGTTGTATT	CTTAAACAAA	100
	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTAAGCGAAT	ATGACTTCCC	AGGTGACGAT	GTACCTGTAA	200
	TCTCTGGTTC	TGCATTAAAA	GCTTTAGAAG	GCGACGCTGA	CTATGAGCAA	250
40	AAAATCTTAG	ACTTAATGCA	AGCTGTTGAT	GACTTCATTC	CAACACCAGA	300
	ACGTGATTCT	GACAAACCAT	TCATGATGCC	AGTTGAGGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTCAAATC	400
	AAAGTCGGTG	AAGAAATCGA	AATCATCGGT	ATGCAAGAAG	AATCAAGCAA	450
	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
45	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTC	ACGTGATGAC	550
	GTACAACGTG	GTCAAGTTTT	AGCTGCTCCT	GGTACTATTA	CACCACATAC	600
	AAAATTCAAA	GCGGATGTTT	ACGTTTTATC	TAAAGATGAA	GGTGGTCGTC	650
	ATACACCATT	CTTCACTAAC	TACCGCCAC	AATTCTATTT		690

50

2) INFORMATION FOR SEQ ID NO: 199

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 723 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: CSG 83

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

	GCATTAGTTG	TATTCTTAAA	CAAAGTTGAC	ATGGTTGACG	ATGAAGAATT	50
	ATTAGAATTA	G TAGAAATGG	AAGTTCGTGA	TTTATTAAGC	GAATATGACT	100
10	TCCCAGGTGA	CGATGTACCT	GTAATCTCTG	GTTCTGCATT	AAAAGCTTTA	150
	GAAGGCGACG	CTGACTATGA	GCAAAAAATC	TTAGACTTAA	TGCAAGCTGT	200
	TGATGACTTC	ATTCCAACAC	CAGAACGTGA	TTCTGACAAA	CCATTTCATGA	250
	TGCCAGTTGA	GGACGTATTC	TCAATCACTG	GTCGTGGTAC	TGTTGCTACA	300
	GGCCGTGTTG	AACGTGGTCA	AATCAAAGTC	GGTGAAGAAA	TCGAAATCAT	350
15	CGGTATGCAA	GAAGAATCAA	GCAAAACAAC	TGTTACTGGT	G TAGAAATGT	400
	TCCGTAAATT	ATTAGACTAC	GCTGAAGCTG	GTGACAACAT	TGGTGCATTA	450
	TTACGTGGTG	TTTCACGTGA	TGACGTACAA	CGTGGTCAAG	TTTTAGCTGC	500
	TCCTGGTACT	ATTACACCAC	ATACAAAATT	CAAAGCGGAT	GTTTACGTTT	550
	TATCTAAAGA	TGAAGGTGGT	CGTCATACAC	CATTCTTCAC	TA ACTACCGC	600
20	CCACAATTCT	ATTTCCGTAC	TACTGACGTA	ACTGGTGTTG	TTA ACTTACC	650
	AGAAGGTACT	GAAATGGTTA	TGCCTGGCGA	TAACGTTGAA	ATGGATGTTG	700
	AATTAATTTC	TCCAATCGCT	ATT			723

25

2) INFORMATION FOR SEQ ID NO: 200

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 697 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: CSsa 18

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

	CGTTGGTGTT	CCAGCATTAG	TTGTATTCTT	AAACAAAGTT	GACATGGTTG	50
	ACGATGAAGA	ATTATTAGAA	TTAGTAGAAA	TGGAAGTTTCG	TGACTTATTA	100
	AGCGAATATG	ACTTCCCAGG	TGACGATGTA	CCTGTAATCT	CTGGTTCTGC	150
45	ATTAAAAGCT	TTAGAAGGCG	ACGCTGACTA	TGAGCAAAAA	ATCTTAGACT	200
	TAATGCAAGC	TGTTGATGAC	TTCAATCCAA	CACCAGAACG	TGATTCTGAC	250
	AAACCATTTCA	TGATGCCAGT	TGAGGACGTA	TTCTCAATCA	CTGGTCGTGG	300
	TACTGTTGCT	ACAGGCCGTG	TTGAACGTGG	TCAAATCAAA	GTCGGTGAAG	350
	AAATCGAAAT	CATCGGTATG	CAAGAAGAAT	CAAGCAAAAC	AACTGTTACT	400
50	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	TACGCTGAAG	CTGGTGACAA	450
	CATTGGTGCA	TTATTACGTG	GTGTTTCACG	TGATGACGTA	CAACGTGGTC	500
	AAGTTTTAGC	TGCTCCTGGT	ACTATTACAC	CACATACAAA	ATTCAAAGCG	550
	GATGTTTACG	TTTTATCTAA	AGATGAAGGT	GGTCGTCATA	CACCATTCTT	600
	CACTAACTAC	CGCCCACAAT	TCTATTTCCG	TACTACTGAC	GTA ACTGGTG	650
55	TTGTTAACTT	ACCAGAAGGT	ACTGAAATGG	TTATGCCTGG	CGATAAC	697

60

2) INFORMATION FOR SEQ ID NO: 201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus sciuri* subsp. *sciuri*
 (B) STRAIN: ATCC 29060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

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15  CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCTCAAACCTC      50
    GTGAGCACAT TCTTTTATCA CGTAACGTAG GTGTTCTGCT ATTAGTAGTA      100
    TTCTTAAACA AAGTTGACAT GGTGACGAT  GAAGAATTAT TAGAATTAGT      150
    TGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGCGACG      200
    ACGTTCCTGT AATTGCTGGT TCAGCATTA  AAGCATTAGA AGGCGACGAA      250
20  GCTTACGAAG ACAAAATCAT GGAATTAATG GATGCTGTTG ATACATTCAT      300
    CCCAACTCCA GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      400
    CGTGGTCAAA TCACTGTTGG TGAAGAAGTT GAAATCATCG GTTTAACTGA      450
    AGAATCTTCT AAAACAACCTG TAACTGGTGT TGAAATGTTT CGTAAATTAT      500
25  TAGACTTCGC TGAAGCTGGA GATAACATCG GTGCATTATT ACGTGGTGTT      550
    GCTCGTGAAG ACGTTAACCG TGGTCAAGTA TTAGCTAAAC CAGGTTCAAT      600
    CACACCTCAC ACTAAATTCA AAGCTGAAGT TTATGTATTA TCTAAAGACG      650
    AAGGTGGACG TCATACTCCA TTCTTCACAA ACTACCGCCC ACAATTCTAT      700
    TTCCGTACTA CTGACGTAAC TGGTGTAGTT AACTTACCAG AAGGTAAGTA      750
30  AATGGTTATG CCTGGCGACA ACGTTGAAAT GGACGTTGAA TTAATTTTAC      800
    CAATCGCTAT TGAAGACGGT ATCGTTTCTC AATCA                      835
  
```

35 2) INFORMATION FOR SEQ ID NO: 202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

```

50  CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACCTC      50
    GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA      100
    TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT      150
    AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG      200
55  ACGTACCTGT AATCGCTGGT TCAGCATTA  AAGCTTTAGA AGGCGACGAA      250
    AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT      300
    TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      400
    CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA      450
60  CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG      500
  
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ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 556
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 600
 ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCA CA ATTCTATTTC 700
 5 CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTECTGAAAT 750
 GGTTATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCAA C 831

10

2) INFORMATION FOR SEQ ID NO: 203

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: CSG 50

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC 50
 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA 100
 TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
 30 AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG 200
 ACGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA 250
 AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT 300
 TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
 35 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 450
 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG 500
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 600
 ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
 40 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCA CA ATTCTATTTC 700
 CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTECTGAAAT 750
 GGTTATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCA 829

45

2) INFORMATION FOR SEQ ID NO: 204

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 839 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bifidobacterium longum*
 (B) STRAIN: ATCC 15707

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

	TGGCGCTATC	CTCGTTGTGG	CCGCCACCGA	CGGCCCGATG	GCCCAGACTC	50
	GCGAGCACGT	GCTGCTCGCC	CGTCAGGTTG	GCGTTCCGAA	GATCCTCGTC	100
5	GCCCTGAACA	AGTGCGACAT	GGTCGACGAT	GAAGAGCTCA	TCGAGCTCGT	150
	CGAAGAAGAG	GTCCGCGACC	TCCTCGACGA	GAACGGCTTC	GACCGTGACT	200
	GCCCGGTCAT	CCACACCTCC	GCTTACGGTG	CTCTGCACGA	CGACGCTCCG	250
	GACCACGAGA	AGTGGGTCCA	GTCCGTTAAG	GACCTCATGG	ACGCTGTCTGA	300
	CGACTACATC	CCGACCCCGG	TTCACGACCT	GGACAAGCCG	TTCCTGATGC	350
10	CGATCGAGGA	CGTCTTCACC	ATCTCCGGCC	GTGGTACCGT	TGTCACCGGT	400
	CGTGTCGAGC	GTGGCCAGCT	GGCCGTCAAC	ACCCCGGTCG	AGATCGTTGG	450
	TATCCGTCCG	ACCCAGCAGA	CCACCGTCAC	CTCCATCGAG	ACCTTCCACA	500
	AGACCATGGA	CGCCTGCGAG	GCTGGCGACA	ACACCGGTCT	GCTTCTGCGT	550
	GGTCTCGGCC	GTGACGATGT	CGAGCGTGGC	CAGGTTGTGG	CCAAGCCGGG	600
15	CTCCGTCACC	CCGCACACCA	AGTTCGAGGG	CGAAGTCTAC	GTGCTGACCA	650
	AGGACGAAGG	CGGCCGTCAC	TCGCCGTTCT	TCTCCAATA	CCGTCCGCAG	700
	TTCTACTTCC	GCACCACCGA	CGTCACCGGC	GTCATCGAGC	TGCCGGAAGG	750
	CGTCGAGATG	GTTCAGCCGG	GCGACCACGC	TACCTTCACC	GTTGAGCTGA	800
	TTCAGCCCAT	CGCTATGGAG	GAAGGCCTGA	CCTTCGCTG		839
20						

2) INFORMATION FOR SEQ ID NO: 205

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stenotrophomonas maltophilia*
 (B) STRAIN: CDC F3338

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

	CGGCGCGATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCGATG	CCGCAGACCC	50
40	GTGAGCACAT	CCTGCTGTCT	CGCCAGGTCG	GCGTGCCGTA	CATCGTCGTG	100
	TTCTGAACA	AGGCCGACAT	GGTCGACGAC	GCCGAGCTGC	TCGAGCTGGT	150
	CGAGATGGAA	GTGCGCGAAC	TGCTGAGCAA	GTACGAGTTC	CCGGGCGACG	200
	ACACCCCGAT	CATCGCCGGT	TCGGCCCGCC	TGGCGCTGGA	AGGCGACCAG	250
	AGCGACATCG	GCGTGCCGGC	CATCCTGAAG	CTGGTCGACG	CGCTGGACAG	300
45	CTGGATTCCG	GAGCCGGAGC	GTGCGATCGA	CAAGCCGTTC	CTGATGCCGG	350
	TGGAAGACGT	GTTCTCGATC	TCGGGCCGCG	GCACCGTGGT	GACCGGTCGT	400
	ATCGAGCGCG	GCGTGATCAA	GGTTGGCGAC	GAAATCGAAA	TCGTCGGCAT	450
	CCGTCCGGTG	CAGAAGACCA	CCGTGACCGG	CGTTGAAATG	TTCCGCAAGC	500
	TGCTGGACCA	GGGTCAGGCA	GGCGACAACG	CTGGCCTGCT	GCTGCGCGGC	550
50	ACCAAGCGTG	ATGACGTCGA	GCGTGGCCAG	GTGCTGGCCA	AGCCGGGCAC	600
	GATCAAGCCG	CACACCAAGT	TCGAAGGCGA	AGTGTACGTC	CTGTCGAAGG	650
	ACGAGGGCGG	CCGCCACACC	CCGTTCTTCA	ACGGCTACCG	TCCGCAGTTC	700
	TACTTCCGCA	CCACCGACAT	CACCGGCGCC	GCTGCACTGC	CGGAAGGCGT	750
	CGAA					754
55						

2) INFORMATION FOR SEQ ID NO: 206

50 (i) SEQUENCE CHARACTERISTICS:

123

(A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

	TGGTGCTATC	CTTGTAAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
15	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAAAA	CCTTATCGTT	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ATCTTCCAGT	TGTTCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATTCA	250
	GCACAAGAAG	ATGTTATCAT	GGAATTGATG	TCAATCGTTG	ACACATACAT	300
20	TCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ATGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTTAA	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CGAAATCTCT	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
25	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACGTTCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGATA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	AAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACTAT	CGAAGTTGAG	TTGATCCACC	800
30	CAATCGCCGT	TGAACAAGGT	ACTACTTTCT	CTATC		835

2) INFORMATION FOR SEQ ID NO: 207

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12403

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

50	CTATCCTTGT	AGTTGCTTCA	ACTGATGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	AGTTGGTGTT	AAACACCTTA	TCGTATTTCAT	100
	GAACAAAGTT	GACCTTGTTG	ATGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATTCT	TGACCTTCTT	TCAGAATACG	ACTTCCCAGG	TGATGACCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCA	CTTGAAGGCG	ACGAAAAATA	250
55	CGAAGACATC	ATCATGGAAT	TGATGAGCAC	TGTTGATGAG	TACATTCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTTTAC	TTCTTCCAGT	TGAAGATGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTTCG	GTCAACGACG	AAGTTGAAAT	CGTTGGTATT	AAAGAAGATA	450
	TCCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACTTGAC	500
50	GAAGGTCTTG	CAGGGGACAA	CGTTGGTGTT	CTTCTTCGTG	GTGTTCAACG	550

TGATGAAATC GAACGTGGTC AAGTTCTTGC TAAACCAGGT TCAATCAACC 600
 CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT 650
 GGACGTCATA CTCCATTCTT CAACAACACTAC CGTCCACAAT TCTACTTCCG 700
 TACAACTGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG 750
 5 TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC 800
 GCCGTAGAAC AAGGTACTA 819

10 2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

25 CTATCCTTGT AGTTGCTTCA ACTGATGGAC CAATGCCACA AACTCGTGAG 50
 CACATCCTTC TTTCACGTCA AGTTGGTGTT AAACACCTTA TCGTATTCAT 100
 GAACAAAGTT GACCTTGTTG ATGATGAAGA ATTGCTTGAA TTGGTTGAAA 150
 TGGAAATTCG TGACCTTCTT TCAGAATACG ACTTCCCAGG TGATGACCTT 200
 30 CCAGTTATCC AAGGTTTCAGC TCTTAAAGCA CTTGAAGGCG ATGAAAAATA 250
 CGAAGACATC ATCATGGAAT TGATGAGCAC TGTGATGAG TACATTCCAG 300
 AACCAGAACG TGATACTGAC AAACCTTTAC TTCTTCCAGT CGAAGATGTA 350
 TTCTCAATCA CTGGACGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG 400
 TACTGTTTCG GTCAACGACG AAGTTGAAAT CGTTGGTATT AAAGAAGATA 450
 35 TCCAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC 500
 GAAGGTCTTG CAGGGGACAA CGTTGGTGTT CTTCTTCGTG GTGTTCAACG 550
 TGATGAAATC GAACGTGGTC AAGTTCTTGC TAAACCAGGT TCAATCAACC 600
 CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT 650
 GGACGTCATA CTCCATTCTT CAACAACACTAC CGTCCACAAT TCTACTTCCG 700
 40 TACAACTGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG 750
 TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC 800
 GCCGTAGAAC AAGGTACTA 819

45

2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 13813

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

```

AGCTATCCTT GTAGTTGCTT CAACTGATGG ACCAATGCCA CAAACTCGTG      50
AGCACATCCT TCTTTCACGT CAAGTTGGTG TTAAACACCT TATCGTATTC      100
ATGAACAAAG TTGACCTTGT TGATGATGAA GAATTGCTTG AATTGGTTGA      150
5  AATGGAAATT CGTGACCTTC TTTCAGAATA CGACTTCCCA GGTGATGACC      200
TTCCAGTTAT CCAAGGTTCA GCTCTTAAAG CACTTGAAGG CGATGAAAAA      250
TACGAAGACA TCATCATGGA ATTGATGAGC ACTGTTGATG AGTACATTCC      300
AGAACCAGAA CGTGATACTG ACAAACCTTT ACTTCTTCCA GTCGAAGATG      350
TATTCTCAAT CACTGGACGT GGTACAGTTG CTTCAGGACG TATCGACCGT      400
10 GGTACTGTTC GTGTCAACGA CGAAGTTGAA ATCGTTGGTA TTAAAGAAGA      450
TATCCAAAAA GCAGTTGTTA CTGGTGTGTA AATGTTCCGT AAACAACCTG      500
ACGAAGGTCT TGCAGGGGAC AACGTTGGTG TTCTTCTTCG TGGTGTTCAA      550
CGTGATGAAA TCGAACGTGG TCAAGTTCTT GCTAAACCAG GTTCAATCAA      600
CCCACACACT AAATTTAAAG GTGAAGTTTA CATCCTTTCT AAAGAAGAAG      650
15 GTGGACGTCA TACTCCATTC TTCAACAACCT ACCGTCCACA ATTCTACTTC      700
CGTACAACCTG ACGTAACAGG TTCAATCGAA CTTCCAGCAG GAACAGAAAT      750
GGTTATGCCT GGTGATAACG TTAATATCGA AGTTGAATTG ATTCACCCAA      800
TCGCCGTAGA ACAAGGTACT AC                                     822

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20

2) INFORMATION FOR SEQ ID NO: 210

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(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 825 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Streptococcus agalactiae
    (B) STRAIN: CDCss-1073

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

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CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC      50
GTGAGCACAT CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA      100
40 TTCATGAACA AAGTTGACCT TGTGATGAT GAAGAATTGC TTGAATTGGT      150
TGAAATGGAA ATTCGTGACC TTCTTTCAGA ATACGACTTC CCAGGTGATG      200
ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA AGGCGACGAA      250
AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT      300
TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG      350
45 ATGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC      400
CGTGGTACTG TTCGTGTCAA CGACGAAGTT GAAATCGTTG GTATTAAAGA      450
AGATATCCAA AAAGCAGTTG TTAAGTGTG TGAAATGTTT CGTAAACAAC      500
TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT TCGTGGTGTT      550
CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT      600
50 CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTTCAATC GAACTTCCAG CAGGAACAGA      750
AATGGTTATG CCTGGTGATA ACGTTACTAT CGAAGTTGAA TTGATTACC      800
CAATCGCCGT AGAACAAGGT ACTAC                                     825

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55

2) INFORMATION FOR SEQ ID NO: 211

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60 (i) SEQUENCE CHARACTERISTICS:

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126

(A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 33397

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

	GGAGCTATCC	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CTCAAACCTCG	50
15	TGAACACATC	CTTCTTTTCAC	GCCAAGTAGG	TGTTAAATAC	CTTATCGTCT	100
	TCATGAATAA	AGTTGACTTG	GTTGACGATG	AAGAATTGCT	TGAATTGGTT	150
	GAAATGGAAA	TCCGTGACCT	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	200
	AATCCCAGTT	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATGAAA	250
	AATATGAAGA	CATCATCATG	GAATTGATGG	ATACTGTTGA	TGAATACATT	300
20	CCAGAACCAG	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTTGAAGA	350
	TGTATTCTCA	ATTACTGGAC	GTGGTACTGT	TGCTTCAGGA	CGTATCGACC	400
	GTGGTACTGT	TAAAGTCAAC	GACGAAGTTG	AAATCGTTGG	TATCCGTGAT	450
	GAAATCCAAA	AAGCAGTTGT	TACTGGTGT	GAAATGTTCC	GTAAACAATT	500
	GGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	GGTTCTTCTT	CGTGGTATCC	550
25	AACGTGACGA	AATCGAACGT	GGACAAGTTC	TTGCTAAACC	AGGTTCAATT	600
	CATCCACACA	CTAAATTCAA	AGGTGAAGTT	TACATCCTTA	CTAAAGAAGA	650
	AGGTGGACGT	CATACTCCAT	TCTTCAACAA	CTACCGTCCT	CAATTCTACT	700
	TCCGTACTAC	AGACGTTACA	GGTTCAATCG	AACTTCCTGC	AGGTACTGAA	750
	ATGGTAATGC	CTGGTGATAA	CGTAACAATC	GACGTTGAAT	TGATCCACCC	800
30	AATTGCCGTA	GAACAAGGAA	CTACAT			826

2) INFORMATION FOR SEQ ID NO: 212

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus bovis*
 (B) STRAIN: ATCC 33317

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

50	TGGTGCTATC	CTTGTAGTAG	CTTCTACAGA	TGGTCCAATG	CCACAAACAC	50
	GTGAACACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATATGATTTC	CCAGGTGATG	200
	AAATCCCTGT	AATCCAAGGT	TCAGCTCTTA	AAGCCCTTGA	AGGTGACACT	250
55	CACTACGAAG	ACATCATCAT	GGAATTGATG	AACACTGTAG	ATGAATACAT	300
	TCCAGAACCA	AAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	CGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	CGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
60	TTGATGAAGG	TATCGCAGGG	GATAACGTTG	GTGTTCTTCT	TCGTGGTATC	550

	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
	CCACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	TCAATTCTAC	700
	TTCCGTACAA	CTGACGTTAC	AGGTTCAATC	GAAGTTCCAG	CAGGTACTGA	750
5	AATGGTAATG	CCTGGTGATA	ACGTTACTAT	CGACGTTGAA	TTGATTCACC	800
	CAATCGCCGT	TGAACAAGGT	ACTACAT			827

10 2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus* (deposited as
Streptococcus constellatus)
 (B) STRAIN: ATCC 27823

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

	GCTATCCTCG	TAGTAGCTTC	AACTGATGGA	CCAATGCCTC	AAACTCGTGA	50
	ACATATCCTT	CTTTCACGTC	AAGTAGGTGT	TAAATACCTT	ATCGTCTTCA	100
	TGAACAAAGT	TGACTTGTTT	GACGATGAAG	AATTGCTTGA	ATTGGTTGAA	150
30	ATGGAAATCC	GTGACCTTCT	TTCAGAATAC	GATTTCCCAG	GTGATGAAAT	200
	CCCAGTTATC	CAAGGTTTCA	CTCTTAAAGC	TCTTGAAGGT	GATGAAAAAT	250
	ATGAAGACAT	CATCATGGAA	TTGATGGATA	CTGTTGATGA	ATACATTCCA	300
	GAACCAGAAC	GTGACACTGA	CAAACCACTT	CTTCTTCCAG	TCGAAGATGT	350
	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	TTCAGGACGT	ATCGACCGTG	400
35	GTACTGTTAA	AGTCAATGAT	GAAGTTGAAA	TTGTTGGTAT	TCGTGACGAA	450
	ATCCAAAAAG	CAGTTGTTAC	TGGTGTTGAA	ATGTTCCGTA	AACAATTGGA	500
	CGAAGGTCTT	GCTGGAGATA	ACGTAGGGGT	TCTTCTTCGT	GGTATCCAAC	550
	GTGACGAAAT	CGAACGTGGA	CAAGTTCTTG	CTAAACCAGG	TTCAATTTCAT	600
	CCACACACTA	AATTCAAAGG	TGAAGTTTAC	ATCCTTACTA	AAGAAGAAGG	650
40	TGGACGTCAT	ACTCCATTCT	TCAACAATA	CCGTCCTCAA	TTCTACTTCC	700
	GTACTACAGA	CGTTACAGGT	TCAATCGAAC	TTCTGCAGG	TACTGAAATG	750
	GTAATGCCTG	GTGATAACGT	AACAATTGAT	GTTGAGTTGA	TCCACCCAAT	800
	TGCCGTAGAA	CAAGGAACTA	C			821

45

2) INFORMATION FOR SEQ ID NO: 214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus cricetus*
 (B) STRAIN: ATCC 19642

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

	GCTATCCTTG	TAGTAGCTTC	TACAGACGGA	CCAATGCCAC	AAACTCGTGA	50
	ACACATCTTG	CTTTCACGCC	AAGTTGGTGT	TAAGAGCCTT	ATCGTCTTCA	100
5	TGAACAAGGT	TGACTTGGTT	GACGATGAAG	AATTGCTTGA	ATTGGTTGAA	150
	ATGGAAATCC	GTGATCTTCT	TTCAGAATAC	GATTTCCCAG	GTGATGATAT	200
	CCCTGTTGTT	CAAGGTTCAG	CTCTTAAAGC	CCTTGAAGGT	GATACAGCTG	250
	CCGAAGACAA	GATCATGGAA	TTGATGGACA	TCGTTGATGA	CTACATTCCA	300
	GAACCAAAAC	GTGATACTGA	TAAGCCATTG	CTTCTTCCAG	TCGAAGACGT	350
10	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	TTCAGGACGT	ATCGACCGTG	400
	GTACTGTTAA	GGTCAATGAC	GAAGTTGAAA	TCGTTGGTAT	CAAGGACGAA	450
	ATCCAAAAAG	CGGTTGTTAC	CGGAGTTGAA	ATGTTCCGTA	AACAATTGGA	500
	TGAAGGTCTT	GCAGGGGATA	ACGTTGGTGT	GCTTCTTCGT	GGTATCCAAC	550
	GTGATGAAAT	CGAACGTGGT	CAAGTATTGG	CTGCACCTGG	TTCAATCCAT	600
15	CCACACACTA	AATTCAAGGG	TGAAGTTTAC	ATCCTTTCTA	AAGATGAAGG	650
	TGGACGTCAC	ACTCCATTCT	TCAACAATA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTAACTGGT	TCAATCGAAT	TGCCAGCAGG	TACTGAAATG	750
	GTTATGCCTG	GTGATAACGT	TACTATCGAC	GTTGAATTGA	TCCACCCAAT	800
	CGCTGTTGAA	AAAGGTACTA	C			821

20

2) INFORMATION FOR SEQ ID NO: 215

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus cristatus*
 35 (B) STRAIN: ATCC 51100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

	TATCCTTGTA	GTAGCTTCAA	CTGACGGACC	AATGCCACAA	ACTCGTGAGC	50
40	ACATCCTTCT	TTCACGTCAG	GTTGGTGTGA	AACACCTTAT	CGTCTTCATG	100
	AACAAGATCG	ACTTGGTTGA	TGACGAAGAA	TTGCTTGAAT	TGGTTGAAAT	150
	GGAAATCCGT	GACCTCTTGT	CAGAATACGA	CTTCCCAGGT	GACGATCTTC	200
	CAGTTATCCA	AGGTTCAGCT	CTTAAAGCTC	TTGAAGGTGA	TACTAAGTAC	250
	GAAGACATCA	TCATGGAATT	GATGAACACT	GTTGATGAGT	ACATCCCAGA	300
45	ACCAGAACGT	GATACTGACA	AACCTCTTCT	TCTTCCAGTC	GAAGACGTAT	350
	TCTCAATCAC	TGGTCGTGGT	ACAGTTGCTT	CAGGACGTAT	CGACCGTGGT	400
	ACTGTTTCGTG	TCAACGATGA	AATCGAAATC	GTTGGTATCA	AAGAAGAAAT	450
	CCAAAAAGCA	GTTGTTACTG	GTGTTGAAAT	GTTCCGTAAA	CAGCTTGACG	500
	AAGGTCTTGC	AGGGGACAAC	GTAGGTGTAC	TTCTTCGTGG	TATCCAACGT	550
50	GATGAAATCG	AACGTGGTCA	AGTTATCGCT	AAACCAGGTT	CAATCAACCC	600
	ACACACTAAA	TTCAAGGGTG	AAGTTTACAT	CCTTACTAAA	GAAGAAGGTG	650
	GACGTCACAC	TCCATTCTTC	AACAACCTAC	GTCCACAGTT	CTACTTCCGT	700
	ACAACCTGACG	TTACAGGTTC	AATCGAACTT	CCAGCAGGTA	CTGAAATGGT	750
	AATGCCTGGT	GATAACGTAA	CTATCGACGT	TGAGTTGATC	CACCCAATCG	800
55	CCGTTGAACA	AGGTACTCCT	T			821

60

2) INFORMATION FOR SEQ ID NO: 216

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus downei*
 (B) STRAIN: ATCC 33748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

15	AGTAGCTTCT	ACTGATGGAC	CAATGCCACA	AACTCGTGAA	CACATCTTGC	50
	TTTCACGTCA	GGTTGGTGTT	AAGAACCTTA	TCGTCTTCAT	GAACAAGGTT	100
	GACTTGGTTG	ACGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	TGGAAATCCG	150
	TGACCTGCTT	TCAGAATACG	ATTTCCCAGG	TGATGATATC	CCTGTTGTTC	200
	AAGGTTTCAGC	TCTTAAGGCT	CTTGAAGGTG	ATACAGCTGC	CGAAGACAAG	250
20	ATCATGGAAT	TGATGGACAT	CGTTGATGAC	TACATTCCAG	AACCAAAACG	300
	TGATACTGAT	AAGCCTTTGC	TTCTTCCAGT	CGAAGATGTA	TTCTCAATCA	350
	CTGGACGTGG	TACTGTAGCT	TCAGGACGTA	TCGACCGTGG	TACTGTTAAG	400
	GTCAACGACG	AAGTTGAAAT	CGTTGGTATC	AAGGACGAAA	TCCAAAAGC	450
	AGTTGTTACC	GGAGTTGAAA	TGTTCCGTAA	ACAATTGGAC	GAAGGTCTTG	500
25	CAGGGGATAA	CGTTGGTGTG	CTTCTTCGTG	GTATCCAACG	TGATGAAATC	550
	GAACGTGGTC	AAGTGTTGGC	TGCGCCTGGT	TCGATTCCAC	CACACACTAA	600
	GTTTAAAGGT	GAAGTTTACA	TCCTTTCTAA	AGAAGAAGGT	GGACGTCATA	650
	CTCCATTCTT	TAACAACACT	CGTCCACAGT	TCTACTTCCG	TACAACTGAC	700
	GTAAGTGGTT	CAATCGAATT	GCCAGCGGGT	ACTGAAATGG	TTATGCCTGG	750
30	TGATAACGTT	ACTATCGACG	TTGAATTGAT	CCACCCAATT	GC	792

2) INFORMATION FOR SEQ ID NO: 217

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus dysgalactiae*
 (B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

50	GTAGTTGCTT	CAACAGACGG	ACCAATGCCA	CAAACCTCGTG	AGCACATCCT	50
	CCTTTCACGT	CAGGTTGGTG	TTAAACACCT	TATCGTGTTT	ATGAACAAAA	100
	TTGACCTTGT	TGACGATGAA	GAATTGCTTG	AATTGGTTGA	AATGGAAATC	150
	CGTGACCTTC	TTTCAGAATA	CGATTTCCCA	GGTGATGACC	TTCCAGTTAT	200
	CCAAGGTTCA	GCTCTTAAAG	CTCTTGAAGG	CGACACTAAA	TTTGAAGACA	250
55	TCATCATGGA	ATTGATGGAT	ACTGTTGATT	CATACATTCC	AGAACCAGAA	300
	CGTGACACTG	ACAAACCATT	GCTTCTTCCA	GTCGAAGACG	TATTCTCAAT	350
	CACAGGTCGT	GGTACAGTTG	CTTCAGGACG	TATCGACCGT	GGTACTGTTC	400
	GTGTCAACGA	CGAAATCGAA	ATCGTTGGTA	TCAAAGAAGA	AACTAAAAAA	450
	GCTGTTGTTA	CTGGTGTTGA	AATGTTCCGT	AAACAACCTG	ACGAAGGTCT	500
50	TGCAGGAGAC	AACGTAGGTA	TCCTTCTTCG	TGGTGTTCAA	CGTGACGAAA	550

	TCGAACGTGG	TCAAGTTATT	GCTAAACCAG	GTTCAATCAA	CCCACACACT	600
	AAATTCAAAG	GTGAAGTATA	TATCCTTTCT	AAAGACGAAG	GTGGACGTCA	650
	CACTCCATTC	TTCAACAAC	ATCGTCCACA	ATTCTACTTC	CGTACAAC	700
	ACGTAACAGG	TTCAATCGAA	CTTCCAGCTG	GTACAGAAAT	GGTTATGCCT	750
5	GGTGATAACG	TGACAATCAA	CGTTGAGTTG	ATCCACCCAA	TCGCC	795

2) INFORMATION FOR SEQ ID NO: 218

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Streptococcus equi* subsp. *equi*
 (B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

25	CGGAGCTATC	CTTGTAAGTTG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAGCA	CCTTATCGTG	100
	TTCATGAACA	AGGTTGACCT	TGTTGACGAT	GAAGAATTGC	TTGAGCTTGT	150
	TGAAATGGAA	ATTCGTGACC	TTCTTTCAGA	ATATGATTTC	CCAGGTGATG	200
	ACCTTCCAGT	TATCCAAGGT	TCAGCGCTTA	AGGCTCTTGA	AGGCGACAGC	250
30	AAATACGAAG	ATATCATCAT	GGAATTGATG	GATACTGTTG	ATTCATACAT	300
	TCCAGAACCA	GAACGTGACA	CAGACAAGCC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGCGGTACTG	TTCGTGTTAA	CGACGAAATC	GAAATCGTTG	GTATCAGAGA	450
	CGAGATCAAA	AAAGCAGTTG	TTACTGGTGT	CGAAATGTTC	CGTAAACAGC	500
35	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAGC	CAGGTTCTAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	ATATATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCAACA	ACTATCGTCC	ACAATTCTAC	700
	TTCCGTACTA	CTGACGTAAC	AGGTTCAATC	GAGCTTCCAG	CAGGTACAGA	750
40	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	TGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	AGAACAAGGT	ACTACATT			828

45 2) INFORMATION FOR SEQ ID NO: 219

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Streptococcus ferus*
 (B) STRAIN: ATCC 33477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

60

	CGGTGCAATC	CTTGTAAGTAG	CTTCTACAGA	TGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTAG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TGCTTTCAGA	ATATGATTTC	CCAGGTGATG	200
5	ACCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATACT	250
	GCTCAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACCGTTG	ATGAGTACAT	300
	CCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ATGTATTCTC	AATCACAGGT	CGTGGTACTG	TAGCTTCAGG	ACGTATCGAT	400
	CGTGGTACTG	TAAGAGTCAA	CGATGAAGTT	GAAATCGTTG	GTATCAAAGA	450
10	CGAAATCACT	AAAGCAGTTG	TTACCGGTGT	TGAAATGTTT	CGTAAACAAT	500
	TGGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTGCTTCT	CCGTGGTGTG	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTA	TTGGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCATACACCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
15	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCCGT	TGAACAAGGT	ACTAC			825

20

2) INFORMATION FOR SEQ ID NO: 220

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| | (A) | LENGTH: 826 bases |
| 25 | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- | | | |
|--|-----|---|
| | (A) | ORGANISM: <i>Streptococcus gordonii</i> |
| | (B) | STRAIN: ATCC 10558 |

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

	CGGAGCTATC	CTTGTAAGTAG	CTTCAACTGA	TGGTCCTATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTCTCA	CGCCAAGTTG	GTGTTAAACA	CTTGATCGTG	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAGTTGGT	150
40	TGAAATGGAA	ATCCGTGACC	TCTTGTGAGA	ATACGACTTC	CCAGGTGACG	200
	ATCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCTCTTGA	AGGTGACTCT	250
	AAATATGAAG	ATATCATCAT	GGAATTGATG	AACACTGTTG	ATGAGTACAT	300
	CCCAGAACCA	GAACGCGACA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
45	CGTGGTATCG	TTAAAGTCAA	TGACGAAATC	GAAATCGTTG	GTATCAAAGA	450
	AGAAATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTGCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	TGGACAAGTT	ATTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTATATCCTT	ACTAAAGAAG	650
50	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTTAC	AGGTTCAATC	GAATTCCAG	CAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	CGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	TGAACAAGGT	ACTACT			826

55

2) INFORMATION FOR SEQ ID NO: 221

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|-------------------|
| 50 | (A) | LENGTH: 799 bases |
|----|-----|-------------------|

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus*
(B) STRAIN: ATCC 27335

10

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 221

	TGTAGTAGCT	TCAACTGACG	GACCAATGCC	TCAAACCTCGT	GAACATATCC	50
	TTCTTTTCACG	TCAAGTAGGT	GTTAAATACC	TTATTGTCTT	CATGAACAAA	100
15	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGATCTT	CTTTCAGAAT	ACGATTTCCT	AGGTGATGAT	ATTCCAGTAA	200
	TCCAAGGTTC	AGCACTTAAA	GCTCTTGAAG	GTGATGAAAA	ATATGAAGAC	250
	ATCATCATGG	AATTGATGAA	TACTGTTGAT	GAATATATTC	CAGAACCAGA	300
	ACGTGATACT	GACAAACCAT	TGCTTCTTCC	AGTCGAAGAT	GTATTCTCAA	350
20	TCACTGGACG	TGGTACTGTT	GCTTCAGGAC	GTATCGACCG	TGGTACTGTT	400
	AAAGTCAACG	ATGAAGTTGA	AATCGTTGGT	ATCCGCGAGG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTG	AAATGTTCCG	TAAACAATTG	GACGAAGGTC	500
	TTGCTGGAGA	TAACGTAGGG	GTTCTTCTTC	GTGGTATCCA	ACGTGACGAA	550
	ATTGAACGTG	GACAAGTTCT	TGCTAAACCA	GGTTCAATTC	ATCCACACAC	600
25	TAAATTCAAA	GGTGAAGTTT	ACATCCTTAC	TAAAGAAGAA	GGTGGACGTC	650
	ATACTCCATT	CTTCAACAAC	TACCGTCCTC	AATTCTACTT	CCGTACTACA	700
	GACGTTACAG	GTTCAATCGA	ACTTCCTGCA	GGTACTGAAA	TGGTAATGCC	750
	TGGTGATAAC	GTAACAATTG	ATGTTGAGTT	GATCCACCCA	ATTGCCGTA	799

30

2) INFORMATION FOR SEQ ID NO: 222

(i)SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus macacae*
(B) STRAIN: ATCC 35911

45

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 222

	TGGTGCTATT	CTTGTAGTAG	CTTCAACTGA	CGGTCCAATG	CCTCAAACGC	50
	GTGAACATAT	CCTTCTTTCA	CGCCAAGTAG	GTGTTAAAAA	CCTTATTGTT	100
50	TTCATGAATA	AAGTTGACTT	AGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTACAGA	ATATGATTTC	CCAGGCGATG	200
	AACTTCCAGT	TATCCAAGGT	TCAGCACTTA	AAGCTCTTGA	AGGTGATACT	250
	AAGTACGAAG	ATATTATCAT	GGAATTGTTG	GATACTGTAG	ATGATTACAT	300
	CCCAGAACCA	CAACGTGATA	CTGACAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
55	ATGTTTTTCTC	TATTACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATTGAC	400
	CGTGGTACTG	TTAAGGTTAA	TGATGAAGTT	GAAATCGTTG	GTATTCGTGA	450
	CGATATTCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTCG	GTGTCCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATTGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGATCAAT	600
60	TCATCCACAT	ACTAAATTCA	AAGGTGAAGT	TTATATTCTT	ACTAAAGAAG	650

AAGGTGGACG	TCATACTCCA	TTCTTTAACA	ACTACCGTCC	ACAGTTCTAC	700
TTCCGTACAA	CTGATGTAAC	TGGTTCAATT	GATTTGCCAG	CAGGTACTGA	750
AATGGTTATG	CCTGGTGATA	ATGTTACGAT	TGATGTTGAA	CTGATCCACC	800
CAATCGCTGT	TGAACAAGGT	ACAAC			825

5

2) INFORMATION FOR SEQ ID NO: 223

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii* (deposited as
 20 *Streptococcus mitis*)
 (B) STRAIN: ATCC 33399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

25	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCC	CTTGAAGGTG	ACACTAAATA	250
30	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TACATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTGC	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACCTTGAC	500
35	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACT	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
40	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	AT			822

45 2) INFORMATION FOR SEQ ID NO: 224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
 (B) STRAIN: ATCC 25175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

50

	CCCTGGTGCT	ATCCTTGTAG	TAGCTTCAAC	TGATGGACCA	ATGCCACAAA	50
	CTCGTGAACA	CATTCTTCTT	TCACGTCAAG	TTGGTGTTAA	ATACCTCATT	100
	GTCTTCATGA	ATAAAGTTGA	TTTGGTTGAC	GATGAAGAAT	TGCTTGAATT	150
	GGTTGAAATG	GAAATCCGTG	ATCTTCTTTC	AGAATATGAT	TTCCCAGGTG	200
5	ATGATATTCC	AGTTATTCAA	GGTTCAGCTC	TTAAAGCTCT	TGAAGGCGAT	250
	ACTGCTCAAG	AAGATATCAT	CATGGAATTA	ATGCATACTG	TTGATGACTA	300
	CATTCCAGAT	CCAGAACGTG	ATACTGACAA	GCCGCTCCTT	CTTCCAGTCG	350
	AAGATGTTTT	CTCAATCACT	GGTCGTGGTA	CTGTTGCTTC	AGGACGTATT	400
	GATCGTGGTA	CTGTAAAGT	TAACGATGAA	GTTGAAATCG	TTGGTATCCG	450
10	TGATGACATT	CAAAAAGCTG	TTGTTACTGG	TGTTGAAATG	TTCCGTAAAC	500
	AATTGGATGA	AGGTATTGCA	GGGGATAATG	TTGGTGTTC	CCTTCGTGGT	550
	ATCCAACGTG	ATGAAATCGA	ACGTGGTCAA	GTTCTTGCTA	AACCAGGTTC	600
	AATTCACCCA	CATACTAAAT	TCAAAGGTGA	AGTTTATATC	CTTACTAAAG	650
	AGGAAGGTGG	ACGTCATACA	CCATTCTTCA	ATAACTATCG	TCCACAATTC	700
15	TACTTCCGTA	CAACTGACGT	AACTGGTTCA	ATTGAGTTGC	CAGCAGGTAC	750
	TGAAATGGTT	ATGCCTGGTG	ATAACGTTAC	TATTGACGTT	GAATTGATCC	800
	ATCCAATCGC	TGTTGAACAA	GGTACTA			827

20

2) INFORMATION FOR SEQ ID NO: 225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus parasanguinis*
 (B) STRAIN: ATCC 15912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

	AGCTATCCTT	GTAGTAGCTT	CAACTGACGG	ACCAATGCCA	CAAACACGTG	50
	AACACATCCT	TCTTTCACGT	CAGGTTGGTG	TTAAACACTT	GATCGTCTTC	100
	ATGAACAAAG	TTGACTTGGT	TGATGATGAA	GAATTGCTTG	AATTGGTTGA	150
40	AATGGAAATC	CGTGACCTTC	TTTCAGAATA	CGATTTCCTA	GGTGATGACC	200
	TTCCAGTTAT	CCAAGGTTCA	GCTCTTAAAG	CTCTTGAAGG	TGACTCTAAA	250
	TATGAAGATA	TCATCATGGA	ATTGATGGAT	ACTGTTGATG	AGTACATCCC	300
	AGAACCAGAA	CGCGATACTG	ACAAACCATT	GCTTCTTCCA	GTCGAAGACG	350
	TATTCTCAAT	CACTGGACGT	GGTACAGTTG	CTTCAGGACG	TATCGACCGT	400
45	GGTGTGTGTC	GTGTCAATGA	TGAAATCGAA	ATCGTTGGTA	TCAAAGAAGA	450
	AATCCAAAAA	GCAGTTGTTA	CTGGTGTGTA	AATGTTCCGT	AAACAACCTG	500
	ACGAAGGTCT	TGCAGGGGAT	AACGTTGGTG	TGCTTCTTCG	TGGTATCCAA	550
	CGTGATGAAA	TCGAACGTGG	ACAAGTTATC	GCTAAACCAG	GTTCAATCAA	600
	CCCACACACT	AAATTCAAAG	GTGAAGTTTA	CATCCTTACT	AAAGAAGAAG	650
50	GTGGACGTCA	TACTCCATTC	TTCAACAAC	ACCGTCCACA	GTTCTACTTC	700
	CGTACAAC	ACGTAAC	ATCTATCGAA	CTTCCACCAG	GAAGTGAAT	750
	GGTAATGCCT	GGTGATAACG	TGACTATCGA	CGTTGAGTTG	ATCCACCCAA	800
	TCGCCGTTGA	ACAAGGTACT	ACAT			824

55

2) INFORMATION FOR SEQ ID NO: 226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases

135

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus ratti*
 (B) STRAIN: ATCC 19645

10

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 226

	TGGTGCTATC	CTTG TAGTAG	CTTCAACTGA	TGGACCAATG	CCGCAA ACTC	50
	GTGAACACAT	CTTGCTTTCA	CGTCAAGTTG	GTGT TAAATA	CCTTATCGTC	100
15	TTCATGAACA	AGGTTGACTT	GGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTT CAGA	ATACGATTTC	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCCCTTA	AAGCTCTTGA	AGGTGACACT	250
	GAACAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACAGTTG	ATGAGTACAT	300
	CCCAGATCCA	GAACGCGATA	CTGATAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
20	ACGTGTTCTC	AATCACTGGA	CGTGGTACTG	TTGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	TGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	TGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTACTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
25	TCATCCGCAT	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCTGT	TGAACAAGGT	ACTA			824

30

2) INFORMATION FOR SEQ ID NO: 227

35 (i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus sanguinis*
 45 (B) STRAIN: ATCC 10556

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 227

	TGTAGTAGCT	TCAACTGACG	GACCAATGCC	ACAAACTCGT	GAGCACATCT	50
50	TGCTTTTACG	TCAGGTTGGT	GT TAAACACT	TGATCGTCTT	CATGAACAAA	100
	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGACCTC	TTGTCAGAAT	ACGACTTCCC	AGGTGACGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGCTCTTAAA	GCTCTTGAAG	GTGACTCTAA	ATATGAAGAC	250
	ATCATCATGG	AATTGATGGA	CACTGTTGAT	GAGTACATCC	CAGAACCAGA	300
55	ACGCGATACT	GACAAGCCAT	TGCTTCTTCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACAGTT	GCTTCAGGAC	GTATCGACCG	TGGTATCGTT	400
	AAAGTCAACG	ACGAAATCGA	AATCGTTGGT	ATCAAAGAAG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTTG	AAATGTTCCG	TAAACAGCTT	GACGAAGGTC	500
	TTGCAGGGGA	CAACGTAGGT	GTGCTTCTCC	GTGGTATCCA	ACGTGATGAA	550
50	ATCGAACGTG	GACAAGTTAT	CGCTAAACCA	GGTTCAATCA	ACCCACACAC	600

TAAATTCAAG	GGTGAAGTTT	ATATCCTTAC	TAAAGAAGAA	GGCGGACGTC	650
ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
GACGTTACAG	GTTCAATCGA	ACTTCCAGCA	GGTACTGAAA	TGGTAATGCC	750
TGGTGATAAC	GTAACAATCG	ACGTTGAGTT	GATCCACCCA	ATCGC	795

5

2) INFORMATION FOR SEQ ID NO: 228

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus sobrinus*
- (B) STRAIN: ATCC 33478

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

TGTAGTAGCT	TCTACTGACG	GACCAATGCC	ACAACTCGT	GAACACATCT	50
25 TGCTTTCACG	CCAAGTTGGT	GTTAAGAACC	TCATCGTCTT	CATGAACAAG	100
GTTGACTTGG	TTGATGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
CCGTGATCTT	CTTTCAGAAT	ACGATTTCCT	AGGTGACGAC	ATTCCTGTTG	200
TTCAAGGTTC	AGCTCTTAAG	GCTCTTGAAG	GTGATACAGC	TGCCGAAGAC	250
AAGATTATGG	AATTGATGGA	CATCGTTGAT	GATTACATTC	CAGAACCAAA	300
30 ACGCGATACT	GATAAGCCAT	TGCTTCTCCC	AGTCGAAGAC	GTATTCTCAA	350
TCACTGGTTCG	TGGTACTGTT	GCTTCAGGAC	GTATTGACCG	TGGTACTGTT	400
AAGGTTAACG	ACGAAGTTGA	AATCGTTGGT	ATCCGTGACG	ATATCCAAAA	450
AGCAGTTGTT	ACTGGAGTTG	AAATGTTCCG	TAAGCAATTG	GACGAAGGTC	500
TTGCTGGAGA	TAACGTTGGT	GTGCTTCTTC	GTGGTATCCA	ACGTGATGAA	550
35 ATTGAACGTG	GTCAAGTATT	GGCTGCACCT	GGTTCAATCC	ACCCACACAC	600
TAAGTTCAAG	GGTGAAGTTT	ACATCCTTTC	TAAAGATGAA	GGTGGACGTC	650
ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
GACGTAAC	GTTCAATCGA	ATTGCCAGCA	GGTACTGAAA	TGGTTATGCC	750
40 TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGC	795

40

2) INFORMATION FOR SEQ ID NO: 229

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus suis*
- (B) STRAIN: ATCC 43765

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

TGTAGTAGCT	TCAACTGACG	GTCCAATGCC	ACAACTCGT	GAGCACATCC	50
50 TTCTTTCACG	TCAGGTTGGT	GTTAAACACC	TTATCGTCTT	CATGAACAAA	100

	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAGTTGGTTG	AAATGGAAAT	150
	CCGTGACCTT	CTTTCAGAAT	ACGATTTCCC	AGGTGATGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGCTCTTAAA	GCTCTTGAAG	GTGACTCTAA	GTACGAAGAC	250
	ATCGTTATGG	AATTGATGAA	CACTGTTGAT	GAGTACATTC	CAGAACCAGA	300
5	ACGCGACACT	GACAAACCAT	TGTTGCTTCC	AGTCGAGGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTA	GCTTCAGGAC	GTATCGACCG	TGGTACTGTT	400
	CGTGTCAACG	ACGAAATCGA	AATCGTTGGT	CTTCAAGAAG	AAAAATCTAA	450
	AGCAGTTGTT	ACTGGTGTTG	AAATGTTCCG	TAAACAACCTT	GACGAAGGTC	500
	TTGCCGGCGA	TAACGTTGGT	GTGCTTCTTC	GTGGTGTACA	ACGTGATGAA	550
10	ATCGAACGTG	GTCAAGTTAT	CTCTAAACCA	GGTTCTATCA	ACCCACACAC	600
	TAAATTCAAA	GGTGAAGTTT	ACATCCTTAC	TAAAGAAGAA	GGTGGACGTC	650
	ACACTCCATT	CTTCGACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAACCT	700
	GACGTAACCTG	GTTCAATCAA	ATTGCCAGAA	GGTACTGAAA	TGGTAATGCC	750
	TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGCCG	797

2) INFORMATION FOR SEQ ID NO: 230

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 793 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus uberis*

30 (B) STRAIN: ATCC 19436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

	TTGTTGTTGC	ATCAACTGAT	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
35	CTTCTTTTCAC	GCCAAGTTGG	TGTTAAACAC	CTTATCGTTT	TCATGAACAA	100
	AATCGACCTT	GTTGACGATG	AAGAATTGCT	TGAATTAGTT	GAAATGGAAA	150
	TCCGTGACCT	TCTTTCAGAA	TACGATTTCC	CAGGTGATGA	CCTACCAGTT	200
	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATTCTA	AATACGAAGA	250
	CATCATCATG	GAATTGATGA	AAACTGTTGA	TGAGTATATT	CCAGAACCAG	300
40	AACGTGATAC	AGACAAACCA	TTACTTCTTC	CAGTCGAAGA	CGTATTCTCA	350
	ATCACAGGTC	GTGGTACTGT	AGCTTCAGGA	CGTATCGATC	GTGGTACTGT	400
	TCGTGTCAAC	GACGAAATTG	AAATCGTTGG	TATCAAAGAA	GAAACTAAAA	450
	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAACCT	TGACGAAGGT	500
	CTTGCAGGAG	ATAACGTAGG	TATCCTTCTT	CGTGGTGTTT	AACGTGACGA	550
45	AATCGAACGT	GGACAAGTTA	TTGCTAAACC	AGGTTCAATC	AACCCACACA	600
	CTAAATTCAA	AGGTGAAGTT	TACATCCTTT	CTAAAGATGA	AGGTGGACGT	650
	CATACTCCAT	TCTTCAACAA	CTACCGTCCT	CAATTCTATT	TCCGTACAAC	700
	TGACGTAACA	GGTTCAATCG	AACTTCCAGC	TGGTACTGAA	ATGGTAATGC	750
	CTGGTGATAA	CGTGACAATC	AGCGTTGAGT	TGATCCACCC	AAT	793

2) INFORMATION FOR SEQ ID NO: 231

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus vestibularis*
 (B) STRAIN: ATCC 49124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

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10 TTGTAGTAGC ATCTACTGAC GGACCAATGC CACAAACTCG TGAGCACATC      50
   CTTCTTTCAC GTCAGGTTGG TGTTAAACAC CTTATCGTCT TCATGAACAA      100
   AGTTGACTTG GTTGACGATG AAGAATTGCT TGAATTGGTT GAAATGGAAA      150
   TCCGTGACCT TCTTTCAGAA TACGATTTC CAGGTGATGA TATTCCAGTT      200
   ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATTCTA AATACGAAGA      250
   CATCATCATG GACTTGATGA ACACGTGTTGA CGAATACATT CCAGAACCAG      300
15 AACGTGACAC TGACAAACCA TTGTTGCTTC CAGTCGAAGA CGTATTCTCA      350
   ATCACTGGTC GTGGTACTGT TGCTTCAGGA CGTATCGACC GTGGTGTGTTGT      400
   TCGTGTTAAT GACGAAGTTG AAATCGTTGG TCTTAAAGAA GAAATCCAAA      450
   AAGCAGTTGT TACTGGTGTA GAAATGTTCC GTAAACAAC TACGAAGGT      500
   ATTGCCGGAG ATAACGTCGG TGTCCTTCTT CGTGGTATCC AACGTGATGA      550
20 AATTGAACGT GGTCAAGTAT TGGCTGCACC TGGTTCAATC AACCACACA      600
   CTAAATTCAA AGGTGAAGTT TACATCCTTT CTAAAGAAGA AGGTGGACGT      650
   CACACTCCAT TCTTCAACAA CTACCGTCCA CAGTTCTACT TCCGTACAAC      700
   TGACGTAACA GGTTCATCG AACTTCCTGC AGGTACTGAA ATGGTTATGC      750
   CTGGTGATAA CGTGACTATC GACGTTGAGT TGATCCACCC AATCGCCG      798
25

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2) INFORMATION FOR SEQ ID NO: 232

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Tatumella ptyseos*
 (B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

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45 GGCGCTATCC TGGTTGTTGC TGCAACTGAC GGCCCTATGC CTCAGACCCG      50
   TGAGCACATC CTGCTGGGCC GCCAGGTAGG CGTTCCTTAC ATCATCGTGT      100
   TCCTGAACAA ATGTGACATG GTTGATGATG AAGAGCTGCT GGAAGTGGTA      150
   GAAATGGAAG TCCGTGACCT GCTGTCACAG TACGACTTCC CGGGTGACGA      200
   CACGCCAATC GTTCGCGGTT CAGCGCTGAA AGCACTGGAA GGTGAAGGCG      250
   AGTGGGAAGA GAAGATTCTG GAGCTGGCTG GCTTCCTGGA TTCTTACATC      300
50 CCTGAGCCAG AGCGTGCTAT CGATCAGCCG TTCCTGCTGC CAATCGAAGA      350
   CGTATTCTCA ATCTCCGGTC GTGGTACAGT TGTTACCGGT CGTGTAGAGC      400
   GCGGGATCAT CAAAGTCGGT GAAGAAGTTG AGATCGTTGG TATCAAAGAT      450
   ACTGCGAAAT CAACCTGTAC CGGTGTTGAA ATGTTCCGTA AACTGCTGGA      500
   CCAGGGTCAG GCGGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAGC      550
55 GTGAAGAGAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCAATCAAA      600
   CCACACACCC AGTTCGAGTC AGAAGTTTAT ATTCTGTCTA AAGACGAAGG      650
   CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
   GTACAACTGA CGTGACCGGA ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
   GTAATGCCTG GTGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCAAT      800
50 CGCGATGGAC GATGGTCTGC GTTTCGCAA      829

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2) INFORMATION FOR SEQ ID NO: 233

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trabulsiella guamensis*
 (B) STRAIN: ATCC 49490

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

20	GGCGCAATCC	TGGTAGTAGC	AGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTC	CGGGCGATGA	200
	CACGCCGATC	GTACGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
25	AGTGGGAAGC	GAAAATCATC	GAAGTGGCAG	GTTTCCTGGA	TTCTTACATT	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTGGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CAACCTGTAC	TGGCGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAC	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAA			829

40 2) INFORMATION FOR SEQ ID NO: 234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
 (B) STRAIN: ATCC 10790

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234

55

	CGGCGCTATC	TTGGTTGTAT	CCGCAGCTGA	CGGCCCTATG	CCTCAAACCTC	50
	GCGAACACAT	CTTGTTGGCT	CGCCAAGTTG	GTGTTCCCTGC	AATCGTAGTA	100
	TTCTTGAACA	AAGCTGACAT	GGTTGACGAT	GAAGAATTGA	TCGAATTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTTTCTTC	CTACGAATTC	CCTGGCGACG	200
60	AAGTACCTAT	CGTTGTAGGT	TCCGCGTTGA	AAGCTTTGGA	AGGCGATGCT	250

	CAATATGTAG	CTAAAATTGA	CGAATTGATG	GACGCTGTAG	ACTCCTACAT	300
	CCCAACACCA	GTTCGTGACA	CTGATAAACC	ATTCTTGATG	CCTGTGGAAG	350
	ATGTTTTCAC	AATCACTGGT	CGTGGTACAG	TAGCAACTGG	CCGTGTTGAA	400
	CGTGGTCAAG	TAAACGTTGG	TGATACTGTT	GAAGTAGTAG	GCTTGAAAGA	450
5	AAAAGCTGAA	CAATACGTAG	TAACAGGTCT	TGAAATGTTC	CGTAAAGTGT	500
	TGGATTCTGC	AGTAGCAGGT	GACAACGTAG	GTGCATTGCT	TCGTGGTGTT	550
	GATCGTAAAG	ACATYGAACG	TGGTCAAGTA	TTGGCTAAAC	CAGGTTCCAT	600
	CAACCCACAY	ACAAAATTCA	AAGCAGAAGT	ATACGTATTG	ACTAAAGAAG	650
	AAGGTGGTCG	TCATACTCCA	TTCTTCTCCA	ACTACCGTCC	ACAATTCTAC	700
10	TTCCGTACAA	CAGACGTAAC	AGGTGTTGTA	AACCTTCCTG	AAGGTGTAGA	750
	AATGTGTATG	CCTGGCGATA	ACGTAACAAT	GGAAATCGAA	TTGATTACTC	800
	CAATCGCTAT	CGAAGAAGGT	CTTCG			825

15

2) INFORMATION FOR SEQ ID NO: 235

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
(B) STRAIN: ATCC 9610

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235

	CGCTATCCTG	GTTGTTGCTG	CAACTGATGG	CCCAATGCCA	CAGACTCGTG	50
	AGCACATCCT	GTTGGGTCGT	CAGGTTGGTG	TTCCTTACAT	CATCGTATTC	100
	ATGAACAAAT	GTGACATGGT	TGACGATGAA	GAGCTGCTAG	AACTGGTAGA	150
35	AATGGAAGTG	CGCGATCTTC	TGTCTACCTA	CGATTTCCCA	GGCGATGATA	200
	CGCCAGTTGT	TCGTGGTTCC	GCGCTGAAAG	CATTGGAAGG	CGAACCTGAG	250
	TGGGAAGCAA	AAATTATCGA	ACTGGCTGGC	TACCTGGATT	CTTACATCCC	300
	AGAACCAGAG	CGTGCTATCG	ATAAGCCGTT	CCTGCTGCCA	ATCGAAGACG	350
	TATTCTCTAT	CTCTGGTCGT	GGTACTGTTG	TAACGGGTCG	TGTAGAGCGC	400
40	GGTATCGTTA	AAGTTGGTGA	AGAAGTCGAA	ATTGTTGGCC	TGAAAGATAC	450
	CGTTAAATCT	ACTTGTA CTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGATG	500
	AAGGCCGTGC	AGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAGCGT	550
	GAAGATATCG	AACGTGGTCA	AGTTCTTGCT	AAACCAGGTT	CGATTAAACC	600
	ACACACCAAA	TTTGAATCAG	AAGTTTATAT	TCTGAGCAAA	GATGAAGGTG	650
45	GTCGCCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCTCAGTT	CTACTTCCGT	700
	ACA ACTGATG	TAACCGGTAC	TATTGAACTG	CCAGAAGGCG	TTGAGATGGT	750
	GATGCCAGGT	GATAACATTC	AAATGATTGT	TAACCTGATT	GCTCCTATCG	800
	CAATGGATGA	CGGCTTGCGC	TTTGC			825

50

2) INFORMATION FOR SEQ ID NO: 236

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yersinia frederiksenii*

(B) STRAIN: ATCC 33641

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236

	GGCGCGATCC	TGGTTGTTGC	TGCCACTGAT	GGCCCGATGC	CACAGACTCG	50
	CGAGCACATT	CTGTTAGGGC	GTCAGGTGGG	TGTTCCCTTAC	ATCCTGGTCT	100
10	TCCTGAACAA	ATGTGACATG	GTTGACGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTCC	CTGGCGACGA	200
	CACTCCAGTT	ATCCGTGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	AAAAATCATC	GAATTGGCTG	AGGCGCTGGA	TAGCTATATT	300
	CCACAGCCAG	AGCGTGCGAT	TGATAAACCA	TTCCTGCTGC	CAATCGAAGA	350
15	CGTATTCTCA	ATCTCTGGCC	GTGGTACTGT	TGTCACCGGT	CGTGTAAGAGC	400
	GCGGTATCGT	TAAAGTCGGC	GAAGAAGTCG	AAATCGTTGG	TATCATTGAT	450
	ACCATCAAGA	CTACCTGTAC	TGGTGTTGAA	ATGTTCCGCA	AATTGCTGGA	500
	CGAAGGCCGT	GCGGGTGAGA	ACGTTGGTGT	TCTGCTACGT	GGTACTAAAC	550
	GTGATGACGT	ACAACGTGGT	CAGGTATTGG	CAAAACCAGG	TTCTATCAAG	600
20	CCACACACCA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
	TGGTCGCCAT	ACTCCGTTCT	TCAAAGGTTA	TCGTCCTCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTGATGCCAG	GTGATAACAT	TCAAATGATT	GTTAACCTGA	TTGCTCCTAT	800
25	CGCAATGGAT	GACGGTCTGC	GCTTTGCG			828

2) INFORMATION FOR SEQ ID NO: 237

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yersinia intermedia*

40 (B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237

	CTTGGTTGTC	GCTGCAACTG	ATGGTCCTAT	GCCACAGACT	CGCGAGCACA	50
45	TCCTGCTAGG	TCGTCAGGTG	GGTGTTCCTT	ACATCCTGGT	CTTCCTGAAC	100
	AAGTGTGACA	TGGTTGACGA	TGAGGAGTTG	CTGGAATTGG	TAGAAATGGA	150
	AGTCCGCGAA	CTTCTGTCTC	AATATGATTT	CCCTGGCGAT	GATACTCCTG	200
	TTATCCGTGG	TTCAGCGCTG	AAGGCGTTGG	AAGGCGAGCC	TGAATGGGAA	250
	GCAAAAATTA	TCGAATTAGC	TGAGGCGCTG	GATAGTTATA	TTCCACAGCC	300
50	AGAGCGCGCG	ATTGATAGAC	CATTCTTGCT	GCCAATCGAA	GACGTATTCT	350
	CTATCTCAGG	TCGTGGTACA	GTCGTCACCTG	GTCGTGTAGA	GCGTGGGATC	400
	GTTAAAGTTG	GCGAAGAAGT	TGAAATCGTT	GGTATTATCG	ATTCCATTAG	450
	AACAACATGT	ACTGGCGTTG	AAATGTTCCG	CAAATTGCTG	GACGAAGGCC	500
	GCGCGGGTGA	GAACGTTGGT	GTTCTACTGC	GTGGGACTAA	ACGTGATGAC	550
55	GTACAGCGTG	GTCAGGTATT	AGCTAAGCCA	GGTTCTATCA	AGCCACATAC	600
	TAAATTCGAA	TCCGAAGTTT	ATATTCTGAG	CAAAGATGAA	GGCGGGCGTC	650
	ACACGCCGTT	CTTCAAAGGC	TACCGTCCTC	AGTTCTACTT	CCGTACAACG	700
	GATGTAAACG	GTACTATTGA	ATTGCCAGAC	GGCGTTGAGA	TGGTGATGCC	750
	AGGTGATAAC	ATTCAAATGA	TTGTTAACCT	GATTGCACCT	ATTGCGATGG	800
60	ATGATGGTCT	GCG				813

2) INFORMATION FOR SEQ ID NO: 238

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pestis*
 (B) STRAIN: KIM D27

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238

20	GGAGCGATCT	TGGTTGTTGC	TGCAACCGAT	GGCCCTATGC	CGCAGACTCG	50
	TGAGCATATC	CTGCTGGGCC	GCCAGGTTGG	TGTCCCATAC	ATTATTGTCT	100
	TCCTGAACAA	ATGTGACATG	GTTGACGATG	AAGAGTTGCT	AGAGTTGGTT	150
	GAAATGGAGG	TTCGTGAGCT	TCTGTCTCAA	TACGATTTC	CAGGCGACGA	200
	CACTCCAGTC	ATCCGTGGTT	CAGCGTTGAA	AGCCCTGGAA	GGTGACGCTG	250
25	AGTGGGAAGC	TAAAATTATC	GAGTTGGCAG	AAGCTCTGGA	TAGCTATATT	300
	CCGCAACCAG	AACGCGCTAT	TGATAGACCA	TTCCTATTGC	CAATTGAAGA	350
	CGTATTCTCT	ATTTCTGGTC	GTGGTACTGT	AGTTACTGGT	CGTGTAAGAAC	400
	GTGGTATTGT	TAAGGTCGGC	GAAGAAGTTG	AAATCGTTGG	TATTATCGAT	450
	ACGATTAAAA	CAACTTGAC	TGGCGTTGAA	ATGTTCCGCA	AGCTGCTGGA	500
30	TGAAGGCCGT	GCTGGTGAAA	ATGTTGGTGT	TCTGCTGCGT	GGTACTAAGC	550
	GTGACGATGT	TCAGCGTGGT	CAAGTACTGG	CGAAACCAGG	TTCTATCAAG	600
	CCACACACGA	AGTTTGAGTC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
	CGGCCGTCAT	ACACCGTTCT	TCAAGGGCTA	CCGTCCTCAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGT	ACCATTGAGC	TGCCAGAAGG	CGTTGAAATG	750
35	GTCATGCCTG	GTGACAACGT	AAACATGGTT	GTTAACCTAA	TTGCTCCTAT	800
	CGCAATGGAT	GATGGTCTGC	GCTTCGCAA			829

40 2) INFORMATION FOR SEQ ID NO: 239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
 (B) STRAIN: ATCC 29833

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239

55

55	TGGAGCGATC	TTGGTTGTTG	CTGCAACCGA	TGGCCCTATG	CCGCAGACTC	50
	GTGAGCATAT	CCTGCTGGGC	CGCCAGGTTG	GTGTCCCATA	CATTATTGTC	100
	TTCCTGAACA	AATGTGACAT	GGTTGACGAT	GAAGAGTTGC	TAGAGTTGGT	150
	TGAAATGGAG	GTTCGTGAGC	TTCTGTCTCA	ATACGATTTC	CCAGGCGACG	200
60	ACACTCCAGT	CATCCGTGGT	TCAGCGTTGA	AAGCCCTGGA	AGGTGACGCT	250

	GAGTGGGAAG	CTAAAATTAT	CGAGTTGGCA	GAAGCTCTGG	ATAGCTATAT	300
	TCCGCAACCA	GAACGCGCTA	TTGATAGACC	ATTCCTATTG	CCAATTGAAG	350
	ACGTATTCTC	TATTTCTGGT	CGTGGTACTG	TAGTTACTGG	TCGTGTAGAA	400
	CGCGGTATTG	TTAAGGTCGG	CGAAGAAGTT	GAAATCGTTG	GTATTATCGA	450
5	TACGATTAAA	ACAACCTTGT	CTGGCGTTGA	AATGTTCCGC	AAGCTGCTGG	500
	ATGAAGGCCG	TGCTGGTGAA	AATGTTGGTG	TTCTGCTGCG	TGGTACTAAG	550
	CGTGACGATG	TTCAGCGTGG	TCAAGTACTG	GCGAAACCAG	GTTCTATCAA	600
	GCCACACACG	AAGTTTGAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GCGGCCGTCA	TACACCGTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700
10	CGTACAACCTG	ACGTGACCGG	TACCATTGAG	CTGCCAGAAG	GCGTTGAAAT	750
	GGTCATGCCT	GGTGACAACG	TAAACATGGT	TGTTAACCTA	ATTGCTCCTA	800
	TCGCAATGGA	TGATGGT				817

15

2) INFORMATION FOR SEQ ID NO: 240

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia rohdei*
(B) STRAIN: ATCC 43380

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCAATG	CCACAGACTC	50
	GCGAGCACAT	CCTGTTGGGT	CGTCAAGTGG	GTGTTCTTTA	CATCTTAGTC	100
	TTCTTGAACA	AGTGTGACAT	GGTTGACGAC	GAAGAGTTGC	TGGAACCTGGT	150
35	TGAAATGGAA	GTTCGTGAGC	TTCTGTCTCA	ATACGATTTC	CCTGGCGATG	200
	ACACTCCGGT	TATTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGAGGCC	250
	GAGTGGGAAG	CCAAAATTAT	TGAACTTGCT	GAAGCACTGG	ATAGCTACAT	300
	TCCACAGCCA	GAGCGCGCGA	TTGATAAACC	ATTCTTGCTG	CCAATCGAAG	350
	ACGTATTCTC	TATCTCAGGC	CGTGGAACAG	TTGTTACCGG	GCGTGTTGAG	400
40	CGCGGTATCG	TCAGAGTGGG	CGAAGAAGTT	GAAATCGTGG	GTATCATCGA	450
	CACCATTTAA	ACCACTTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCCGGTGAG	AACGTTGGTG	TTCTGCTGCG	CGGTACTAAA	550
	CGCGATGACG	TGCAACGTGG	TCAAGTGTTG	GCTAAACCAG	GTTCTATTAA	600
	GCCGCATACC	AAATTTGAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
45	GTGGTCGTCA	TACTCCGTTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGACG	GTGTTGAGAT	750
	GGTGATGCCA	GGTGATAACA	TTCAAATGAT	TGTTAACCTG	ATTGCGCCTA	800
	TTGCAATGGA	TGACGGTCTA	CGATTTGCA			829

50

2) INFORMATION FOR SEQ ID NO: 241

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yokenella regensburgei*

(B) STRAIN: ATCC 35313

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241

	TGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCGGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	AACTCCGAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
	GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GTTCGTGCTA	TCGACCTGCC	GTTCTTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGTGGCACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GTTCCATCAA	600
20	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	TATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGC					804

25

2) INFORMATION FOR SEQ ID NO: 242

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Achromobacter xylosoxidans* subsp. *denitrificans*

40

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242

45	TCAGTTCCCC	CGCGATCACA	TGCCCAAGAT	CTACGAAGCG	CTTACTCTGG	50
	CCGACGAGGG	TTCCTCGTTC	GCCGAAAAGG	GTCTGACGCT	GGAAGTGCAG	100
	CAACAGCTGG	GCGACGGCGT	GGTGCGTACC	ATCGCGCTGG	GCTCCAGCGA	150
	CGGCCTGCGC	CGCGGTATGA	AGGTCACCGG	TACGGGCGCG	CCGATCTCGG	200
	TGCCGGTCGG	CACCGGCACG	CTGGGCCGCA	TCATGGACGT	GCTGGGTCGT	250
50	CCCATCGACG	AAGCCGGCCC	GATCCAGCAC	GAAGAAAAGC	GTGGCATTCA	300
	CCAGCCGGCT	CCCCGTTTCG	ACGAACTGTC	GCCGTCGGTG	GAAGTCTGG	350
	AAACCGGCAT	CAAGGTTATT	GACCTGGTCT	GCCCGTTTCG	CAAGGGCGGC	400
	AAGGTCGGCC	TGTTTCGGCG	CGCCGGCGTG	GGCAAGACCG	TCAACATGAT	450
	GGAAGTATC	AACAACATCG	CCAAGCAGCA	CAGCGGCTTG	TCGGTGTTCG	500
55	CCGGCGTGGG	CGAGCGTACC	CGCGAAGGCA	ACGACTTCTA	CCACGAAATG	550
	GAAGAGTCGA	ACGTTCTGGA	CAAGGTTGCG	ATGGTGTTCG	GTCAGATGAA	600
	CGAACCCCCG	GGCAACCGTC	TGCGCGTGGC	GCTGACCGGC	CTGACCATGG	650
	CCGAGAAGTT	CCGCGACGAA	GGCCGCGACA	TCCTGTTCTT	CGTGGACAAC	700
	ATCTACCGCT	ACACCCTGGC	CGGTACGGAA	GTGTCCGCGC	TGCTGGGCCG	750
60	TATGCCGTCG	GCAGTGGGCT	ACCAGCCCAC	GCTGGCCGAA	GAAATGGGCA	800

5 2) INFORMATION FOR SEQ ID NO: 243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
(B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243

20 TGAAACTACT TTAGAAGTTC AGCAACAAC TGGTGATGGT GTTGTTTCGTA 50
CCATCGCAAT GGGTTCTACA GAAGGTCTTA AACGTGGTCT TACTGTAACT 100
AGCACAAACG CACCGATCTC TGTTCCAGTT GGTACAGCCA CTCTTGGCCG 150
TATCATGGAC GTTTTAGGTC GTCCTATCGA TGAAGCAGGT CCTGTTGCGA 200
25 CTGAAGAACG TTTGCCGATT CACCGTCAAG CGCCTTCTTA TGCTGAACAA 250
GCAGCTTCTA CTGACCTTTT AGAAACTGGT ATTAAAGTCA TCGACTTACT 300
TTGCCCCGTTT GCGAAAGGTG GTAAAGTTGG TTTATTCGGT GGTGCTGGTG 350
TTGGTAAAC CGTTAACATG ATGGAATTGA TCAACAACAT CGCGAAAGCA 400
CACTCAGGTT TATCTGTGTT TGCTGGTGTT GGTGAGCGTA CTCGTGAAGG 450
30 TAATGACTTC TATCACGAAA TGAAAGATTC TAACGTTCTT GACAAAGTAG 500
CAATGGTCTA CGGTCAGATG AACGAGCCAC CAGGTAACCG TTTACGCGTA 550
GCGTTAACTG GTTTGACTAT GGCTGAATAC TTCCGTGATG AAAAAGACGA 600
AAACGGTAAA GGTCGTGACG TATTATTATT CGTCGACAAC ATCTACCGTT 650
ATACACTTGC AGGTACTGAA GTATCAGCAT TGTTAGGTCG TATGCCATCT 700
35 GCGGTAGGTT ACCAACCTAC ACTTGCAGAA GAAATGGGTG TTCTTCAAGA 750
GCGTATTACA TCTACTAAAT CTGGTTCGAT CACTTCG 787

40 2) INFORMATION FOR SEQ ID NO: 244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
(B) STRAIN: CDCF 3697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244

55 GTTCCTAAGA TCTATGACGC TCTCCACGTT GATGGCACTG AAACCTACATT 50
AGAAGTTCAG CAACAACCTG GTGATGGCGT AGTTCGTACT ATTGCAATGG 100
GTTCTACTGA AGGCCTTAAG CGTGGTTTGA ACGTAACTAA CACTAACGCG 150
CCGATTCTG TACCAGTAGG TACAGCGACT CTAGGTCGTA TCATGGACGT 200
50 TCTTGGTGCG CCAATCGACG AAGCTGGTCC AGTTGCGACT GAAGCGCGTT 250

	TGCCGATTCA	CCGTCAAGCA	CCTTCTTATG	CTGAACAAGC	AGCTTCTACT	300
	GACCTTTTAG	AAACTGGTAT	TAAAGTCATC	GACTTACTTT	GCCCGTTCGC	350
	TAAAGGTGGT	AAAGTTGGTC	TGTTCGGTGG	TGCCGGTGTT	GGTAAAACTG	400
	TAAACATGAT	GGAGTTGATC	AACAACATCG	CTAAAGCGCA	CTCAGGTTTA	450
5	TCTGTATTCT	CTGGTGTTGG	TGAGCGTACT	CGTGAAGGTA	ATGACTTCTA	500
	TCACGAGATG	AAAGACTCAA	ACGTTCTAGA	CAAAGTAGCA	ATGGTCTACG	550
	GTCAGATGAA	CGAGCCACCG	GGTAACCGTT	TACGCGTAGC	GTTGACTGGT	600
	TTGACCATGG	CTGAGTACTT	CCGTGACGAG	AAAGACGAAA	ACGGCAAAGG	650
	CCGTGACGTA	CTATTGTTCT	TAGATAACAT	CTACCGTTAT	ACACTAGCAG	700
10	GTACTGAAGT	ATCAGCACTT	CTAGGTCGTA	TGCCGTCTGC	AGTAGGTTAC	750
	CAACCGACAC	TTGCAGAAGA	GATGGGTGTT	CTTCAAGAAC	GTATTACATC	800
	GACTAAGTCT	GGTTCGATTA	CGTCA			825

15

2) INFORMATION FOR SEQ ID NO: 245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSG-197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
35	TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCA	GTTGGTGATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTTCGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
40	TTCGGTGGCG	CTGGTGTAGG	TAAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
45	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

50

2) INFORMATION FOR SEQ ID NO: 246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Alcaligenes faecalis*

(B) STRAIN: ATCC 15554

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246

	TTCCCCCGCG	ACAGCATCCC	TAAAGTCTAC	GAAGCATTGA	CGCTCGTTGA	50
	CGAAAGTTTCG	GCTTTCGCAG	AAAAAGGCCT	GACTTTTGAA	GTACAGCAAC	100
10	AATTGGGTGA	CGGTGTAGTT	CGCACCATCG	CCATGGGTTC	CAGCGACGGC	150
	CTGCGCCGCG	GTATGGAAGT	GGCCGGTTCG	GGCGCTCCCA	TCTCCGTTCC	200
	CGTGGGTGTC	GGCACCCTGG	GTCGCATTAT	GGACGTTCTG	GGTCGCCCTA	250
	TTGACGAAGT	CGGTCCTATT	CAGTCCGACG	AGCGTCGCGC	CATTCACCAG	300
	CCTGCGCCTA	CTTTCGACGA	ACTGTCGCCT	TCCGTAGAGC	TGCTGGAAAC	350
15	CGGTATTAAA	GTGATTGACC	TGGTTTGCCC	GTTCGCCAAG	GGTGGTAAGG	400
	TTGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	AGACCGTGAA	CATGCTGGAG	450
	CTGATCAACA	ACATCGCCAA	GGCACACAGC	GGTCTGTCCG	TGTTTGCCGG	500
	TGTGGGTGAG	CGTACCCGTG	AAGGTAACGA	CTTCTACCAC	GAAATGGCCG	550
	ATGCTGGCGT	TATCCAGATG	GACAACCTGA	GCGAGTCCAA	AGTGGCCATG	600
20	GTGTTTCGGTC	AGATGAACGA	ACCTCCAGGC	AACCGTCTGC	GTGTGGCACT	650
	GTCCGGCCTG	ACCATGGCCG	AGAAGTTCCG	TGACGAAGGC	CGTGACATCC	700
	TGTTCTTTGT	GGACAACATC	TACCGCTACA	CGCTGGCCGG	TACAGAAGTG	750
	TCCGCTCTGC	TGGGTCGTAT	GCCTTCCGCA	GTGGGTACC	AGCCTACGCT	800
	GGCCGAGGAA	ATGGGTAAGC	TGCAAGAGCG	CATTACCTCC	ACCAAGACCG	850
25	G					851

2) INFORMATION FOR SEQ ID NO: 247

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

35

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247

45	GATGGCGGAA	AGCTACCAGA	AATCTACAAC	GCCCTTACGG	TAAAACAGAG	50
	CAACGAAAAC	GGAACAAGCA	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	100
	TAGGTGATGA	CACAGTTCGT	ACAGTTGCAA	TGTCTTCCAC	AGATGGACTT	150
	GTTCGTGGCA	CAGAAGTAGA	AGATACTGGT	AAAGCAATCT	CTGTACCAGT	200
	TGGTGATGCA	ACACTTGGTC	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	250
50	ACTTAGATGG	TGAGGTTCCT	GCGGATGTAC	GTCGTGATCC	AATTCACCGT	300
	CAAGCACCTG	CATTCGAAGA	ATTATCTACT	AAAGTAGAAA	TTCTTGAAAC	350
	TGGTATTAAA	GTAGTAGACT	TACTTGCTCC	TTACATTAAG	GGTGGTAAGA	400
	TCGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACGGTATT	AATTCAGGAA	450
	TTAATCAATA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCTGG	500
55	TGTAGGTGAG	CGTACTCGTG	AGGGTAATGA	CTTATACCAC	GAAATGAGCG	550
	ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
	CCACCTGGAG	CACGTCAACG	TGTTGCGTTA	ACAGGTTTAA	CAATGGCTGA	650
	GCATTTCCGT	GATGAGCAAG	GACAAGATGT	ACTTCTGTTC	ATCGATAATA	700
	TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGGCCGT	750
50	ATGCCATCTG	CGGTAGGTTA	CCAACCAACA	CTTGCAACAG	AAATGGGTCA	800

5 2) INFORMATION FOR SEQ ID NO: 248

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248

20 CCAGAAATCT ACAATGCCCT TACGGTAAAA CAAAGCAACG AAAACGGAAG 50
CATGAACTTA ACATTTGAAG TTGCACTTCA TTTAGGTGAT GATACAGTTC 100
GTACAGTTGC GATGTCTTCC ACAGATGGAC TTGTTCTGTG CACAGAAGTA 150
GAAGATACTG GTAAAGCAAT CTCTGTACCA GTTGGTGATG CAACACTTGG 200
25 ACGTGTATTC AACGTATTAG GTGATGCAAT TGA CTTAGAT GGTGAACTTC 250
CTGCGGATGT ACACCGTGAT CCAATTCACC GTCAAGCACC TGCATTCGAA 300
GAATTATCTA CTAAAGTAGA AATTCTTGAA ACTGGTATTA AAGTAGTAGA 350
CTTACTTGCT CCTTACATTA AGGGTGGTAA GATCGGCCTA TTCGGTGGTG 400
CCGGCGTAGG TAAACAGTA TTAATTCAGG AGTTAATCAA TAACATCGCA 450
30 CAAGAGCACG GTGGTATCTC TGTATTGCTG GGTGTAGGTG AGCGTACTCG 500
TGAGGGTAAT GACTTATACC ACGAAATGAG CGATTCTGGC GTAATCAAGA 550
AAACTGCGAT GGTATTCTGA CAAATGAACG AGCCACCTGG AGCACGTCAA 600
CGTGTTGCAT TAACAGGTTT AACAATGGCT GAGCATTTCG GTGATGAGCA 650
AGGACAAGAC GTACTTCTGT TCATCGATAA CATCTTCCGT TTCACGCAAG 700
35 CGGGTTCTGA AGTATCTGCC CTTCTTGGTC GTATGCCATC TCGGGTAGGT 750
TACCAACCAA CACTTGCAAC AGAAATGGGT CAATTACAAG AGCGTATTAC 800
ATCTACAAAT 810

40 2) INFORMATION FOR SEQ ID NO: 249

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 944 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacteroides distasonis*
(B) STRAIN: ATCC 8503

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249

CTTTGATTAT GGGACAGAAG AAACAGTAAC CCTCCCCCGT ATCCACGACG 50
CCATGGAGAT TTCCCGCCCA AACGGAAAGA TCTTGATCGT CGAAGTTCAG 100
CAACACATCG GGGAAAACAC CGTCCGTACC GTAGCGATGG ATACGACCGA 150
50 CGGATTGAGA CGAGGCATGG AGGCCGTGTC ATACGGAATG CCCATCACCA 200

	TGCCGACCGG	CGACCAAGTC	AAAGGACGTT	TAATGAATGT	CACCGGCGAC	250
	CCTATCGATG	GCATGGCCCA	GCTTACTAAA	GACGGGGCTC	TTCCCATCCA	300
	TCGTGAGCCT	CCTAAATTCG	AGGATCTGAC	AACGACCCAA	GAGGTCTTGT	350
	ACACGGGTAT	TAAAGTAATC	GATTTATTGG	AACCTTACGC	CAAAGGAGGC	400
5	AAGATCGGAC	TTTTCGGAGG	AGCCGGAGTC	GGCAAAACGG	TATTGATCAT	450
	GGAATTGATC	AACAACATCG	CAAAGAAAAA	CAACGGATTC	TCCGTCTTCG	500
	CCGGTGTGGG	TGAACGTACA	CGTGAAGGAA	ATGACCTATT	GCGTGAAATG	550
	ATCCAATCCG	GTGTCATCCG	ATACGGCGAG	GAGTTTAAGA	AGAGTATGGA	600
	GGCAGGCAAC	TGGGACTTGT	CGAAGATCGA	TTACGATGAA	TTGGCTAAGT	650
10	CGCAGGCTAC	CTTGGTATTC	GGGCAGATGA	ACGAACCGCC	GGGCGCCCGC	700
	TCGTCCGTGG	CCTTATCCGG	TTTGACGATC	GCCGAATCCT	TCCGTGACAA	750
	AGCCTCTGAG	GGAGAAAGAA	AAGATATATT	ATTCTTCATC	GATAATATCT	800
	TCCGTTTCAC	CCAAGCCGGT	TCCGAGGTTT	CCGCCTTGCT	GGGGCGTATG	850
	CCTTCCGCCG	TAGGTTACCA	ACCGACATTG	GCCACGGAAA	TGGGAGCTAT	900
15	GCAAGAGCGT	ATCACTTCAA	CCAAGAAGGG	CTCCATCACC	TCCG	944

2) INFORMATION FOR SEQ ID NO: 250

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Bacteroides ovatus*
 (B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250

35	TTGAGGGTAC	GGATGCAGAA	TTGGTGCTGC	CAAGCATCCA	CGACGCACTG	50
	GAGATAAAGA	GGCCAAACGG	CAAAATACTG	GTTGTAGAAG	TTCAGCAACA	100
	TATCGGCGAA	AATACGGTGC	GTACCGTAGC	GATGGACAGT	ACTGACGGAC	150
	TTCAGAGAGG	CATGAAAGTG	TATCCCACCG	GAGGCCCGAT	CACGATGCCG	200
	ATTGGCGAAC	AGATTAAAGG	ACGACTGATG	AACGTAGTCG	GTGATTTCGAT	250
40	CGACGGTATG	AAAGGACTCG	ACCGCAAAGG	TGCATATTCC	ATTCATCGCG	300
	ACCCCCCTAA	GTTTGAGGAT	TTGACTACTG	TGCAAGAGGT	GCTCTTCACA	350
	GGTATCAAAG	TGATCGACCT	GCTCGAACCG	TATGCCAAAG	GTGGTAAAAT	400
	CGGTTTGTTT	GGCGGTGCCG	GTGTAGGAAA	GACTGTATTG	ATTCAGGAAC	450
	TTATCAATAA	TATCGCCAAG	AAACATAATG	GATTCTCTGT	ATTTGCCGGA	500
45	GTAGGTGAAC	GTACCCGTGA	AGGTAACGAC	TTGCTGCGCG	AAATGATTGA	550
	ATCCGGTGTA	ATCCGTTACG	GCGAAGCATT	CAAAGAAGGA	ATGGAGAAAG	600
	GTCACGGGGA	TCTTTCGAAA	GTGGATTATA	ACGAACTGGA	GAAATCGCAA	650
	GTGTCTCTGA	TTTTCGGTCA	GATGAACGAG	CCTCCGGGCG	CACGTGCCTC	700
	TGTGGCATTG	TCCGGAATGA	CGGTGGCGGA	ATCTTTCCGC	GACGCAGGAA	750
50	AAGAAGGTGA	GAAACGCGAT	ATTCTGTTCT	TTATTGATAA	TATCTTCCGT	800
	TTCACGCAAG	CAGGTTTCAG	AGTGTCCGCC	CTTTTGGGAC	GTATGCCCTC	850
	CGCTGTTGGT	TACCAGCCCA	CGTTGGCTAC	GGAAATGGGT	GCGATGCAGG	900
	AACGTATCAC	GTCTACCCGC	AAAGGTTCTA	TCACCTCCG		939

55

2) INFORMATION FOR SEQ ID NO: 251

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 833 bases

150

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leclercia adecarboxylata*
 (B) STRAIN: ATCC 23216

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251

	CGAATTCCCT	CAGGATGCCG	TACCGCGCGT	GTACGATGCT	CTTGAGGTTC	50
	AGAATGGTAA	TGAGAGCCTG	GTGCTGGAAG	TTCAGCAGCA	GCTCGGCGGC	100
15	GGTATTGTGC	GTACCATCGC	CATGGGTTCT	TCCGACGGTC	TGCGTCGTGG	150
	TCTGGAAGTT	AAAGACCTCG	AGCACCCAAT	CGAAGTACCA	GTAGGTAAAG	200
	CAACCCTGGG	CCGTATCATG	AACGTCCTGG	GTCAGCCGAT	CGACATGAAA	250
	GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGTT	CAGCACCTTC	300
	CTATGAAGAG	CTGTCCAGCT	CTCAGGAACT	GCTGGAAACC	GGCATCAAAG	350
20	TTATCGACCT	GATGTGTCCG	TTCGCGAAGG	GCGGTAAAGT	TGGTCTGTTC	400
	GGCGGTGCGG	GTGTAGGTAA	AACCGTAAAC	ATGATGGAGC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCCGT	GTTTGCAGGC	GTGGGTGAGC	500
	GTAATCGTGA	GGGTAACGAC	TTCTACCACG	AAATGACCGA	CTCCAACGTT	550
	CTGGACAAAG	TATCCCTGGT	TTACGGCCAG	ATGAACGAGC	CACCAGGAAA	600
25	CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAGTTCCGTG	650
	ACGAAGGTCG	TGACGTACTG	CTGTTCTGTTG	ACAACATCTA	CCGTTACACC	700
	CTGGCCGGTA	CGGAAGTATC	CGCACTGCTG	GGTCGTATGC	CATCAGCAGT	750
	AGGCTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGTGTTCTG	CAGGAACGTA	800
	TCACCTCTAC	CAAAACCGGT	TCTATCACCT	CCG		833

30

2) INFORMATION FOR SEQ ID NO: 252

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Stenotrophomonas maltophilia*
 (B) STRAIN: CDC F3338

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252

	GTGTACGACG	CACTGAAGGT	GGAAAACACC	GAGATCACCC	TCGAAGTCCA	50
50	GCAGCAGCTG	GGCGACGGCG	TGGTGC GTAC	CATCGCCCTC	GGTTCCACCG	100
	ACGGCCTGAA	GCGCAACCTG	GTTGCCGTCA	ACACCGGCCG	TGGCATCTCG	150
	GTGCCGGTCG	GCGCCGGCAC	CCTGGGCCGC	ATCATGGACG	TGCTGGGCCG	200
	TCCGATCGAC	GAAGCCGGCC	CGGTCGCTGC	CAGCGACAAC	TGGGAAATCC	250
	ACGCGCTGCTG	GCCGTCGTAT	GAAGACCAGT	CCCCGGCCAC	CGAGCTGCTG	300
55	GAAACCGGCA	TCAAGGTCAT	CGACCTGATG	TGCCC GTTCG	CCAAGGGCGG	350
	CAAGGTCGGC	CTGTTCTGGC	GCGCCGGCGT	CGGCAAGACC	GTCAACATGA	400
	TGGAAC TGAT	CAACAACATC	GCCAAGGCGC	ACAGCGGCCT	GTCCGTGTTC	450
	GCCGGCGTGG	GTGAGCGTAC	CCGTGAGGGC	AACGACTTCT	ACCACGAGAT	500
	GAAGGACTCC	AACGTCCTGG	ACAAGGTGGC	GATGGTGTAC	GGCCAGATGA	550
60	ACGAGCCGCC	GGGCAACCGT	CTGCGCGTGC	CCCTGACCGG	CCTGACCATG	600

	GCCGAGTACT	TCCGCGATGA	GAAGGACGAA	AACGGCAAGG	GCAAGGACGT	650
	CCTGCTGTTC	GTCGACAACA	TCTACCGCTA	CACCCTGGCC	GGTACCGAAG	700
	TGTCGGCACT	GCTGGGCGCG	ATGCCGTCCG	CGGTGGGTTA	CCAGCCGACC	750
	CTGGCCGAGG	AAATGGGCGT	CCTGCAGGAG	CGCATCACCT	CGACCAAGAA	800
5	TGGTTCGATC	ACCTCGATC				819

2) INFORMATION FOR SEQ ID NO: 253

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Bartonella henselae*
 (B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253

25	AGTTTGAAGG	CCCTTTGCCA	AATATTCTCA	ATGCATTAGA	AACAGATAAT	50
	TTGGGCAATC	GGCTAGTTTT	AGAAGTTGCT	CAGCATTTGG	GTGAAAATAC	100
	CGTGCGTACC	ATTGCCATGG	ATACTACCGA	TGGTCTTGTC	CGTGGTCAAA	150
	AAGTTTTTGA	TACAGGAACA	CAGATCAGTG	TTCCCGTGGG	AGAAGCAACA	200
	CTTGGTCGTA	TTATGAATGT	GATTGGAGAG	CCGGTTGATA	ATGTTGGCCC	250
30	AATTGCTACA	AGCAAAACCC	GTTCCATTCA	CCAAGAGGCT	CCTGAATATG	300
	TGGAGCAATC	AACCGCATCA	GAAATCCTTG	TGACTGGTAT	TAAAGTCGTT	350
	GATCTGTTAG	CTCCTTATTC	TAAAGGGGGG	AAGGTTGGTT	TGTTTGGAGG	400
	TGCCGGTGTT	GGTAAAACCG	TTCTCATTAT	GGAGCTTATC	AACAATATTG	450
	CAAAGGCGCA	TGGTGGCTAT	TCAGTGTTTG	CCGGTGTTGG	TGAACGTACA	500
35	CGTGAGGGAA	ATGATCTTTA	TTATGAAATG	ATCGAAAGCC	GTGTGAATGT	550
	GAATCCAAA	GACAACAATG	GTTCAACAGA	AGGATCAAAA	TGTGCACTCG	600
	TTTATGGGCA	AATGAATGAA	CCACCAGGGG	CGCGTGCACG	TGTGGCTCTT	650
	TCAGGATTGA	CCATTGCAGA	AAGTTTCCGT	GATGAGGGAC	AAGATGTTTT	700
	GTTCTTCGTA	GATAATATTT	TCCGTTTTAC	GCAAGCAGGC	GCTGAAGTGT	750
40	CAGCTCTTTT	AGGGCGTATT	CCTTCTGCTG	TAGGGTATCA	GCCAACTTTG	800
	GCAACTGATA	TGGGGGCTTT	GCAAGAGCGT	ATTACCAGTA	CAAGAACAGG	850
	CTCTATTACC	TCTG				864

45

2) INFORMATION FOR SEQ ID NO: 254

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 866 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254

152

	TTCCCGGTGG	GCCACCTGCC	CGACATTTAC	AATGCACTTA	CCGTTGAACT	50
	GKCCAACACC	GGYGTCCACG	AASAGGGCGA	GACCACCAAG	AAGATCACCC	100
	TTGMGGTTGA	ACAGCATCTT	GGCGATTCCA	CCGTGCGTAC	CGTCGCTCTG	150
5	AAGCCGACTG	ACGGCCTTGT	GCGTGCGGCC	ACCGTGTATG	ACACCGGCGG	200
	CCCGATCTCT	GTGCCGGTTG	GCGATGTCAC	CAAGGGCCAC	GTATTTCGACG	250
	TGTCCGGCAA	CATCCTCAAC	AAGAAGGCCG	ACGAGACCGT	TAAGGTTACC	300
	GAACGTTGGT	CTATCCACCG	TAACCCGCCG	GCATTTCGACC	AGCTGGAGTC	350
	CAAGACCCAG	ATGTTTCGAAA	CCGGTATCAA	GGTCATCGAT	TTGCTGACCC	400
10	CGTATGTGCA	GGGCGGCAAG	ATCGGTCTGT	TCGGCGGCGC	AGGCGTCGGC	450
	AAGACCGTGC	TGATCCAGGA	AATGATTTCAG	CGTGTGGCTC	AGAACCACGG	500
	CGGTGTGTCC	GTGTTTCGCAG	GCGTCGGCGA	GCGTACCCGT	GAGGGTAACG	550
	ATCTGATCGG	CGAAATGGAC	GAAGCCGGCG	TGCTCGAGAA	GACCGCACTG	600
	GTCTTCGGCC	AGATGGATGA	GCAGCCGGGT	ACCCGTCTGC	GCGTGCCGCT	650
15	GACCGCACTG	ACCATGGCAG	AGTACTTCCG	TGACGTACAG	AATCAGGACG	700
	TGCTGCTGTT	CATCGATAAC	ATCTTCCGTT	TCACCCAGGC	TGGTTCCGAG	750
	GTGTCCACCC	TGCTCGGCCG	TATGCCGTCC	GCAGTGGGCT	ACCAGCCGAA	800
	CCTGGCCGAT	GAGATGGGCG	CGCTGCAGGA	GCGAATCACT	TCGACCCGTG	850
	GACACTCCAT	CACCTC				866
20						

2) INFORMATION FOR SEQ ID NO: 255

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 842 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Brucella abortus*
 - 35 (B) STRAIN: S2308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255

	AAGGCCAGCT	GCCGCTGATC	CTGAACGCGC	TTGAAGTGGA	CAATCAGGGC	50
40	CATCGTCTGG	TTCTCGAAGT	TGCCCAGCAC	CTCGGCGAAG	ACACCGTGCG	100
	CACCATCGCC	ATGGACGCGA	CCGAAGGTCT	CGTTCGCGGT	CAGGAAGCAC	150
	GCGACACTGG	CGAACCGATC	ATGGTGCCGG	TCGGCGTCTGA	AACGCTTGGC	200
	CGCATCATGA	ACGTCATCGG	CGAGCCGGTT	GACGAAGCAG	GCCCCATCAA	250
	GACCAAGGCA	ACCCGCGCCA	TCCACCAGAA	CGCGCCGGAA	TATATCGAAC	300
45	AGTCGACCGA	AGCCGAAATT	CTGGTCACGG	GCATCAAGGT	CGTCGACCTT	350
	CTGGCGCCTT	ACGCCAAGGG	CGGCAAGATC	GGCCTCTTCG	GCGGTGCAGG	400
	CGTCGGCAAG	ACCGTTCTCA	TCATGGAAct	CATCAACAAC	GTCGCCAAGG	450
	CGCACGGCGG	TTATTCCGTG	TTCGCAGGCG	TCGGTGAGCG	TACCCGTGAG	500
	GGCAACGACC	TTTACCACGA	AATGATCGAG	TCGGGCGTGA	ACAAGCTCGG	550
50	CGGCGGCGAA	GGCTCCAAGG	CAGCCCTCGT	TTACGGCCAG	ATGAACGAAC	600
	CCCCGGGTGC	CCGCGCCCGC	GTTGCCCTTT	CCGGTCTGAC	GTTTGCTGAA	650
	AACTTCCGTG	ACCAGGGCCA	GGACGTTCTG	TTCTTCGTGG	ACAACATCTT	700
	CCGCTTCACG	CAGGCAGGTT	CGGAAGTGTC	GGCTCTTCTC	GGCCGTATTC	750
	CTTCCGCTGT	GGGTTATCAG	CCGACGCTGG	CAACCGACAT	GGGCGCCATG	800
55	CAGGAACGCA	TCACCACGAC	GACCAAGGGT	TCGATCACCT	CG	842

2) INFORMATION FOR SEQ ID NO: 256

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea davisae*
 (B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256

15	CGAGTTCCCT	CAGGACGGCG	TACCGCGCGT	TKATGATGCG	CTTGAAGTAC	50
	AAAATAACAG	CGAGCAGCTG	GTGCTGGAAG	TTCAGCAGCA	GCTCGGCGGC	100
	GGTATCGTGC	GTACCATCGC	TATGGGTTCT	TCCGACGGTC	TGCGTCGTGG	150
	TCTGGAAGTT	AAAGACCTCG	AGCACCCGAT	CGAAGTCCCG	GTAGGTAAAG	200
	CGACCCCTTG	CCGTATCATG	AACGTGCTGG	GTCAGCCGAT	CGACATGAAA	250
20	GGCGATATCG	GCGAAGAAGA	CCGTTGGGCT	ATTCACCGCG	CTGCACCTTC	300
	CTATGAAGAG	CTGTCCAGCT	CTCAGGAACT	GCTGGAAACC	GGCATCAAAG	350
	TAATCGACCT	TATCTGTCCG	TTCGCTAAGG	GCGGTAAAGT	AGGTCTGTTC	400
	GGTGGTGCGG	GCGTGGGTAA	AACCGTAAAC	ATGATGGAGC	TTATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GCTACTCCGT	GTTTGCGGGC	GTGGGTGAGC	500
25	GTACTCGTGA	GGGTAACGAC	TTCTATCACG	AAATGACCGA	CTCCAACGTT	550
	CTGGACAAAG	TTGCCCTGGT	TTACGGCCAG	ATGAACGAGC	CACCGGGTAA	600
	CCGTCTGCGC	GTAGCGCTGA	CCGGTCTGAC	CATCGCGGAG	AAATTCCGTG	650
	ACGAAGGTCG	TGACGTTCTG	CTGTTTCGTTG	ATAACATCTA	CCGTTACACC	700
	CTGGCCGGTA	CTGAAGTATC	CGCGCTGCTG	GGTCGTATGC	CTTCTGCGGT	750
30	AGGTTACCAG	CCAACCTCTG	CGGAAGAGAT	GGGTGTTCTT	CAGGAGCGTA	800
	TTACCTCCAC	CAAGACCGGT	TCCATCACCT	CCG		833

35 2) INFORMATION FOR SEQ ID NO: 257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257

50	TTCCCTCAGG	ACGGCGTACC	GCGCGTATAT	GACGCGCTTG	AGGTACAGAA	50
	TAACAGCGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
	TCGTACGTAC	CATCGCAATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GAAGTGAAAG	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	200
55	TCTGGGTCGT	ATCATGAACG	TGCTGGGTCA	GCCAATTGAT	ATGAAAGGCG	250
	ACATCGGCGA	AGAAGATCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAT	300
	GAAGAGCTGT	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	350
	CGACCTGATT	TGTCCGTTCTG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	400
	GTGCGGGCGT	AGGTAAAACC	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	450
50	GCGATCGAGC	ACTCCGGTTA	CTCCGTGTTT	GCAGGCGTGG	GTGAGCGTAC	500

TCGTGAGGGT AACGACTTCT ACCACGAGAT GACCGACTCC AACGTTCTGG 550
 ACAAAGTTGC ACTGGTTTAC GGCCAGATGA ACGAGCCGCC AGGTAACCGT 600
 CTGCGCGTAG CGCTGACCGG TCTGACCATC GCGGAGAAAT TCCGTGACGA 650
 AGGCCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG 700
 5 CCGGTACAGA AGTTTCTGCA CTGCTGGGTC GTATGCCATC TGCGGTAGGT 750
 TATCAGCCTA CTCTGGCAGA AGAGATGGGT GTTCTTCAGG AGCGTATTAC 800
 CTCCACCAAG ACCGGTTCCA TCACTTCCG 829

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2) INFORMATION FOR SEQ ID NO: 258

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cedecea neteri*
 (B) STRAIN: ATCC 33855

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258

TCCCTCAGGA CGGCGTACCG CGCGTTTATG ACGCGCTTGA GGTACAGAAC 50
 AACAATGAGA AGCTGGTGCT GGAAGTTCAG CAGCAGCTCG GCGGCGGTAT 100
 CGTGCGTACC ATCGCAATGG GTTCTTCCGA CGGTCTGCGT CGTGGTCTGG 150
 30 TAGTAACAGA CCTCGAGCAC CCGATCGAAG TCCCGGTAGG TAAAGCGACC 200
 CTTGGCCGTA TCATGAACGT GCTGGGTCAG CCGATCGACA TGAAAGGCGA 250
 CATCGGCGAA GAAGACCGTT GGGCGATTCA CCGCGCAGCA CCTTCCTACG 300
 AAGAGCTGTC CAGCTCTCAG GAATTGCTGG AAACCGGCAT CAAAGTTATC 350
 GACCTGATTT GTCCGTTCGC TAAGGGCGGT AAAGTAGGTC TGTTCGGTGG 400
 35 TGCGGGCGTA GGTAACACCG TAAACATGAT GGAGCTGATC CGTAACATTG 450
 CGATCGAGCA CTCCGGTTAT TCCGTGTTTG CGGGCGTGGG TGAGCGTACT 500
 CGTGAGGGTA ACGACTTCTA CCACGAAATG ACCGACTCCA ACGTTCTGGA 550
 TAAAGTAGCA CTGGTTTACG GCCAGATGAA CGAGCCACCA GGTAACCGTC 600
 TGCGCGTAGC GCTGACCGGT CTGACCATCG CGGAAAAATT CCGTGACGAA 650
 40 GGCCGCGACG TTTTGCTGTT CGTTGATAAC ATCTACCGTT ATACCCTGGC 700
 CCGTACCGAA GTATCTGCAC TGCTGGGTCG TATGCCTTCT GCGGTAGGTT 750
 ATCAGCCAAC TCTGGCAGAA GAGATGGGTG TTCTTCAGGA GCGTATTACC 800
 TCCACCAAGA CCGGTTCTAT CACCTCCGTA 830

45

2) INFORMATION FOR SEQ ID NO: 259

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 931 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chryseobacterium meningosepticum*
 (B) STRAIN: CDC B7681

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259

	TTTCAGGAAG	TAGAGGAACT	ACCAAACATT	TATGACGCAC	TTGAAGTTGT	50
	CAGAGAAGGC	CAGAAAGGTC	TGATCTTAGA	AGTTGAACAA	CACATCGGTG	100
5	AGGATACAGT	GAGATGTATC	GCTATGGATG	CAACAGACGG	ACTTCAAAGA	150
	GGACAATCTG	TAATAGGACA	TGGAAGACAA	ATTACTATGC	CTATTGGTGA	200
	AGAAGTAAAT	GGTAGATTGT	TCAACGTGGT	AGGAGATGCT	ATCGACGGAC	250
	TTCAGGAATT	ATCTAAAGAC	AATGGTTTGC	CAATCCACAG	AGAAGCACCT	300
	AAATTTCGATC	AGTTATCAAC	TTCTGCTGAA	GTACTATATA	CAGGTATCAA	350
10	AGTAATCGAC	CTTATCGAGC	CTTATGCAAA	AGGTGGTAAA	ATTGGTTTGT	400
	TCGGTGGTGC	TGGTGTAGGT	AAAACAGTAT	TGATCCAGGA	ATTGATTAAT	450
	AACATTGCTA	AAGGACACGG	TGGTCTTTCT	GTATTCGCAG	GAGTAGGTGA	500
	GAGACAAGA	GAAGGAAATG	ACCTTCTTCG	TGAGATGTTA	GAGTCTGGTA	550
	TTATTAAATA	TGGTGACGAA	TTCATGCATT	CTATGGAGAA	CGGTGGATGG	600
15	GATCTTTCTA	AAGTTGACAG	TGAGTTGATG	AAAGAGTCTA	AAGCTGCTTT	650
	CGTTTTTCGGA	CAGATGAACG	AGCCACCAGG	TGCAAGAGCA	CGTGTAGCCC	700
	TTTCTGGTCT	TACTTTAGCT	GAATACTACC	GTGATGGTGG	CGAAAGCGGA	750
	CAAGGTAGAG	ACGTTCTTTT	CTTCGTAGAC	AACATCTTCC	GTTTTACACA	800
	GGCTGGTTCT	GAGGTGTCTG	CACTTCTAGG	TCGTATGCCT	TCAGCGGTAG	850
20	GTTACCAACC	AACTCTAGCT	TCTGAGATGG	GTGCAATGCA	GGAGAGAATT	900
	ACTTCAACTA	AAAACGGATC	TATTACATCT	G		931

25 2) INFORMATION FOR SEQ ID NO:260

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter amalonaticus*

(B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260

40	GTATCGTACG	TACCATCGCA	ATGGGTTCTT	CCGACGGTCT	GCGTCGTGGT	50
	CTGGAAGTCA	AAGACCTCGA	GCACCCGATC	GAAGTCCCGG	TAGGTAAAGC	100
	AACCCTGGGT	CGTATCATGA	ACGTCCTGGG	TCACCCGATC	GACATGAAAG	150
	GCGATATCGG	TGAAGAAGAG	CGTTGGGCTA	TCCACCGCGC	AGCACCGTCC	200
45	TATGAAGAGC	TGTCCAGCTC	TCAGGAACTG	CTGGAAACCG	GTATCAAAGT	250
	TATCGACCTG	ATGTGTCCGT	TCGCGAASGG	CGGTAAAGTG	GGTCTGTTCG	300
	GTGGTGCGGG	TGTAGGTAAA	ACCGTAAACA	TGATGGAGCT	TATCCGTAAC	350
	ATCGCGATCG	AGCACTCCGG	TTACTCCGTG	TTTGCGGGCG	TAGGTGAACG	400
	TACTCGTGAG	GGTAACGACT	TCTACCACGA	AATGACCGAC	TCCAACGTTC	450
50	TGGATAAAGT	ATCCCTGGTA	TATGGCCAGA	TGAACGAGCC	GCCGGGAAAC	500
	CGTCTGCGCG	TTGCACTGAC	CGGTCTGACC	ATGGCAGAGA	AATTCCGTGA	550
	CGAAGGTCGT	GACGTACTGC	TGTTCTGTCGA	TAACATCTAT	CGTTACACCC	600
	TGGCCGGTAC	GGAAGTTTCC	GCACTGCTGG	GTCGTATGCC	ATCAGCGGTA	650
	GGTTACCAGC	CGACCCTGGC	GGAAGAGATG	GGTGTCTGCT	AGGAACGTAT	700
55	CACTTCTACC	AAAACCGGTT	CTATCA			726

50 2) INFORMATION FOR SEQ ID NO: 261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261

15	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTTATGAATG	GTAAAGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACCA	100
	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAT	150
	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACTC	TGGGTCGTAT	200
	CATGAACGTC	CTGGGTCACC	CGATCGACAT	GAAAGGCGAT	ATCGGTGAAG	250
20	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTATGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTGCT	AAGGGCGGTA	AAGTTGGTCT	GTTGCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAACAC	450
	TCCGGTTACT	CCGTGTTTGC	GGGCGTGGGT	GAACGTAATC	GTGAGGGTAA	500
25	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAT	AAAGTATCCC	550
	TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCT	600
	CTGACCGGTC	TGACCATGGC	AGAGAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTC	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACAGAAG	700
	TATCCGCTCT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCGACC	750
30	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAC	800
	CGGTTCTATC	AC				812

35 2) INFORMATION FOR SEQ ID NO: 262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262

50	GCGCGTGTAC	GACGCCCTTG	AGGTGCAGAA	TGGTAATGAA	CATCTGGTGC	50
	TGGAAGTTCA	GCAGCAGCTC	GGTGGCGGTA	TCGTACGTAC	CATCGCCATG	100
	GGTTCTTCCG	ACGGCCTGCG	TCGTGGTCTG	GATGTGAAAG	ACCTTGAGCA	150
	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	GCTGGGTCGT	ATCATGAACG	200
55	TACTGGGCGA	ACCAGTAGAC	ATGAAAGGCG	AGATCGGTGA	AGAAGAGCGT	250
	TGGGCTATCC	ACCGTGCGGC	ACCGTCCTAC	GAAGAGTTGT	CAAACCTCTCA	300
	GGAAGTGTCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	TGCCCCGTTCTG	350
	CGAAGGGCGG	TAAAGTGGGT	CTGTTCCGGT	GTGCGGGTGT	AGGTAAAACC	400
	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAAC	ACTCCGGTTA	450
50	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	AACGACTTCT	500

	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	CCTGGTTTAC	550
	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	CGCTGACCGG	600
	CCTGACCATG	GCGGAGAAAT	TCCGTGACGA	AGGTCGTGAC	GTTCTGCTGT	650
	TCGTGACAA	CATCTACCGT	TACACCCTGG	CCGGTACGGA	AGTATCCGCA	700
5	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TACCAGCCGA	CCCTGGCGGA	750
	AGAGATGGGT	GTTTTGCAGG	AACGTATCAC	CTCCACCAAA	ACCGGTTCTA	800
	TCACCTCCGT	A				811

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2) INFORMATION FOR SEQ ID NO: 263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263

	GATGCCGTAC	CGCGCGTGTA	CGATGCTCTT	GAGGTTATGA	ATGGTAAAGA	50
	GAGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGCGGCGGT	ATCGTACGTA	100
	CCATCGCGAT	GGGTTCCTCC	GACGGTCTGC	GTCGTGGTCT	GGAAGTAAAA	150
30	GACCTCGAAC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCAA	CTCTGGGTCG	200
	TATCATGAAC	GTCCTGGGTC	ACCCGATCGA	CATGAAAGGC	GATATCGGTG	250
	AAGAAGAGCG	TTGGGCTATC	CACCGCGCAG	CGCCATCCTA	TGAAGAGCTG	300
	TCCAGCTCTC	AGGAACTGCT	GGAAACCGGT	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTCCGGT	GGTGCGGGTG	400
35	TAGGTAA AAC	CGTAAACATG	ATGGAACTCA	TCCGTAA CAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCCGTGTT	TGCGGGCGTA	GGTGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGATTC	CAACGTTCTG	GATAAAGTAT	550
	CCCTGGTATA	TGGCCAGATG	AACGAGCCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GTCTGACCAT	GGCAGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
40	CGTACTGCTG	TTCGTCGATA	ACATCTATCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCAT	CAGCGGTAGG	CTACCAGCCA	750
	ACCCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CTTCTACCAA	800
	AACCGGTTCT	ATTACC				816

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2) INFORMATION FOR SEQ ID NO: 264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264

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AGGATGCCGT ACCGCGCGTG TACGATGCTC TTGAGGTTAT GAATGGTAAA      50
GAGAGCCTGG TGCTGGAAGT TCAGCAGCAG CTCGGCGGCG GTATCGTACG      100
5  TACCATCGCC ATGGGTTCTT CTGACGGTCT GCGTCGTGGT CTGGAAGTTA      150
AAGACCTCGA GCACCCGATC GAAGTCCCGG TAGGTAAAGC AACGCTGGGT      200
CGTATCATGA ACGTTCTGGG TCACCCGATC GACATGAAAG GCGATATCGG      250
TGAAGAAGAG CGTTGGGCTA TCCACCGTGC AGCACCTTCC TACGAAGAGC      300
TGTC AAGCTC TCAGGAACTG CTGGAAACCG GTATCAAAGT TATCGACCTG      350
10 ATGTGTCCGT TCGCTAAGGG CGGTAAAGTT GGTCTGTTCG GTGGTGCGGG      400
TGTAGGTAAA ACCGTAAACA TGATGGAGCT GATCCGTAAC ATCGCGATCG      450
AACACTCCGG TTA CTCCGTG TTTGCGGGCG TAGGTGAACG TACTCGTGAG      500
GGTAACGACT TCTACCACGA AATGACCGAC TCCAACGTTT TGGACAAAGT      550
ATCCCTGGTA TATGGCCAGA TGAACGAGCC GCCTGGAAAC CGTCTGCGTG      600
15 TTGCGCTGAC CGGTCTGACC ATGGCTGAGA AGTTCCGTGA CGAAGGTCGT      650
GACGTTCTGC TGTTCGTTGA TAACATCTAT CGTTACACCC TGGCCGGTAC      700
AGAAGTATCT GCACTGCTGG GTCGTATGCC ATCAGCGGTA GGCTACCAGC      750
CGACCCTGGC GGAAGAGATG GGTGTTCTGC AGGAACGTAT CACCTCCACC      800
AAAACCGGTT CTATCACCT                                     819

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2) INFORMATION FOR SEQ ID NO: 265

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 35 (B) STRAIN: ATCC 27028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265

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GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTGCAGA ATGGTAATGA      50
40 ACATCTGGTG CTGGAAGTTC AGCAGCAGCT CCGTGCGCGT ATCGTACGTA      100
CCATCGCCAT GGGTTCTTCC GACGGCCTGC GTCGTGGTCT GGATGTGAAA      150
GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAGCAA CGCTGGGTCG      200
TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GAGATCGGTG      250
AAGAAGAGCG TTGGGCTATC CACCGTGCGG CACCGTCCTA CGAAGAGTTG      300
45 TCAAACCTCT AGGAACTGTT GGAAACCGGT ATCAAAGTTA TCGACCTGAT      350
GTGTCCGTTT GCGAAGGGCG GTAAAGTGGG TCTGTTTCGGT GGTGCGGGTG      400
TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAA      450
CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG      500
TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT      550
50 CCTTGGTTTA CGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT      600
GCGCTGACCG GCCTGACCAT GCGGAGAAA TTCCGTGACG AAGGTCGTGA      650
CGTTCTGCTG TTCGTCGACA ACATCTACCG TTACACCCTG GCCGGTACGG      700
AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTACCAGCCG      750
ACCCTGGCGG AAGAGATGGG TGTTTTGCAG GAACGTATCA CCTCCACCAA      800
55 AACCGGTTCT ATCACCTCCG TA                                     822

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2) INFORMATION FOR SEQ ID NO: 266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266

15	GATGCCGTAC	CGCGCGTGTA	CGACGCCCTT	GAGGTACAGA	ATGGTAATGA	50
	GCGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGTGGCGGT	ATTGTACGTA	100
	CCATCGCCAT	GGGTTCTTCC	GACGGTCTGC	GTCGTGGTCT	GGAAGTAAAA	150
	GACCTTGAGC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCAA	CGCTGGGTCG	200
	TATCATGAAC	GTACTGGGCG	AACCAGTAGA	CATGAAAGGC	GACATCGGTG	250
20	AAGAAGAGCG	TTGGGCTATC	CACCGTGCCG	CGCCGTCCTA	TGAAGAGTTG	300
	TCTAACTCTC	AGGAACTGCT	GGAAACCGGC	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTCCGT	GGTGCGGGCG	400
	TAGGTAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
25	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	GACAAAGTAT	550
	CCCTGGTGTA	CGGCCAGATG	AACGAGCCGC	CTGGAAACCG	TCTGCGCGTC	600
	GCACTGACCG	GTCTGACCAT	GGCTGAGAAG	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGCTG	TTCGTCGATA	ACATCTATCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTAGG	TTATCAGCCG	750
30	ACTCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CCTCAACCAA	800
	AACCGGTTCT	ATCACCTCCG				820

35 2) INFORMATION FOR SEQ ID NO: 267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267

50	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTTATGAATG	GTAAAGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACCA	100
	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACCC	TGGGTCGTAT	200
55	CATGAACGTC	CTGGGTCATC	CGATCGACAT	GAAAGGCGAT	ATCGGTGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCAGCAC	CTACCTATGA	AGAACTGTCC	300
	AGTTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGG	AAGGGCGGTA	AAGTTGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAACAC	450
50	TCCGGTTACT	CAGTGTTTGC	GGGCGTTGGT	GAACGTACTC	GTGAGGGTAA	500

	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACCATGGC	TGAGAAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTC	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
5	TATCTGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCAACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACCT	CTACCAAAC	800
	CGGTTC					806

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2) INFORMATION FOR SEQ ID NO: 268

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 810 bases
15	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Citrobacter youngae</i>
	(B)	STRAIN: ATCC 29935

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268

	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTTATGAATG	GTAAAGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACCA	100
	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
30	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTT	CTGGGTCACC	CGATCGACAT	GAAAGGCGAT	ATCGGAGAAG	250
	AAGAGCGTTG	GGCTATTCAC	CGCGCAGCAC	CTTCCTATGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCT	AAGGGCGGTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
35	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGTGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGATTCCAA	CGTTCTGGAT	AAAGTATCCC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
40	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACTT	CTACCAAAC	800
	CGGTTCTATC					810

45

2) INFORMATION FOR SEQ ID NO: 269

(i) SEQUENCE CHARACTERISTICS:

50	(A)	LENGTH: 827 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Clostridium innocuum</i>
	(B)	STRAIN: ATCC 14501

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269

```

5  TTGAGAACGG AGATTTGCCG CAGCTATTGA CCGCTATTGA AATTCCTCTG      50
   AAAGACAGTG AATCTCTGAT TGTCTGAAGTT GCTCAGCATA TCGGTGATGA      100
   ACGTGTCCGC TGTATCGCTA TGGGCGGTAC AGATGGTCTG GTTCGTGGAA      150
   TGGAAGCCAT TGATACAGGA TCCGCAATCC GTGTACCGGT GGGAAAAGAA      200
   ATTCTGGGAA GAATGTTCAA TGTCTCGGA CGTGAAATTG ATGGTCTGGG      250
   ACCTGTAGGA ACGGATAACA CACTGCCGAT CCACAGACAG GCACCGGGCT      300
   TTGAGGAGCA GCAGACATCC GCAGAAATGC TGGAAACAGG AATTAAGGTC      350
10 ATTGACCTGT TATGTCCATA TTCCAAGGGT GGTAAGATTG GTTTGTTTGG      400
   TGGTGCGGGA GTAGGTAAAA CCGTACTGAT TCAGGAGCTG ATTCATAATA      450
   TCGCCAAGGA ACATGGTGGA ATGTCCGTCG TTACCGGTGT AGGGGAGAGA      500
   ACCCGTGAAG GAAACGACAT GTATCATGAA ATGAAGGACA GCGGTGTCCT      550
   TGATAAGACC GTACTGGTTT ACGGACAGAT GAATGAATCA CCGGGTGCCA      600
15 GAATGCGTGT CCGTCTGACC GGGCTGACGA TGGCGGAATA TTTCCGTGAT      650
   CACGACCATC AGGATGTATT GCTGTTTATT GATAATATTT TCCGTTTTAC      700
   CCAGGCGGGA AGTGAAGTAA GTGCCCTGCT GGGACGTATG CCAAGTGCAG      750
   TAGGCTATCA GCCGACACTT GCGACAGAAA TGGGACAGCT GCAGGAGCGC      800
   ATTACATCCA CGAAGGATGG TTCCATT                                827
20

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2) INFORMATION FOR SEQ ID NO: 270

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25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 829 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30
    (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Clostridium perfringens
35        (B) STRAIN: ATCC 13124

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270

```

40 GCAAATGATG AACTTCCTAA TATATTTAAT GCAATACACA TAAAAATGGA      50
   CGATGGAAAA ATCTTAGTTT GTGAGGTAGA GCAACACGTA GGAGACGATA      100
   TAGTTAGAAC TATAGCTATG GAAGCTACTG AAGGACTAAG AAGAGGTGTA      150
   GAAGCTGTTG ATACAGGAGC ACCTATATCA GTACCAGTTG GTGAATGCGT      200
   ATTAGGAAGA ATATTTAACG TATTAGGTAA ACCACTAGAT AGTGGAGCTG      250
   AAGTTAATAA CGAAGAAAAA TATCCAATTC ATAGACCAGC TCCATCATTT      300
45 GAAGAACAAT CAGTTGTTCC TCAAATGTTT GAGACAGGAA TAAAGGTTAT      350
   CGACCTTTTA GCACCTTACC AAAGAGGGGG AAAAATCGGT CTATTTGGAG      400
   GTGCAGGTGT TGGTAAAACA GTTCTTATCC AAGAGCTTAT AAACAACATA      450
   GCTAAAGAGC ACGGTGGACT TTCTGTATTC ACAGGAGTTG GAGAAAGATC      500
   AAGAGAAGGT AATGACCTTT ACTATGAAAT GATGGAATCA GGAGTTATAA      550
50 AAAATACAGC ATTAGTATTT GGACAAATGA ACGAACCACC TGGAGCAAGA      600
   ATGAGAGTTG CTTTAACAGG ACTTACTATG GCTGAGTACT TCAGAGACCA      650
   AGGTCAAGAC GTGTTATTAT TCATAGATAA CATATTCAGA TTCTCACAAG      700
   CTGGATCAGA GGTTTCAGCT TTATTAGGAA GAATACCATC AGCTGTTGGT      750
   TACCAACCAA CTCTTGCTAC AGAGATGGGA GCTCTTCAAG AGAGAATCAC      800
55 ATCAACTACC CATGGATCAA TTACATCAG                                829

```

2) INFORMATION FOR SEQ ID NO: 271

50

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271

10

TTGTCCACGT TGGATRTCTT CA

22

15 2) INFORMATION FOR SEQ ID NO: 272

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272

30

CCCGCGTGGC	GAGCTGCCGG	CACTGTACAA	CGCGTTGACT	GTCGAGGTCA	50
CCCTCGAGGC	AGTCGCTAAG	ACCATTACCC	TTGAGGTTGC	CCAGCACTTG	100
GGCGACAACC	TCGTTGCGCG	CGTGTCCATG	GCCCCTACCG	ACGGCCTCGT	150
CCGTGGTGCT	GTTGTGACCG	ACTCGGGCAA	GCCAATCTCC	GTGCCAGTTG	200
35 GCGACGTTGT	TAAAGGCCAC	GTTTTCAACG	CACTGGGCGA	TTGCTTGGAT	250
GAGCCAGGTC	TCGGCCGCGA	TGGTGAGCAG	TGGGGAATTC	ACCGCGATCC	300
ACCACCATTC	GATCAGCTCG	AAGGTAAGAC	CGAAATCCTC	GAGACCGGTA	350
TTAAGGTCAT	CGACTTGCTC	ACCCCTTACG	TTAAGGGCGG	CAAGATTGGT	400
CTGTTTCGGTG	GTGCAGGTGT	GGGTAAGACC	GTGCTCATCC	AGGAGATGAT	450
40 CACTCGTATT	GCTCGCGAGT	TCTCCGGTAC	CTCCGTCTTC	GCTGGCGTTG	500
GTGAGCGTAC	CCGTGAGGGC	ACCGACCTCT	TCCTCGAAAT	GGAAGAAATG	550
GGCGTTCTTC	AGGACACCGC	TCTCGTGTTT	GGCCAGATGG	ACGAGCCACC	600
AGGAGTCCGT	ATGCGCGTTG	CTCTGTCCGG	TCTGACCATG	GCGGAGTACT	650
TCCGCGATGT	TCAGCACCAG	GACGTGCTTC	TGTTTCATCGA	TAACATTTTC	700
45 CGTTTCACCC	AGGCCGGTTC	CGAGGTTTCG	ACCCTTCTTG	GTCGTATGCC	750
TTCCGCCGTG	GGTTACCAGC	CAACCTTGGC	TGACGAGATG	GGTGTTCTCC	800
AGGAGCGTAT	TACCTCTA				818

50

2) INFORMATION FOR SEQ ID NO: 273

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273

	CGATGCCTGC	TCTGTACAAC	GCGCTGACTG	TCGAGGTCAC	CCTCGAGGCA	50
	GTCGCCAAGA	CCATCACGCT	TGAGGTTGCA	CAGCACCTCG	GCGATAACCT	100
	GATCCGGACC	ATTGCGTTGG	CACCTACGGA	CGGTCTCGTC	CGTGGCGCTG	150
10	AGGTTATCGA	CACTGGTAAG	CCAATTACTG	TTCCCGTCGG	CGATGCCGTC	200
	AAAGGACACG	TCTTCAATGC	GCTCGGTGAG	TGTTTGGACG	AACCAGGATT	250
	GGGCCGCGAC	GGCGAACAGT	GGGGAATCCA	CCGCGATCCG	CCACCATTCG	300
	ATGCGCTGGA	GGGCAAAACC	GAGATTCTGG	AGACTGGAAT	CAAGGTTATC	350
	GACCTCCTTA	CCCCTTACGT	TAAGGGTGGC	AAAATTGGTC	TGTTCGGTGG	400
15	CGCCGGCGTC	GGCAAGACCG	TTCTTATCCA	GGAAATGATC	ACTCGTATCG	450
	CTCGTAACTT	CTCCGGTACT	TCCGTGTTCC	CCGGCGTCGG	TGAGCGTACC	500
	CGTGAGGGTA	CTGACCTGTT	CCTGGAAATG	GAAGAGATGG	GCGTGTTGCA	550
	AGACACCGCC	CTTGTCTTCG	GTCAAATGGA	CGAACCACCA	GGGGTTCGTA	600
	TGCGCGTGGC	CTTGTCTGGT	CTAACCATGG	CTGAATATTT	CCGCGACGTT	650
20	CAAAACCAGG	ACGTTTTGTT	GTTTATTGAC	AACATCTTCC	GTTTTACTCA	700
	GGCAGGTTCC	GAGGTTTCCA	CGCTGTTGGG	CCGTATGCCT	TCCGCCGTGG	750
	GTTATCAGCC	AACATTGGCT	GATGAGATGG	GTGTTTTGCA	GGAACGGATT	800
	ACCTCTACAC	GTGGTAAGTC	AATTACTTCC	CTG		833

25

2) INFORMATION FOR SEQ ID NO: 274

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 417 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
 (B) STRAIN: NCTC 8665

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274

	CCGTGCTCAT	CCAGGAGATG	ATCACCCGTG	TGGCCCGCAA	CTTCGGCGGC	50
	ACCTCTGTGT	TCGCCGGCGT	CGGCGAGCGC	ACCCGTGAGG	GCAACGACCT	100
15	CTGGGTCGAG	ATGGACGAGG	CCGACGTGCT	CAAGGACACC	GCCCTGGTGT	150
	TCGGCCAGAT	GGACGAGCCG	CCGGGAACCC	GTCTGCGCGT	GGCCCTGTCC	200
	GCGCTGACCA	TGGCGGAGTA	CTTCCGCGAT	GTGCAGAACC	AGGACGTGCT	250
	GCTGTTCATC	GACAACATCT	TCCGCTTCTC	CCAGGCCGGC	TCCGAGGTCT	300
	CCACCCTGCT	GGGCCGCATG	CCCTCCGCGG	TGGGCTACCA	GCCGAACCTG	350
50	GCGGACGAGA	TGGGTGTGCT	GCAGGAGCGC	ATCACCTCGA	CTCGCGGCCA	400
	CTCCATCACC	TCGATGC				417

55 2) INFORMATION FOR SEQ ID NO: 275

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium urealyticum*

(B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275

10 GGCAGCAGC CAGCACTATT CAACGCGCTG CACGTCGAGG TTGACCTCGA 50
 GGCAGTTGCG AAGACCATTA CCCTGGAGGT CGCACAGCAC CTGGGTGACA 100
 ACCTGGTGCG CACCGTCTCC ATGGCCCCGA CCGACGGCCT GGTCCGCGGT 150
 GCAGAGGTCA AGGACACCGG TAAGCCGATC TCTGTGCCAG TCGGCGATGT 200
 15 TGTCAAGGGG CACGTCTTCA ACGCCCTGGG CGACTGCCTG GATGAGCCAG 250
 GTCTCGGCCG CGACGGCGAG CAGTGGGGCA TCCACCGCGA GCCACCGGCA 300
 TTCGACGAGC TCGAGGGTAA GACCGAGATC CTGGAGACCG GCGTTAAGGT 350
 CATCGACCTG CTGACCCCTT ACGTCAAGGG CGGCAAGATT GGCCTCTTCG 400
 GTGGTGCAGG TGTGGGTAAG ACCGTCCTGA TTCAGGAGAT GATTACCCGT 450
 20 ATCGCCCGCG AGTTCTCCGG TACCTCCGTG TTCGCCGGCG TCGGCGAGCG 500
 TACCCGTGAG GGTACGGACC TCTTCCTCGA GATGGAGGAG ATGGGCGTGC 550
 TCCAGGACAC CGCGCTGGTG TTCGGTCAGA TGGATGAGCC GCCGGGAGTC 600
 CGTATGCGCG TGGCTCTGTC CGGTCTGACC ATGGCGGAGT ACTTCCGCGA 650
 TGTTCAAGGC CAGGACGTGC TGCTGTTCAT CGACAACATC TTCCGTTTCA 700
 25 CCCAGGCAGG TTCTGAGGTC TCCACGCTGC TCGGCCGCAT GCCGTCCGCA 750
 GTGGGTTACC AGCCGACCCT GGCTGACGAG ATGGGTGTTC TGCAGGAGCG 800
 CATTACCTCC ACGAAGGGTA AGTCCATTAC CTCCC 835

30

2) INFORMATION FOR SEQ ID NO: 276

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coxiella burnetii*

(B) STRAIN: Nine Mile phase II

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276

CCCGTCACGC TGTCCCGAAA GTGTACGATG CTTTGCAGGT GGATGAAAAT 50
 AATTTAACGC TCGAAGTCCA ACAGCAACTC GGGGACGGTG TCGTGCGCAC 100
 AATTGCCATG GGCAGCACTG AGGGCTTAAA ACGCGATATC GCCGTAAAAA 150
 50 ATACGGAAAA ACCGATTGAA GTTCCCGTAG GAAAAGAAAC TTTAGGTCGT 200
 ATCATGAACG TGCTGGGTGA GCCGATCGAT GAGTTAGGTC CCATTAATTC 250
 AAAAGAAAAA CTCCCTATTC ATCGTCCTGC GCCGAGCTTT ATTGAGCAAT 300
 CTGGCGCTAC CGAATTATTA GAAACCGGTA TTAAAGTGGT CGATTTGCTT 350
 TGCCCCTTTG CTAAGGGAGG CAAAGTGGGT CTTTTTGGAG GCGCGGGCGT 400
 55 TGGA AAAACG GTTAATATGA TGGAATTAAT CCGTAATATC GCCATTGAAC 450
 ACAGCGGTTA TTCTGTTTTT GCGGGTGTGG GAGAAAGAAC GCGAGAAGGC 500
 AATGATTTTT ATCATGAAAT GAAAGAATCC AATGTCTTGG ATAAAGTGGC 550
 GTTGGTGTAC GGACAAATGA ACGAGCCGCC AGGGAACCGC TTGCGGGTGG 600
 GTTTGACGGG GCTTACGCTG GCGGAAGCCT TCCGTGACGA AGGACGCGAC 650
 50 GTTCTGTTAT TTATCGATAA TATCTTTCGT TACACTTTGG CAGGGGTTGA 700

AGTCTCTGCC	CTCCTCGGTC	GGATGCCATC	GGCTGTGGGT	TATCAGCCGA	750
CGTTGGCCGA	AGAGATGGGG	GCCCTGCAAG	AACGCATTAC	TTCCACTAAA	800
AAAGGGTCCA	TTACGTCG				818

5

2) INFORMATION FOR SEQ ID NO: 277

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 (B) STRAIN: ATCC 33379

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277

TTCCCGCAGG	ACGCCGTGCC	GAAGGTGTAT	AACGCACTGG	AAGTAAAAGG	50
CGGTGCCACG	AAACTGGTAC	TGGAAGTGCA	GCAGCAGCTG	GGTGGCGGCG	100
25 TAGTTCGCTG	CATCGCGATG	GGCTCTTCCG	ACGGTCTGCG	CCGTGGGCTA	150
GAGGTTGAAG	ACCAAGACCA	TCCGATCGAG	GTTCTGTGTG	GCAAGGCGAC	200
TCTGGGCCGT	ATCATGAACG	TACTGGGTGA	TCCGGTCGAC	ATGAAGGGCG	250
AGATCGGTGA	AGAAGAGCGT	TGGGCTATCC	ATCGTGCTGC	ACCGAGCTAT	300
GAAGATCTGT	CTAACTCTCA	GGAAGTGTG	GAGACCGGCA	TTAAGGTTAT	350
30 CGACCTGATT	TGCCCCGTTCG	CTAAAGGCGG	TAAAGTGGGC	CTGTTCCGGT	400
GGGCCGGTGT	GGGTAAGACC	GTTAACATGA	TGGAGCTTAT	CCGTAACATC	450
GCTATCGAGC	ACTCCGGTTA	CTCAGTCTTC	GCCGGTGTGG	GTGAGCGTAC	500
CCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GACCGATTCC	AACGTATTGG	550
ATAAAGTTTC	TCTGGTGTAT	GGTCAGATGA	ACGAGCCACC	GGGAAACCGT	600
35 CTGCGCGTGG	CGCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGATGA	650
AGGTCGTGAT	GTACTGTTGT	TCATCGATAA	CATCTACCGT	TATACCTTGG	700
CCGGTACTGA	AGTCTCCGCT	CTGCTGGGCC	GTATGCCGTC	GGCGGTAGGT	750
TATCAGCCGA	CTCTGGCGGA	GGAAATGGGG	GTGCTGCAAG	AGCGTATTAC	800
CTCCACTAAG	ACCGGGTCCA	TCACCTCTG			829

40

2) INFORMATION FOR SEQ ID NO: 278

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*
 55 (B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278

GCCGTGCCGA	AGGTGTATAA	CGCACTGGAA	GTAAAAGGCG	GTGCCACGAA	50
50 ACTGGTACTG	GAAGTGCAGC	AGCAGCTGGG	TGGCGGCGTC	GTTCGCTGCA	100

	TCGCGATGGG	CTCCTCCGAC	GGTCTGCGCC	GTGGGCTGGT	GGTTGAAGAC	150
	CAAGACCATC	CGATCGAGGT	TCCGGTCGGT	AAGGCGACCC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGATC	CGGTCGACAT	GAAGGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCGC	CGAGCTATGA	AGATCTGTCC	300
5	AACTCTCAGG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	CCCGTTTCGCC	AAAGGCGGTA	AAGTTGGCCT	GTTCGGTGGT	GCCGGTGTGG	400
	GTAAGACCGT	TAACATGATG	GAGCTTATCC	GTAACATCGC	TATCGAGCAC	450
	TCCGGTTACT	CCGTATTTGC	CGGTGTAGGC	GAGCGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAGATGA	CCGACTCCAA	CGTATTGGAT	AAAGTTTCTC	550
10	TGGTATACGG	CCAGATGAAT	GAGCCGCCGG	GAAACCGTCT	GCGTGTGGCG	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGCGATGT	650
	GTTGTTGTTC	ATCGATAACA	TTTATCGTTA	TACCTTGGCT	GGTACCGAAG	700
	TTTCTGCTCT	GCTGGGTCGT	ATGCCGTCGG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	GTTGCAAGAG	CGTATCACCT	CAACGAAGAC	800
15	GGGCTCTAT					809

2) INFORMATION FOR SEQ ID NO: 279

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279

35	TTTCCGCGTA	CCGCCATTCC	GCGTGTTTAC	GATGCACTCA	AACTGGTTGA	50
	TACTGATTTG	ACGCTGGAAG	TACAGCAGCA	GCTTGGTGAC	GGCGTTGTCC	100
	GTACCATTGC	GATGGGTAAG	ACAGACGGTT	TGAAACGTGG	CTTGGCTGTG	150
	CAAAATACTG	GTGCACCGAT	TACTGTGCCG	GTGGGGAAAG	CCACCCTAGG	200
	CCGCATCATG	GACGTTCTGG	GCAACCCCGT	GGACGAACAA	GGTCCGATCG	250
40	GTTCTGACCA	AACCCGTGCT	ATTCATCAAT	TTGCACCTAA	GTTTCGACGAA	300
	CTCTCCAGCA	CTACCGAATT	GTTGGAAACA	GGCATTAAAG	TGATCGATTT	350
	GCTTTGTCCG	TTTGCTAAAG	GTGGTAAAGT	GGGTCTGTTT	GGCGGTGCCG	400
	GTGTGGGCAA	AACCGTGAAC	ATGATGGAGC	TGATTAACAA	CATTGCCAAA	450
	GCGCACAGTG	GTCTTTCCGT	ATTCGCCGGT	GTGGGTGAGC	GTACTCGTGA	500
45	AGGTAACGAC	TTCTACCACG	AAATGAAAGA	CTCCAACGTG	TTGGATAAAG	550
	TGGCAATGGT	GTATGGCCAG	ATGAACGAGC	CGCCTGGTAA	CCGCTTGCGT	600
	GTTGCTCTAA	CTGGTTTGTC	GATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	650
	CGAAAACGGC	AAAGGCCGTG	ACGTATTATT	CTTTGTGGAT	AATATCTACC	700
	GCTATACTCT	GGCGGGTACC	GAAGTGTCGG	CTCTGCTTGG	CCGTATGCCT	750
50	TCTGCTGTGG	GTTATCAGCC	AACTTTGGCT	GAAGAAATGG	GTCGTTTGCA	800
	GGAGCGTATT	ACCTCCACCC	AAACTGGTTC	CATTACCTCT		840

55 2) INFORMATION FOR SEQ ID NO: 280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter agglomerans*

(B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280

10
 GCCGTACCAC GAGTGTACGA TGCACTTGAG GTAAAGAATG GTGAAGAGCG 50
 TCTGGTGCTG GAAGTTCAGC AACAGCTCGG CGGTGGCGTT GTACGTACCA 100
 TCGCAATGGG TTCTTCTGAT GGTCTGCGTC GTGGTCTGGA AGTAACGGAC 150
 CTGGCTCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
 15 CATGAACGTA CTGGGCGAAC CAGTAGACAT GAAAGGCGAC ATCGGTGAAG 250
 AAGAGCGTTG GGCGATCCAC CGTGCAGCAC CGTCCTACGA AGAGTTGTCA 300
 AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTTCGCT AAGGGCGGTA AAGTGGGTCT GTTCGGTGGT GCGGGTGTAG 400
 GTAAAACCGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC 450
 20 TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAC AAAGTATCCC 550
 TGGTGTATGG TCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG 600
 CTGACCGGTC TGACCATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
 ACTGTTGTTC GTTGACAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700
 25 TATCCGCACT GCTGGGCCGT ATGCCTTCTG CGGTAGGTTA TCAGCCGACG 750
 CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAC 800
 CGG 803

30

2) INFORMATION FOR SEQ ID NO: 281

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter amnigenus*

(B) STRAIN: ATCC 33072

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281

CGAATTCCCT CAGGATGCCG TACCGCGCGT GTACGATGCT CTTGAGGTAC 50
 AGAATGGTAA CGAGAGTCTG GTGCTGGAAG TTCAGCAGCA GCTCGGTGGT 100
 GGTATCGTAC GTACTATCGC CATGGGTTCT TCCGACGGTC TCGTCTGTGG 150
 50 TCTGGCTGTT AAAGATCTCG AACACCCGAT CGAAGTCCCG GTAGGTAAAG 200
 CAACACTGGG TCGTATCATG AACGTTTTGG GTCAACCAAT CGACATGAAA 250
 GGCGACATCG GTGAAGAAGA CCGTTGGGCA ATCCACCGTG CAGCACCTTC 300
 CTATGAAGAG CTGTCTAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG 350
 TTATCGACCT GATGTGTCCG TTCGCTAAGG GCGGTAAAGT TGGTCTGTTC 400
 55 GGCGGTGCGG GCGTGGGTAA AACTGTAAAC ATGATGGAGC TGATCCGTAA 450
 CATCGCGATC GAGCACTCCG GTTACTCCGT GTTTGCAGGC GTGGGTGAGC 500
 GTACTCGTGA GGGTAACGAC TTCTACCACG AAATGACCGA TTCCAACGTT 550
 CTGGATAAAG TATCCCTGGT TTATGGCCAG ATGAACGAGC CACCAGGAAA 600
 CCGTCTGCGC GTTGCGCTGA CCGGTCTGAC TATGGCTGAG AAGTTCCGTG 650
 50 ACGAAGGTCG TGACGTACTG CTGTTCTGTAG ATAACATCTA CCGTTACACC 700

CTGGCCGGTA	CTGAAGTATC	TGCGCTGCTG	GGCCGTATGC	CTTCAGCGGT	750
AGGTTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	800
TCACTTCTAC	CAAACCGGT	TCTATCACCT	CCG		833

5

2) INFORMATION FOR SEQ ID NO: 282

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282

GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
25 TCGCGATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTCAAAGAC	150
CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
30 TCCGTTTCGG	AAGGGCGGTA	AAGTCCGTCT	GTTCCGGTGGT	GCGGGTGTG	400
GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
TCCGGTTACT	CCGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
35 CTGACCGGTC	TGACGATGGC	TGAGAAGTTC	CGTGATGAAG	GCCGTGACGT	650
TCTGCTGTTC	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	CCAGCCTACG	750
CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAC	800
CGGTTCTATC					810

40

2) INFORMATION FOR SEQ ID NO: 283

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283

GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTACAGAATG	GTAACGAGAG	50
60 CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACTA	100

	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTAAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTATT	CCGTGTTTGC	GGGCGTGGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTTGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACCGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CAACCAAAAC	800
15	CGGTTCTATC	A				811

2) INFORMATION FOR SEQ ID NO: 284

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284

35	GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
40	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTTCG	AAGGGCGGTA	AAGTTGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CCGTATTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
15	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACTGGTC	TGACGATGGC	TGAGAAGTTC	CGTGACGAAG	GCCGTGACGT	650
	TCTGCTGTTC	GTTGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
50	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAAC	800
	CGGTTCTATC	ACTTCCG				817

55 2) INFORMATION FOR SEQ ID NO: 285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter gergoviae*

(B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285

10 AATGAGAGCC TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATCGT 50
 GCGTACCATC GCAATGGGTT CTTCTGACGG TCTGCGTCGC GGTCTGGAAG 100
 TTAAAGATCT CGAACATCCG ATCGAAGTCC CGGTAGGTAA AGCGACCCTC 150
 GGCCGTATTA TGAACGTGCT GGGTCAGCCG GTTGATATGA AAGGCGATAT 200
 15 CGGCGAAGAA GAGCGTTGGG CGATCCACCG CGCTGCGCCG TCCTATGAAG 250
 AGCTCTCCAG CTCTCAGGAA CTGCTGGAAA CCGGTATCAA GGTAATGGAC 300
 CTGATTTGCC CGTTCGCGAA GGGCGGTAAA GTCGGTCTGT TCGGCGGTGC 350
 GGGCGTTGGT AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA 400
 TCGAGCACTC CGGCTACTCC GTGTTTGCGG GCGTGGGTGA ACGTACTCGT 450
 20 GAGGGTAACG ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGACAA 500
 AGTATCCCTG GTGTACGGCC AGATGAACGA GCCGCCGGGA AACCGTCTGC 550
 GCGTGGCGCT GACCGGTCTG ACCATGGCTG AGAAATTCCG TGACGAAGGT 600
 CGTGACGTTT TGCTGTTCGT CGATAACATC TACCGCTATA CCCTCGCCGG 650
 TACTGAAGTA TCCGCACTGC TGGGCCGTAT GCCTTCTGCA GTAGGTTACC 700
 25 AGCCGACGCT GGC GGAAGAG ATGGGTGTTT TGCAGGAACG TATCACCTCC 750
 ACCAAAACCG GTTCTA 766

30 2) INFORMATION FOR SEQ ID NO: 286

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter hormaechei*

(B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286

45 GCCGTACCAC GCGTGTACGA CGCGCTTGAG GTACAGAATG GTAACGAGAG 50
 CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA 100
 TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTGAAAGAC 150
 CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACGC TGGGTCGTAT 200
 50 CATGAACGTA TTGGGTCAGC CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250
 AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTACGA AGAGCTGTCC 300
 AGCTCTCAGG AACTGCTGGA AACC GG CATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTTGCG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
 GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
 55 TCCGGTTACT CCGTGTTTGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC 550
 TGGTTTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
 CTGACTGGCC TGACGATGGC TGAGAAGTTC CGTGACGAAG GCCGTGACGT 650
 TCTGCTGTTC GTCGATAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700
 50 TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTAA TCAGCCAACG 750

CTTGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CGACCAAAC 800
CGGTT 805

5

2) INFORMATION FOR SEQ ID NO: 287

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 791 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakasaki*
(B) STRAIN: ATCC 29544

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287

25 TACGACGCCC TTGAGGTAAC GAATGGTAAT GAGCGTCTGG TGCTGGAAGT 50
CCAGCAGCAG CTCGGCGGCG GTATCGTACG TACCATCGCG ATGGGCTCTT 100
CCGACGGTCT GCGTCGCGGT CTGCCTGTTG CAGACCTTGA GCACCCGATC 150
GAAGTGCCGG TAGGTAAAGC GACGCTGGGT CGTATCATGA ACGTCCTGGG 200
TCAGCCTATC GACATGAAAG GCGACATCGG CGAAGAAGAG CGTTGGGCGA 250
TTCATCGCGC GGCGCCGTCC TATGAAGAGC TGTCCAGCTC TCAGGAACTG 300
CTGGAAACCG GCATCAAAGT TATCGACCTG ATGTGTCCGT TCGCGAAGGG 350
CGGTAAAGTC GGTCTGTTTC GTGGTGCAGG TGTAGGTAAA ACCGTAAACA 400
30 TGATGGAGCT TATTCGTAAC ATCGCGATTG AGCACTCCGG TTA CTCCGTG 450
TTTGCGGGCG TGGGCGAACG TACCCGTGAA GGTAACGACT TCTACCACGA 500
AATGACCGAC TCCAACGTAC TGGATAAAGT ATCCCTGGTG TACGGCCAGA 550
TGAACGAGCC GCCGGGAAAC CGTCTGCGCG TTGCGCTGAC CGGCCTGACC 600
ATGGCTGAGA AATTCCGTGA CGAAGGTCGT GACGTTCTGC TGTTCGTCGA 650
35 CAACATCTAC CGTTACACCC TGGCCGGTAC TGAAGTATCC GCACTGCTGG 700
GCCGTATGCC TTCAGCGGTA GGTTATCAGC CGACCCTGGC GGAAGAGATG 750
GGTGTCTGTC AGGAGCGTAT CACCTCCACC AAAACCGGTT C 791

40

2) INFORMATION FOR SEQ ID NO: 288

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
(B) STRAIN: ATCC 14025

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288

60 TTTCTTTAGA TCAATCCTTA CCAGACATCA ACAATGCGTT GATTGTTTAC 50
AAAAAAGATA AAACAAAAGT TGTTCTTGAA GTTGCTTTGG AACTTGGTGA 100
TGGTGTTATC CGCACAATCG CTATGGAGGC TACTGATGGA TTGCAACGTG 150
GAATGGAAGT TGTCGATACT GGCAAATCAA TCTCCGTTCC TGTAGGTAAA 200

	GATACTCTAG	GTCGTGTGTT	TAACGTATTA	GGTGAAACGA	TTGATAAAGA	250
	AGCACCTTTT	CCAGAAGATG	CAGAAAGAAG	CGGCATTTCAT	AAAAAGGCGC	300
	CTGCTTTTGA	AGACCTTAGT	ACAAGTAACG	AGATTTTGGG	AACAGGGATC	350
	AAGGTTATCG	ACTTATTAGC	CCCTTATTTA	AAAGGTGGGA	AAGTCGGACT	400
5	ATTCGGTGGT	GCCGGTGTG	GTAAAACCGT	TTTGATCCAA	GAATTAATTC	450
	ATAATATCGC	CCAAGAACAC	GGTGGTATTT	CAGTGTTTAC	CGGTGTTGGG	500
	GAACGTACTC	GTGAAGGGAA	CGACCTTTAT	TATGAAATGA	AAGACTCTGG	550
	CGTTATTGAG	AAAACAGCCA	TGGTGTTTCG	ACAAATGAAC	GAGCCGCCTG	600
	GTGCACGTAT	GCGTGTTGCC	TTGACTGGTT	TGACATTAGC	TGAATATTTT	650
10	CGTGATGAAG	AAGGACAAGA	TGTGTTGCTA	TTTATTGACA	ACATCTTCCG	700
	CTTTACTCAA	GCCGGATCAG	AAGTTTCTGC	CTTATTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	GTATCAACCA	ACTTTGGCAA	CTGAAATGGG	GCAATTACAA	800
	GAACGAATCA	CTTCAACCAA	AAAAGGTTTC	ATCACTTCA		839

15

2) INFORMATION FOR SEQ ID NO: 289

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 847 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: ATCC 25788

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289

	TTCTCTCTAG	ACCAATCATT	ACCAGATATC	AACAATGCGT	TGATTGTTTA	50
	CAAAAAAGAT	GAGCAGAAAA	CAAAAGTTGT	GTTAGAAGCT	GCCTTAGAAC	100
35	TTGGCGACGG	CGTTATCCGT	ACGATTGCCA	TGGAATCAAC	AGATGGCTTA	150
	CAACGAGGAA	TGGAAGTAAT	CGATACAGGC	GCCTCCATTT	CTGTTCCAGT	200
	TGGGACAGAA	ACCTTAGGAC	GGGTGTTTAA	TGTCCTTAGGG	GACACCATCG	250
	ATTTAGAAGC	GCCGTTCCCT	GAAGAAGCAC	CCCGCAGTGG	GATTCACAAA	300
	AAAGCACCTG	ACTTTGATGA	ATTGTCAACA	AGTACGGAGA	TCCTTGAAAC	350
40	TGGGATCAAA	GTTATCGATT	TGTTAGCCCC	TTATTTAAAA	GGGGGGAAAG	400
	TTGGACTTTT	CGGTGGTGCC	GGTGTTGGTA	AAACCGTCTT	GATCCAAGAA	450
	TTGATCCACA	ACATCGCCCA	AGAGCATGGT	GGGATCTCTG	TCTTCACAGG	500
	TGTTGGTGAA	CGGACACGTG	AAGGAAATGA	CCTTTATAAT	GAAATGAAAG	550
	AATCTGGCGT	TATCGAAAAA	ACAGCCATGG	TGTTTGGACA	AATGAACGAA	600
45	CCACCAGGTG	CTCGGATGCG	GGTAGCCTTG	ACTGGTTTGA	CATTAGCCGA	650
	GTACTTCCGT	GATGTGGAAG	GACAAGACGT	GCTCTTGTTT	ATCGATAATA	700
	TCTTCCGCTT	CACTCAAGCA	GGTTCTGAAG	TATCTGCCTT	ACTAGGTCGG	750
	ATGCCGTCTG	CCGTTGGGTA	TCAGCCAACA	TTAGCAACTG	AGATGGGGCA	800
	ATTACAAGAA	CGGATCACAT	CGACGAAGAA	AGGTTCCGTT	ACGTCTA	847

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2) INFORMATION FOR SEQ ID NO: 290

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 845 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus durans*
 5 (B) STRAIN: ATCC 19432

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 290

	TTTCTTTAGA	CCAATCCTTA	CCAGATATCA	ACAACGCTTT	AGTTGTTTAT	50
10	AAAAATGATG	AGAAGAAATC	GAAAGTTGTT	CTTGAAACAG	CGCTAGAATT	100
	AGGTGACGGT	GTCATCCGTA	CAATCGCGAT	GGAATCAACA	GATGGTTTAC	150
	AACGCGGAAT	GGAAGTCATT	GATACAGAAA	AAGCAATTTC	TGTACCAGTG	200
	GGTAAAGAAA	CGTTAGGTCG	TGTATTCAAT	GTATTAGGAG	ATACGATCGA	250
	TTTATCTGCA	CCTTTCCCAG	AAGATGCAAA	ACGTAGCGAA	ATCCATAAAA	300
15	AAGCACCAAA	CTTTGATGAG	TTAAGTACAA	GTACTGAGAT	CCTTGAAACT	350
	GGGATCAAAG	TTATTGACTT	GCTTGCTCCT	TACTTAAAAG	GTGGGAAAGT	400
	TGGATTATTC	GGTGGTGCCG	GTGTAGGTAA	AACTGTATTG	ATCCAAGAAT	450
	TGATCCATAA	TATCGCTCAA	GAACACGGTG	GTATTTCTGT	ATTTACTGGT	500
	GTTGGTGAAC	GTACACGTGA	AGGTAATGAC	CTTTATTATG	AAATGAAAGA	550
20	TTCAGGAGTT	ATTGAAAAAA	CAGCCATGGT	GTTTGGTCAA	ATGAACGAAC	600
	CACCAGGTGC	ACGTATGCGT	GTTGCCTTGA	CTGGTTTGAC	GATTGCTGAA	650
	TACTTCCGTG	ATGTTGAAGG	GCAAGACGTG	CTATTGTTTA	TTGATAATAT	700
	TTTCCGTTTC	ACTCAAGCCG	G TTCAGAAGT	TTCTGCCCTA	TTAGGTCGTA	750
	TGCCTTCTGC	CGTTGGGTAC	CAACCAACGC	TAGCAACAGA	AATGGGTCAA	800
25	TTACAAGAAC	GGATCACTTC	AACGAAAAAA	GGTTCAATCA	CTTCA	845

2) INFORMATION FOR SEQ ID NO: 291

30

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

40 (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: ATCC 29212

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 291

45	TTAGATCAAT	CCTTACCCGA	TATTAACAAC	GCTTTAGTCG	TTTATAAAAA	50
	TGGCGAAGCA	AAACAAAAAG	TAGTACTTGA	AGTCGCTTTA	GAAGTAGGTG	100
	ATGGAGTGAT	TCGTTCTATC	GCCATGGAAT	CGACAGATGG	TTTACAACGT	150
	GGAATGGAAG	TTATCGATAC	AGGAAAATCA	ATTTCAGTTC	CTGTTGGTAA	200
	AGATACATTA	GGTCGTGTGT	TTAACGTTTT	AGGAGACACA	ATTGACTTAG	250
50	AAGCGCCATT	CCCTGCAGAT	GCTGAACGTA	GTGGGATTCA	TAAAAAAGCG	300
	CCAGCATTTG	ATGAATTAAG	TACCAGTAAT	GAAATTTTAG	AAACAGGGAT	350
	TAAAGTTATT	GACTTATTAG	CACCTTATCT	AAAAGGTGGT	AAAGTCGGAC	400
	TTTTCGGTGG	TGCCGGTGTT	GGTAAAACCG	TCTTAATTCA	AGAATTAATT	450
	CATAATATTG	CCCAAGAACA	TGGAGGGATT	TCCGTCTTTA	CTGGTGTGG	500
55	TGAACGGACA	CGTGAAGGGA	ACGATCTGTA	CTATGAAATG	AAAGATTTCAG	550
	GCGTTATTGA	AAAAACAGCC	ATGGTTTTTG	GTCAAATGAA	CGAACCGCCA	600
	GGTGCACGGA	TGCGTGTGGC	CTTAAC TGGG	TTAACGATTG	CTGAATATTT	650
	CCGTGATGTG	GAAGGACAAG	ACGTGCTATT	ATTTATTGAT	AACATTTTCC	700
	GTTTCACCCA	AGCCGGTTCA	GAAGTTTCTG	CCCTTTTAGG	TCGGATGCCG	750
60	TCAGCCGTTG	GTTACCAACC	AACCTTAGCG	ACTGAAATGG	GACAATTACA	800

AGAACGGATT ACTTCAACGA AAAAAGGATC AATTACCTCT

840

5 2) INFORMATION FOR SEQ ID NO: 292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292

20 TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCATT AGTTGTTTAT 50
 AAAAATGACG AAAATAAATC AAAAGTTGTT CTTGAAGCAG CGTTAGAATT 100
 AGGGGACGGA GTGATCCGGA CCATTGCGAT GGAATCAACA GATGGTTTAC 150
 AAAGAGGAAT GGAAGTCATT GATACAGGCA AAGCAATCTC TGTTCTGTGTA 200
 25 GGTAAAGAAA CATTAGGTCG CGTATTCAAC GTACTAGGAG ATACGATCGA 250
 TTTAGAAACA CCTTTCCCAG AAGATGCGGA AAGAAGCGAA ATTCATAAAA 300
 AAGCACCAGC CTTTGACGAA TTAAGTACAA GTACAGAAAT TTTGGAAACA 350
 GGGATCAAAG TTATCGATTT GCTTGCCCCA TATTTAAAAG GTGGGAAAGT 400
 CGGACTATTC GGTGGTGCCG GTGTTGGTAA AACCGTACTG ATCCAAGAAC 450
 30 TGATCCATAA TATCGCCCAA GAACATGGTG GTATTTCTGT ATTTACCGGT 500
 GTAGGTGAAC GTACTCGTGA AGGTAATGAC TTGTATTATG AAATGAAAGA 550
 TTCAGGAGTT ATCGAAAAAA CAGCCATGGT GTTCGGACAA ATGAACGAAC 600
 CACCAGGTGC ACGTATGCGT GTTGCTTTGA CTGGTTTGAC GATTGCGGAA 650
 TATTTCCGTG ATGTAGAAGG TCAAGATGTA CTGTTGTTTA TCGACAACAT 700
 35 TTTCCGTTTC ACTCAAGCTG GATCTGAAGT ATCAGCCTTG TTAGGACGGA 750
 TGCCTTCTGC GGTGTTGTTAT CAACCAACAT TGGCAACAGA AATGGGTCAA 800
 TTGCAAGAAC GTATCACATC TACGAAAAAA G 831

40

2) INFORMATION FOR SEQ ID NO: 293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: ATCC 49573

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293

CCTTACCAGA TATCAACAAT GCGTTGATCG TTTACAAAAA AGACGAGAAA 50
 AAAACAAAAG TAGTATTGGA AGCCGCTTTA GAACTAGGGG ATGGTGTGAT 100
 CCGCACCATC GCAATGGAAT CTACAGACGG TTTGCAACGA GGAATGGAAG 150
 60 TCATCGATAC CGGTGCCTCA ATCTCTGTCC CTGTAGGAAC AGATACTCTA 200

	GGCCGAGTAT	TTAATGTACT	AGGCGATACT	ATCGACTTGG	AAGCACCATT	250
	CCCAGAAGAT	GCCAAACGTA	GTGGCATCCA	CAAAAAAGCC	CCAGATTTCG	300
	ATGAATTGTC	AACAAGTACA	GAAATCCTTG	AAACTGGGAT	CAAAGTTATC	350
	GATTTATTAG	CTCCTTACTT	AAAAGGTGGT	AAAGTCGGCT	TGTTTCGGTG	400
5	TGCCGGTGTT	GGTAAAACCG	TATTGATTCA	AGAATTGATT	CACAATATCG	450
	CTCAAGAGCA	TGGGGGAATT	TCAGTATTTA	CCGGTGTTGG	CGAACGGACG	500
	CGTGAAGGTA	ATGACTTGTA	TTATGAAATG	AAAGAATCAG	GCGTTATCGA	550
	AAAGACAGCC	ATGGTTTTTCG	GTCAAATGAA	TGAACCACCA	GGTGCCCGGA	600
	TGCGGGTTGC	TTTGACTGGT	TTGACCATTG	CTGAGTATTT	CCGTGACGTT	650
10	GAAGGACAAG	ATGTGCTCTT	GTTTATCGAT	AATATTTTCC	GTTTCACACA	700
	AGCGGGTTCT	GAAGTATCTG	CCTTGTTAGG	CCGGATGCCA	TCAGCCGTTG	750
	GTTATCAACC	AACTCTAGCA	ACTGAAATGG	GTCAATTACA	AGAACGAATC	800
	ACTTCTACGA	AAAAAGGATC	TGTAAC			826

15

2) INFORMATION FOR SEQ ID NO: 294

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus saccharolyticus*
- (B) STRAIN: ATCC 43076

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294

	TTTCTTTGGA	CCAATCCTTA	CCAGACATCA	ACAATGCGTT	GGTGGTCTAT	50
	AAAAAGAATG	ATGAAAAAAC	AAAAGTGGTA	CTTGAAACAG	CTTTAGAACT	100
35	TGGTGATGGT	GTCGTACGTA	CGATTGCTAT	GTCGTCAACA	GACGGTTTGC	150
	AACGTGGGAT	GGAAGTCATC	GATACAGGAG	CATCAATTTT	TGTTCTCTGT	200
	GGGAAAGAGA	CATTAGGACG	TGTATTTAAC	GTTTTAGGGG	AGACTATCGA	250
	CTTAGATGGT	CCATTCCCAG	AAGAAGTAGC	ACGAGATGGT	ATTCATAAAA	300
	AGGCACCTGA	TTTTGATGAA	TTAAGTACAA	GTACGGAGAT	TCTTGAAACA	350
40	GGGATTAAAG	TAATCGATTT	ATTAGCGCCT	TACTTAAAAG	GTGGGAAAGT	400
	TGGTTTATTC	GGTGGTGCCG	GTGTAGGTAA	AACGGTATTA	ATTCAAGAAT	450
	TGATTAACAA	TATTGCGCAA	GAACATGGTG	GTATTTTCAGT	ATTTGCGGGT	500
	GTTGGTGAGC	GTA CTCGTGA	AGGAAATGAC	CTTTATTATG	AAATGAAAGA	550
	GTCGGGCGTT	ATTGAGAAAA	CAGCGATGGT	TTTTGGACAA	ATGAACGAAC	600
15	CACCAGGTGC	ACGTATGCGA	GTTGCTTTAA	CTGGTTTAAAC	CATTGCAGAA	650
	TACTTCCGTG	ATGTTGAAGG	ACAAGATGTA	TTACTATTTA	TTGATAACAT	700
	TTTCCGTTTT	ACTCAAGCTG	GTTCAGAAGT	TTCAGCTTTA	TTAGGACGTA	750
	TGCCTTCAGC	GGTAGGGTAT	CAACCGACAT	TAGCAACAGA	AATGGGACAA	800
	TTACAAGAAC	GTATTACGTC	AACGAAAAAA	GGCTCAATTA	CATCAA	846

50

2) INFORMATION FOR SEQ ID NO: 295

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*
 5 (B) STRAIN: ATCC 35469

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 295

	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTGCAAAATG	GTAATGAGCG	50
10	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGTGGTATC	GTGCGTACCA	100
	TCGCAATGGG	GTCCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCGACTC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGTGAAG	250
	AAGAGCGTTG	GGCGATTCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300
15	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCT	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAAAACGTG	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CTGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
20	TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTT	GTTGACAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTTCAGGAA	CGTATCACCT	CCACCAAAC	800
25	TGG					803

2) INFORMATION FOR SEQ ID NO: 296

30

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

40 (A) ORGANISM: *Escherichia hermannii*
 (B) STRAIN: ATCC 33650

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 296

45	GATGCCGTAC	CGCGCGTGTA	CGATGCTCTT	GAGGTGCAAA	ATGGTGATGA	50
	GCGTCTGGTG	CTGGAAGTGC	AGCAGCAGCT	CGGCGGCGGT	ATCGTGCGTA	100
	CCATCGCAAT	GGGTTCCTCC	GACGGTCTGC	GTCGTGGTCT	GACTGTCGTC	150
	GACCTCGAGC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCGA	CCCTGGGCCG	200
	TATCATGAAC	GTGCTGGGTC	AGCCGATCGA	CATGAAAGGC	GATATCGGTG	250
50	AAGAAGAGCG	TTGGGCGATT	CACCGCGCGG	CGCCGTCCTA	TGAAGAGCTG	300
	TCCAGCTCTC	AGGAACTGCT	GGAAACCGGC	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTC	GCGAAGGGCG	GTAAAGTCGG	TCTGTTCCGGT	GGTGCGGGCG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
55	TAACGACTTC	TACCATGAAA	TGACCGACTC	CAACGTTCTG	GACAAAGTAT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAACCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCACTGACCG	GCCTGACCAT	GGCTGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGTTG	TTCGTCGACA	ACATCTACCG	TTACACCCTG	GCCGGTACTG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CTGCGGTAGG	TTACCAGCCG	750
50	ACCCTGGCGG	AAGAGATGGG	CGTTCTGCAG	GAGCGTATCA	CCTCCACCAA	800

5 2) INFORMATION FOR SEQ ID NO: 297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
(B) STRAIN: ATCC 33821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297

20 CCGAACGTGT ACGACGCCCT CGAAGTGACA AATGGTAATG AGCGTCTGGT 50
GCTGGAAGTT CAGCAGCAGC TCGGCGGCGG TATCGTACGT ACCATCGCTA 100
TGGGTTCTTC CGACGGTCTG CGTCGTGGTC TGGAAGTTCA GGACCTCGAG 150
CACCCGATCG AAGTGCCGGT AGGTAAAGCG ACCCTGGGTC GTATCATGAA 200
25 CGTACTGGGT CAGCCGATCG ATATGAAAGG CGACATCGGT GAAGAAGAGC 250
GTTGGGCTAT TCACCGTGCA GCACCGTCCT ATGAAGAGCT CTCCAGCTCT 300
CAGGAACTGC TGGAAACCGG CATCAAGGTT ATCGACCTGA TGTGTCCGTT 350
CGCCAAGGGC GGTAAGTCG GCCTGTTCGG CGGCGCGGGC GTGGGTAAAA 400
CCGTAAACAT GATGGAGCTG ATCCGTAAAC TCGCGATCGA GCACTCCGGT 450
30 TACTCCGTGT TTGCAGGCGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT 500
CTACCACGAG ATGACCGACT CCAACGTTCT GGACAAAGTA TCCCTGGTGT 550
ACGGCCAGAT GAACGAGCCG CCGGGAACCC GTCTGCGCGT GGCCTGACC 600
GGCCTGACCA TGGCTGAGAA GTTCCGTGAC GAAGGTCGTG ACGTTCTGCT 650
GTTCGTTGAC AACATCTATC GTTACACCCT GGCCGGTACG GAAGTATCTG 700
35 CACTGCTGGG CCGTATGCCT TCAGCGGTAG GTTACCAGCC GACGCTGGCG 750
GAAGAGATGG GCGTTCTGCA GGAGCGTATC ACCTCCACCA AAACCGGTTC 800
TATCACCT 808

40 2) INFORMATION FOR SEQ ID NO: 298

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*
(B) STRAIN: ATCC 43055

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298

TTTCCCCCTG ATCAGCTGCC GCGGATTTAC AACGCGCTGA CGGTTGATGC 50
CAAGACCCTG GCGGGCGACT TGCACCTCGT GCTCGAGGTC GAGACGCACC 100
TGCCGGGCAA CCTTGTCGCG TCGGTGGCCA TGAGCTCGAC GGACGGTCTC 150
50 GTCCGCGGCC TCGAGGTCGT CGACACGGGC AACCCGATCA TGATGCCCGT 200

	GGGTCCCGAG	ACCCTGGGTC	GCATCTGGAA	CGTCATGGGC	GAGCCCGTGG	250
	ACGAGAAGCC	GATGCCCCGAG	GTGAAGGGCT	ACATGCCCCAT	CCACCGTCCG	300
	GCTCCGGACT	ACGACGAGCT	GTCCACCACC	ACCGAGATCT	TCGAGACCGG	350
	CATCAAGGCC	ATCGACCTCG	TCGAGCCCTT	CGTCAAGGGC	GGCAAGACGG	400
5	GTCTGTTCGG	CGGCGCCGGC	GTGGGCAAGA	CGGTTATCAT	CCAGGAGCTC	450
	ATCAACAACC	TGGCCCAGGA	GCACGGCGGC	ACGTCGGTGT	TCACGGGCGT	500
	GGGCGAGCGT	ACCCGCGAGG	GTACCGACCT	CTACCTGGAG	ATGAGCGACT	550
	CGGGCGTCAT	CAACAAGACC	TGCCTCGTGT	ACGGTCAGAT	GAACGAGCCT	600
	CCGGGAGCGC	GTCTGCGCGT	GGGTCTCGCG	GGCCTCACCG	AGGCGGAGTA	650
10	CTTCCGCGAT	CAGGGCCAGG	ACGTGCTTCT	GTTCTGTGGAC	AACATCTTCC	700
	GCTTCACGCA	GGCCGGCTCC	GAGGTGTCCG	CTCTGCTGGG	CCGCATGCCC	750
	TCTGCCGTGG	GTTACCAGCC	GACGCTGGCA	ACCGAGATGG	GCGACCTGCA	800
	GGAGCGCATC	ACGTCGACGT	CCACCGGCTC	CATCACGTCC	GTG	843

15

2) INFORMATION FOR SEQ ID NO: 299

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 829 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ewingella americana*

(B) STRAIN: ATCC 33852

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299

	TCCCTCAGGA	TGCAGTACCG	AACGTGTACA	ATGCTCTTGA	GGTAGAAAAC	50
	GGTGCCCTCCA	AACTGGTTCT	GGAAGTTCAG	CAACAGTTAG	GCGGCGGCGT	100
35	TGTTTCGTTGT	ATCGCAATGG	GTACCTCAGA	CGGCCTTCGT	CGCGGTCTGA	150
	AAGTGAACAA	CCTGGAACAC	CCAATTGAAG	TTCCGGTTGG	TAAAGCGACT	200
	CTGGGTTCGTA	TCATGAACGT	ATTGGGTGAA	CCAATCGACA	TGAAAGGTGA	250
	AATCGGCGAA	GAAGAACGTC	GTGCAATTCA	CCGTCCAGCG	CCTTCTTATG	300
	AAGAGCTGGC	TAACTCCCAA	GAATTGCTGG	AAACCGGTAT	CAAAGTTATG	350
40	GACCTGATGT	GTCCGTTCGC	TAAGGGCGGT	AAAGTCGGTC	TGTTTCGGTGG	400
	TGCGGGTGTT	GGTAAAACTG	TAAACATGAT	GGAGCTGATC	CGTAACATCG	450
	CGATCGAGCA	CTCCGGTTAC	TCAGTGTTTG	CAGGCGTGGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACTGACTCCA	ACGTTATCGA	550
	CAAAGTTTCC	CTGGTCTATG	GTCAGATGAA	TGAGCCACCA	GGTAACCGTC	600
45	TGCGCGTTGC	ACTGACCGGC	CTGACCATGG	CGGAGAAATT	CCGTGATGAA	650
	GGTCGTGACG	TACTGCTGTT	CGTTGACAAC	ATTTACCGTT	ACACCCTGGC	700
	AGGTACCGAA	GTGTCCGCAC	TTCTGGGCCG	TATGCCATCG	GCGGTAGGTT	750
	ATCAGCCAAC	GCTGGCGGAA	GAGATGGGTG	CTCTGCAAGA	GCGTATCACC	800
	TCTACCAAAA	GTGGTTCTAT	CACCTCCGT			829

50

2) INFORMATION FOR SEQ ID NO: 300

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

5 (A) ORGANISM: *Francisella tularensis*
(B) STRAIN: LVS

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 300

	AACACGCCTA	AAGTATATGA	TGCTTTAAAT	GTAGTAGAAG	CTGGTTTAGT	50
10	ATTAGAAGTT	CAGCAACAAA	TTGGTGATGG	CGTAGTTCGT	ACAATTGCTA	100
	TGGGATCTAG	TGATGGTCTT	AGACGTGGTA	TGGAAGTTAA	GAACACAAAT	150
	GCGCCTATTT	CTGTTCCAGT	TGGACATGGC	ACACTTGGAC	GTATCATGAA	200
	TGTTTTAGGT	GAACCAATTG	ATGAAGCTGG	TCCAATTGAA	TATACTGAGA	250
	AAAGATCTAT	CCATCAAGCT	CCTCCTGCAT	ATGATGAGTT	AGCATTAAGT	300
15	ACAGAAATAT	TAGAAACAGG	TATCAAAGTA	GTTGACCTTA	TTTGTCCATT	350
	TGCTAAGGGC	GGTAAAGTTG	GTTTATTTGG	CGGTGCAGGT	GTTGGTAAAA	400
	CTGTAACGAT	GATGGAACCT	ATCAACAATA	TTGCAAAAGA	ACATAGTGGC	450
	TACTCTGTAT	TTTCCGGTGT	TGGTGAAAGA	ACTCGTGAAG	GTAATGACTT	500
	CTACTATGAG	ATGAAATATT	CTAATGTATT	GGATAAAGTA	TCATTAGTAT	550
20	ATGGTCAGAT	GAATGAGCCG	CCTGGAAACA	GATTAAGAGT	AGCTCTTAGT	600
	GGCTTAACAA	TAGCAGAAGG	ATTCCGTGAT	GAAAAGCGTG	ATGTTTTGAT	650
	GTTTATCGAT	AACATCTATC	GTTATACATT	AGCAGGTACA	GAGGTATCGG	700
	CGCTACTTGG	TCGTATGCCA	TCTGCTGTGG	GTTATCAGCC	AACGCTTGCA	750
	GCTGAGATGG	GTGCTTTACA	GGAGCGTATT	ACATCTACTA	AGACAGGATC	800
25	TATTA					805

2)INFORMATION FOR SEQ ID NO: 301

30

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

40 (A) ORGANISM: *Fusobacterium gonidiaformans*
(B) STRAIN: ATCC 25563

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 301

45	GACGAATTGC	CAAAAATATA	CAATGCATTA	AAGGTGCAAG	TTGGAGAAAA	50
	AGAACTTGTA	TTGGAAGTGC	AACAACATTT	GGGAAATAAT	GTTGTGAGAA	100
	CAGTAGCGAT	GGACTCAACA	GATGGATTGC	TTCGAGGAAT	GGAAGTAATG	150
	GATACCGGAG	CACCGATTAC	TGTTCCAGTA	GGGAAGGCGG	TTTTAGGAAG	200
	AATATTGAAT	GTTTTGGGAG	AGCCTGTGGA	TCAAAAAGGG	CCTGTGGAAA	250
50	CAGAAGAATA	TTTACCTATC	CATAGAGAAG	CACCAAAATT	TGAAGAACAA	300
	GAAACAGTAA	CAGAAATTTT	TGAAACAGGA	ATTAAAGTCA	TAGATTTGTT	350
	AGCCCCCTTAT	ATCAAAGGAG	GAAAGACAGG	TCTATTTCGGT	GGAGCCGGAG	400
	TAGGGAAAAC	AGTTTTAATT	ATGGAATTAA	TTAATAACAT	TGCAAAGGGC	450
	CACGGAGGAA	TTTCTGTGTT	TGCAGGAGTT	GGAGAAAGAA	CAAGAGAAGG	500
55	AAGAGATTTA	TACAACGAAA	TGACAGAGTC	CGGAGTTTTG	AATAAGACCT	550
	CGTTGGTGTA	TGGTCAAATG	AATGAGCCGC	CCGGAGCAAG	ACTTCGTGTG	600
	GCGTTGACAG	GATTAACGGT	TGCTGAAAAC	TTTAGAGATA	AAGAAGGGCA	650
	AGATGTATTG	TTGTTTATCG	ACAATATCTT	CCGTTTCACA	CAAGCAGGAT	700
	CAGAAGTATC	GGCTCTATTG	GGAAGAATTC	CATCGGCAGT	AGGATATCAA	750
60	CCGAACCTAG	CGACAGAAAT	GGGAACCTTA	CAAGAAAGAA	TTACTTCTAC	800

5 2) INFORMATION FOR SEQ ID NO: 302

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fusobacterium necrophorum* subsp.
necrophorum
(B) STRAIN: ATCC 25286

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302

ACAATGCATT	AAAGGTACAG	GTGGGAGAAA	GGGAACTTGT	GTTGGAAGTG	50
CAGCAACATT	TAGGAAATAA	TGTTGTCAGA	ACAGTAGCAA	TGGATTCAAC	100
AGACGGATTA	CTTCGGGGAA	TGGAAGTGAG	AGATACAGGA	GTTCCCATTA	150
25 CTGTTCCGGT	AGGAAAGGCG	GTTTTGGGAA	GAATATTAAA	TGTCTTAGGG	200
GAGCCTGTGG	ACGAAAAAGG	TCCGATAGAG	ACAGAAGAAT	ATTTACCAAT	250
ACATAGAGAA	GCACCGAAAT	TTGAAGAACA	GGAAACGGTG	ACAGAAATTT	300
TTGAAACAGG	AATTAAAGTC	ATTGATTTGT	TAGCTCCTTA	TATTAAAGGA	350
GGAAAAACAG	GCCTATTCGG	AGGAGCCGGA	GTAGGAAAAA	CCGTTTTGAT	400
30 TATGGAAGTG	ATCAATAATA	TTGCAAAAGG	TCATGGAGGA	ATTTCTGTTT	450
TTGCAGGAGT	TGGAGAAAGA	ACGAGAGAGG	GAAGAGATCT	ATACAACGAA	500
ATGACAGAGT	CCGGAGTTTT	GAATAAAACT	TCTTTGGTAT	ATGGGCAAAT	550
GAATGAGCCG	CCCGGAGCAA	GACTTCGAGT	GGCTTTAACC	GGACTIONT	600
TTGCCGAAAA	TTTCAGAGAT	AAAGAGGGAC	AGGATGTCTT	ATTGTTTATT	650
35 GACAATATTT	TCCGTTTCAC	ACAAGCAGGT	TCGGAAGTAT	CGGCACTTTT	700
GGGGAGAATT	CCTTCTGCAG	TGGGATATCA	ACCGAAGTTG	GCGACAGAAA	750
TGGGAAGCTT	ACAAGAAAGA	ATTACTTCTA	CAAAATCCGG	TTCTATCACT	800
TCCGTG					806

40

2) INFORMATION FOR SEQ ID NO: 303

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
(B) STRAIN: ATCC 10953

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303

GATGAATTGC	CTGCAATATA	TAATGCTTTA	AAAGTAAAAT	TAGAAGATAA	50
GGAAGTTGTT	CTAGAAGTTG	AACAACATCT	TGGTAACAAT	GTTGTAAGAA	100
50 CTGTTGCTAT	GGATTCAACT	GATGGATTAA	AAAGAGGAAT	GGAAGTTATA	150

	GATACAGGTA	AACCAATTAC	AGTACCAGTT	GGTAAAGCTG	TTCTTGGTAG	200
	AATATTAAAT	GTTTTAGGAG	AACCTGTTGA	TAATCAAGGT	CCTATAAATG	250
	CTGAAACATT	TTTACCTATT	CATAGAGAAG	CACCAGAATT	TGATGACTTA	300
	GAAACTGAAA	CTGAAATATT	TGAAACAGGA	ATAAAAGTTA	TAGACTTATT	350
5	AGCACCATAT	ATTAAAGGTG	GAAAAATAGG	ATTATTTGGT	GGAGCTGGAG	400
	TAGGAAAAAC	AGTTTTAATA	ATGGAACTTA	TCAACAACAT	TGCAAAAGGA	450
	CATGGAGGAA	TTTCAGTTTT	TGCAGGAGTT	GGAGAAAGAA	CAAGAGAAGG	500
	TAGAGACTTA	TATGGTGAAA	TGACTGAATC	AGGAGTTATC	ACAAAAACAG	550
	CTCTTGTTTA	TGGACAAATG	AATGAGCCAC	CTGGAGCAAG	ACTTAGAGTT	600
10	GCATTAACAG	GGCTTACTGT	TGCAGAAAAC	TTTAGAGATA	AAGATGGGCA	650
	AGATGTTCTT	CTATTTATAG	ATAATATATT	TAGATTTACA	CAAGCAGGTT	700
	CAGAAGTTTC	AGCTTTACTT	GGAAGAATAC	CATCAGCTGT	TGGATATCAA	750
	CCAAACCTAG	CAACTGAAAT	GGGTGCTTTA	CAAGAAAGAA	TAACATCTAC	800
	AAAATCTGGT	TCAATTACAT	C			821
15						

2) INFORMATION FOR SEQ ID NO: 304

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*
 30 (B) STRAIN: ATCC 49145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304

	TTCCCAGTTG	GCTATCTTCC	AGATATTTAT	AATGCTCTCA	AGGTTGATAT	50
35	CAACACCGTT	GGAAACACGG	AGGGAGATAC	CGTCCACGAG	ATTACATTGG	100
	AAGTTGAGCA	GCACCTTGGT	GATTCAACTG	TGCGAGCAGT	GGCACTTAAG	150
	CCTACGGACG	GCTTGGTCCG	TGGTGCTTTA	GTGCGAGATA	CTGGTGGCCC	200
	AATTTCTGTG	CCTGTTGGAG	ATGTTACAAA	AGGTCACGTT	TTTGACGTAA	250
	CTGGTAACAT	TTTAAACGCT	AAACCAGGCG	AAAACATTGA	GGTGACCGAG	300
40	CGCTGGCCAA	TCCACCGCAA	CCCACCTGCT	TTCGATCAGC	TTGAGTCTAA	350
	GACTCAAATG	TTTGAAACAG	GCATTAAGGT	TATCGATTTG	CTTACGCCTT	400
	ACGTTTCAGG	CGGAAAGATT	GGTCTGTTCT	GTGGTGCAGG	CGTTGGTAAA	450
	ACTGTGTTGA	TTCAGGAGAT	GATTCAGCGC	GTTGCACAGA	ACCACGGCGG	500
	TGTGTCTGTG	TTTGCTGGCG	TTGGCGAACG	TACTCGTGAG	GGTAACGATT	550
45	TGATTGGCGA	AATGGCTGAG	GCTGGCGTTT	TGGAGAAAAC	AGCGCTTGTC	600
	TTTGGTCAGA	TGGATGAGCC	TCCTGGGACT	CGTCTTCGTG	TGCCTCTTAC	650
	TGCTTTGACT	ATGGCTGAGT	ATTTCCGTGA	TGTTTCAGAAT	CAGGATGTGT	700
	TGCTGTTTAT	CGACAACATC	TTCCGCTTTA	CTCAGGCAGG	TTCTGAGGTT	750
	TCCACGTTGC	TTGGTCGTAT	GCCTTCTGCA	GTTGGTTATC	AGCCAAACTT	800
50	GGCGGATGAA	ATGGGTGCGT	TGCAGGAGCG	CATTACTTCT	ACGCGCGGTC	850
	ATTCTATTAC	GTCG				864

55 2) INFORMATION FOR SEQ ID NO: 305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella haemolysans*

(B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305

10 TCGAATCAGG GCATATGCCA AATCTATTAA ACGCTTTAGA AGTTTACATA 50
 GAAAAAGGCG ATGGGAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA 100
 AATTGGTGAT AACGTAGTAA GAACAATCGC TATGTCATCT ACTGATGGAT 150
 TAAATAGGGG AGCAGAAGTA GTAGATACAG GAGCACCAAT TACAGTTCCT 200
 15 GTAGGTAAC TACACATTAGG TCGTGTGTTC AACGTATTAG GTGAAGCAGT 250
 TGACCACGGT GAAGAAGCAG GAGCAGAAGT TCGTAAAGAT TCAATTCACA 300
 AAGAAGCTCC AACATTGAT GAATTATCAA CTCACGTTGA GGTTCTTGAA 350
 ACAGGTATTA AAGTTATCGA CTTACTTGCA CCATATATTA AAGGTGGTAA 400
 AATCGGTCTT TTCGGTGGTG CGGGAGTTGG TAAAACGGTT CTTATCCAAG 450
 20 AACTTATCAA CAACGTTGCG CAACAACACG GTGGATTATC AGTATTCACA 500
 GGTGTAGGTG AGCGTACTCG TGAAGGAAAT GACTTATACT ATGAAATGAA 550
 AGATTCTGGT GTTATTAACA AAACAGCCAT GGTATTCGGA CAAATGAACG 600
 AACCACCAGG TGCTCGTATG CGTGTAGCAT TAACAGGATT AACAAATGGCG 650
 GAATACTTCC GTGATGAAGA AGGACAAGAC GTGCTTCTAT TCATCGATAA 700
 25 CATTTTCCGT TTCACACAAG CAGGTTCTGA GGTTCCTGCG TTATTAGGAC 750
 GTATGCCATC AGCCGTTGGT TACCAACCAA CACTTGCTAC AGAGATGGGA 800
 CGTTTACAAG AACGTATAAC ATCAACTAAA AAAGGTTCTG TTACATCT 848

30

2) INFORMATION FOR SEQ ID NO: 306

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 848 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella morbillorum*

(B) STRAIN: ATCC 27824

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306

TCGAATCAGG GCATATGCCT AATCTACTAA ACGCTTTAGA AGTTTATATA 50
 GAAAAAGGCG ATGGAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA 100
 AATCGGGGAT AATGTCGTAA GAACTATTGC GATGTCATCT ACTGATGGAT 150
 50 TAAACAGAGG GGCAGAAGTA GTTGATACTG GAGCGCCAAT TACAGTGCCA 200
 GTAGGTAAC ATACATTAGG ACGTGTGTTC AACGTATTAG GTGAAGCAGT 250
 TGACCACGGA GAAGAAGCTG GAGCAGAAGT TCAAAAAGAA TCTATTCATA 300
 AAGAAGCTCC AACTTTGAA GAATTATCAA CACATGTTGA GGTTATTAGAA 350
 ACAGGTATTA AAGTTATCGA CCTTCTTGCA CCATATATTA AAGGTGGTAA 400
 55 GATTGGACTA TTCGGTGGTG CTGGAGTTGG GAAAACAGTT CTTATCCAAG 450
 AACTTATTAA CAACGTAGCA CAACAACACG GAGGACTTTC AGTATTTACT 500
 GGGGTAGGTG AACGTACTCG TGAGGGTAAC GACTTGTAAT ATGAAATGAA 550
 AGACTCTGGA GTTATTAATA AAACAGCCAT GGTATTTGGT CAAATGAATG 600
 AGCCACCAGG TGCACGTATG CGTGTTCGCT TAACAGGATT AACAAATGGCA 650
 60 GAGTACTTCC GTGATGAAGA AGGACAAGAC GTACTATTAT TTATCGATAA 700

TATCTTCCGT	TTCACACAAG	CAGGGTCTGA	GGTATCTGCA	TTATTAGGGC	750
GTATGCCTTC	AGCCGTTGGA	TATCAACCAA	CTCTTGCAAC	AGAAATGGGA	800
CGTCTTCAAG	AACGTATTAC	ATCAACTAAA	AAAGGATCTG	TTACATCT	848

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2) INFORMATION FOR SEQ ID NO: 307

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307

GATGCAGTAC	CAAAAGTATA	TGATGCTTTA	AAAGTTGAAT	CAGGTTTAAC	50
CTTAGAAGTT	CAACAACAAT	TAGGTGGTGG	TTTAGTACGT	TGTATCGCAT	100
25 TAGGTACCTC	AGATGGTTTA	AAGCGTAGCT	TAAAGGTTGT	AAATACAGGT	150
AACCCTATTC	AAGTTCCTGT	AGGCACTAAA	ACATTAGGCC	GTATTATGAA	200
TGTATTAGGC	GAACCAATTG	ATGAAAAAGG	ACCTATTAGC	GAAGAAGCTC	250
GTTGGGATAT	TCATCGTGCG	GCTCCAAATT	ATGAAGAACA	GTCAAATAGT	300
ACTGAATTAC	TTGAAACCGG	TATCAAAGTT	ATTGACTTAA	TTTGTCCATT	350
30 TGCAAAAGGT	GGTAAAGTCG	GCTTATTTGG	TGGAGCTGGT	GTAGGTAAAA	400
CCGTTAATAT	GATGGAATTG	ATCCGTAATA	TTGCTATTGA	GCACTCAGGT	450
TATTCGGTTT	TTGCTGGTGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGATTT	500
TTATCATGAA	ATGACGGATT	CTAATGTATT	AGATAAAGTA	TCACTAGTAT	550
ATGGTCAAAT	GAATGAACCA	CCAGGTAACC	GCCTACGTGT	TGCGTTAACA	600
35 GGTTTAACTA	TGGCTGAAAA	ATTCCGTGAT	GAAGGTCGTG	ATGTATTATT	650
TTTCGTAGAT	AATATTTATC	GTTATACTTT	AGCCGGTACA	GAAGTTTCTG	700
CTTTATTAGG	CCGTATGCCA	TCAGCGGTAG	GTTATCAACC	AACCCTTGCA	750
GAAGAAATGG	GTGTATTACA	AGAACGTATT	ACCTCAACTA	AAACTGGTTC	800
AATCACGGCA	GTA				813

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2) INFORMATION FOR SEQ ID NO: 308

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*
 55 (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308

TGAATTTCCA	CAAGATGCAG	TGCCAAAAGT	TTACGATGCA	TTAAAAGTTG	50
50 AATCAGGTTT	AACACTTGAG	GTGCAACAAC	AATTAGGTGG	CGGTGTGGTA	100

	CGTTGTATCG	CATTAGGTGC	TTCTGACGGT	TTAAAACGTG	GTTTAAAAGT	150
	AGAAAACACG	AATGATCCGA	TTCAAGTACC	GGTAGGCACA	AAAACCCTTG	200
	GTCGTATCAT	GAATGTATTG	GGTGAACCAA	TTGACGAACA	AGGTCCAATC	250
	GGTGAAGAAG	AGCGTTGGGC	TATCCATCGT	TCTGCACCAA	GCTATGAAGA	300
5	ACAATCAAAC	AGTACGGAAT	TATTAGAGAC	TGGTATCAAA	GTTATCGACT	350
	TAATTTGTCC	ATTCGCAAAA	GGTGGTAAAG	TTGGTCTATT	CGGTGGTGCG	400
	GGTGTAGGTA	AAACCGTTAA	CATGATGGAA	TTAATCCGTA	ACATCGCGAT	450
	CGAGCACTCA	GGTTACTCCG	TATTTGCGGG	TGTAGGTGAA	CGTACTCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGAAAG	ATTCTAACGT	ATTAGATAAA	550
10	GTATCTTTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGTA	ACCGTTTACG	600
	TGTTGCGTTA	ACTGGTTTAA	CCATGGCAGA	AAAATTCCGC	GATGAAGGTC	650
	GTGATGTATT	ATTCTTCGTG	GATAATATCT	ATCGTTATAC	CCTTGCTGGT	700
	ACGGAAGTAT	CTGCGTTATT	AGGTCGTATG	CCATCTGCGG	TAGGTTACCA	750
	ACCAACTCTT	GCTGAAGAAA	TGGGTGTGTT	ACAAGAACGT	ATCACTTCAA	800
15	CCAAAACAGG	TTCTATTACA	TCTGTA			826

2) INFORMATION FOR SEQ ID NO: 309

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Haemophilus parahaemolyticus*
 (B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309

35	GATGCAGTAC	CAAAAGTATA	TGATGCGTTA	AAAGTTGAAT	CAGGTTTAAC	50
	GCTTGAAGTT	CAACAACAAT	TAGGCGGTGG	CTTAGTGCGC	TGTATCGCAT	100
	TAGGTACGTC	TGATGGTTTA	AAACGTGGCT	TAAAAGTAGA	AAATACAGGC	150
	AACCCAATTG	AAGTGCCAGT	GGGCACTAAA	ACCCTTGGTC	GTATTATGAA	200
	CGTATTGGGT	GAGCCGATTG	ACGAAAAAGG	TCCTATCGGT	GAAGAAGCAC	250
40	GCTGGGCAAT	CCACCGTGCA	GCACCAAGCT	ACGAAGAGCA	ATCAAATAGC	300
	ACGGAATTAC	TCGAAACAGG	TATCAAAGTT	ATCGACTTAA	TCTGCCCATT	350
	CGCAAAAGGG	GGTAAAGTTG	GTTTATTTGG	TGGTGCAGGT	GTAGGTAAAA	400
	CCGTAAATAT	GATGGAGTTA	ATCCGTAAAC	TCGCGATCGA	ACACTCTGGT	450
	TACTCTGTAT	TTGCAGGGGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGACTT	500
45	CTACCACGAA	ATGACAGACT	CTAACGTATT	AGATAAAGTA	TCGTTAGTGT	550
	ATGGTCAAAT	GAACGAACCA	CCAGGTAACC	GTTTACGCGT	AGCTTTAACA	600
	GGCTTAACCA	TGGCGGAAAA	ATTCCGCGAT	GAAGGTCGTG	ACGTATTATT	650
	CTTCGTCGAT	AACATCTACC	GTTATACCCT	AGCAGGTACG	GAAGTGTCAG	700
	CACTTCTCGG	TCGTATGCCA	TCTGCGGTAG	GTTATCAGCC	AACCTTAGCA	750
50	GAAGAAATGG	GTGTATTACA	AGAGCGTATC	ACTTCAACCA	AAACTGGTTC	800
	TATCACCTC					809

55 2) INFORMATION FOR SEQ ID NO: 310

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*

(B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310

10 CGAATTTCCA CAAGATGCAG TACCAAAAGT TTATGATGCA TTAAAAGTTG 50
 AATCGGGTTT AACCCTTGAA GTTCAACAAC AATTAGGTGG TGGTGTGGTA 100
 CGTTGTATCG CACTGGGAGC TTCTGACGGT TTAAAACGCA GTTTAAGCGT 150
 TGAAAATACC AATAAACCAA TTTCAGTACC GGTTGGTGTA AAAACTCTCG 200
 15 GTCGTATTAT GAACGTATTG GGCGAACCGA TTGATGAAAG AGGTCCTATC 250
 GGTGCGGAAG AAGAATGGGC AATTCACCGT TCTACTCCAA GTTATGAAGA 300
 ACAGTCCAAC AGTACCGAAT TATTAGAAAC CGGTATCAAA GTTATCGACT 350
 TAATTTGTCC ATTCGCGAAG GGTGGTAAAG TTGGTTTATT CGGTGGTGCG 400
 GGTGTAGGTA AGACCGTAAA TATGATGGAA TTAATCCGTA ATATTGCGAT 450
 20 TGAGCACTCA GGTTACTCCG TATTTGCCGG TGTAGGTGAG CGTACCCGTG 500
 AAGGTAACGA CTTCTACCAT GAAATGACAG AATCTAACGT ATTAGACAAA 550
 GTATCCCTAG TTTACGGACA AATGAATGAG CCGCCGGGTA ACCGTTTACG 600
 TGTTGCTTTA ACCGGTTTAA CCATGGCAGA AAAATTCCGT GACGAAGGTC 650
 GTGATGTATT ATTCTTCGTG GATAACATCT ATCGTTATAC CCTTGCAGGG 700
 25 ACTGAAGTAT CGGCACTTTT AGGCCGTATG CCATCAGCGG TAGGTTATCA 750
 GCCGACACTT GCAGAAGAAA TGGGTGTGTT ACAAGAACGT ATTACATCAA 800
 CCAAACAGG TTCTATTACT TCTG 824

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2) INFORMATION FOR SEQ ID NO: 311.

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Hafnia alvei*

(B) STRAIN: ATCC 13337

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311

GCCGTGCCTA AAGTGTATAA CGCACTTGAG GTGAAAGGCG GTGCCACTAA 50
 ACTGGTACTG GAAGTTCAGC AGCAGCTAGG CGGCGGCGTT GTACGCTGTA 100
 TCGCTATGGG TACTTCTGAC GGTCTGCGTC GCGGACTGGA CGTTGTTGAC 150
 50 CTGGAGCACC CGATTGAAGT CCCAGTAGGT AAAGCGACCT TAGGCCGCAT 200
 TATGAACGTA CTGGGTGAGC CAATTGATAT GAAGGGTGAT ATCGGCGAAG 250
 AAGATCGCTG GGCTATTCAC CGTGAAGCTC CAAGCTACGA AGAACTGTCT 300
 AACTCGCAAG AACTGCTGGA AACTGGTATC AAGGTAATGG ACCTGATTTG 350
 TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTG 400
 55 GTAAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
 TCAGGTTACT CTGTATTTGC CGGCGTGGGT GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTATTGGAC AAAGTATCAC 550
 TGGTTTATGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
 CTGACCGGTC TGACTATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
 60 ACTGCTGTTC ATCGATAACA TCTACCGTTA TACCTTGGCC GGTACCGAAG 700

TATCTGCACT	GTTGGGTCGT	ATGCCTTCTG	CGGTAGGTTA	TCAGCCAACG	750
CTGGCGGAAG	AGATGGGTGT	TCTGCAAGAA	CGTATCACCT	CGACCAAAAC	800
GGGTTCAATC	A				811

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2) INFORMATION FOR SEQ ID NO: 312

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 831 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kingella kingae*

(B) STRAIN: ATCC 23330

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312

GCGATGCTAT	TCCACGCGTT	TACGATGCGT	TGAAACTGGT	TGATGTGGAC	50
TTGACATTAG	AAGTGCAACA	ACAACTGGGC	GATGGCGTAG	TGCGTACCAT	100
25 TGCGATGGGT	AGTACCGATG	GTTTGAAACG	CGGCTTAGCC	GTGAACAACA	150
CAGGCGCACC	TATTACAGTG	CCTGTTGGTA	AAGCAACATT	GGGTCGTATT	200
ATGGACGTAT	TGGGTAATCC	TGTTGATGAA	GCAGGTCCAA	TTGGTTCTGA	250
CCAAACGCGT	GCTATTCACC	AACCAGCTCC	TAAATTTGAT	GAACGTGCTA	300
GCGCAACCGA	ATTGCTGGAA	ACAGGCATCA	AAGTGATTGA	CTTGCTTTGC	350
30 CCATTTGCAA	AAGGTGGTAA	AGTAGGTTTG	TTTGGTGGTG	CAGGTGTGGG	400
CAAACTGTG	AACATGATGG	AGTTGATTAA	CAACATTGCC	AAAGCGCACA	450
GTGGTTTGTG	TGTATTTGCA	GGCGTGGGTG	AACGTACTCG	CGAAGGTAAT	500
GACTTCTATC	ACGAGATGAA	AGATTCTAAC	GTGTTGGATA	AAGTTGCCAT	550
GGTGTATGGT	CAAATGAATG	AACCTCCTGG	CAACCGTTTG	CGCGTTGCAT	600
35 TGACTGGTTT	GTCTATGGCA	GAACACTTCC	GTGATGAAAA	AGACGAAAAT	650
GGCAAAGGTC	GCGATGTATT	GTTCTTTGTG	GACAACATCT	ATCGCTACAC	700
ATTGGCAGGT	ACAGAAGTAT	CGGCATTGCT	GGGTCGTATG	CCCTCTGCGG	750
TAGGTTATCA	ACCAACATTG	GCAGAAGAAA	TGGGTCGTTT	GCAAGAGCGT	800
ATTACTTCAA	CGCAAACAGG	TTCGATTACT	T		831

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2) INFORMATION FOR SEQ ID NO: 313

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 812 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*

55 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313

ATGCCGTACC	ACGCGTGTAC	GAAGCCCTTG	AGGTACAGAA	TGGTAATGAA	50
50 GTTCTGGTGC	TGGAAGTTCA	GCAGCAGCTG	GGCGGCGGTA	TCGTACGTAC	100

	CATCGCCATG	GGTTCTTCTG	ATGGTCTGCG	CCGCGGTCTG	GATGTAAAG	150
	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TACTGGGTCA	ACCGGTTGAC	ATGAAAGGCG	ACATCGGCGA	250
	AGAAGAGCGT	TGGGCTATCC	ACCGCGCGGC	ACCGTCCTAT	GAAGAGCTGT	300
5	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CCAAGGGCGG	TAAAGTTGGT	CTGTTCGGCG	GTGCGGGTGT	400
	AGGTAAACT	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAGCGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ATAAAGTATC	550
10	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTAAGTCTGT	TCGTGATAA	CATCTATCGT	TACACCCTGG	CCGGTACTGA	700
	AGTATCCGCG	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAA	800
15	ACCGGTTCTA	TC				812

2) INFORMATION FOR SEQ ID NO: 314

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Klebsiella ornithinolytica*
 (B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314

35	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTACAGAA	TGGTAATGAG	50
	AGCCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGTGGTA	TCGTACGTGC	100
	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	GAAGTTAAAG	150
	ACCTTGAGCA	CCCGATCGAA	GTCCCGGTTG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TGCTGGGTCA	GCCAATCGAT	ATGAAAGGCG	ACATCGGCGA	250
40	AGAAGAGCGT	TGGGCTATTC	ACCGTGCAGC	TCCGTCTCTAT	GAAGAGCTGT	300
	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTCGGTG	GTGCGGGTGT	400
	AGGTAAACC	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
45	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTCTGG	ATAAAGTATC	550
	CCTGGTTTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTTCTGCTGT	TCGTGATAA	CATCTATCGT	TATACCCTGG	CCGGTACTGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
50	CCCTGGCGGA	AGAGATGGGT	GTTCTGCAGG	AACGTATCAC	CTCCACCAA	800
	ACCGGTTCTA	TC				812

55 2) INFORMATION FOR SEQ ID NO: 315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315

10 GTACCGCGCG TGTACGAGGC TCTTGAGGTA CAAAATGGTA GTGAGAATCT 50
 GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CGGTATTGTT CGTACCATCG 100
 CCATGGGTTC TTCCGACGGT CTGCGTCGCG GTCTGGAAGT CAAAGACCTC 150
 GAGCATCCGA TCGAAGTCCC GGTAGGTAAA GCAACGCTGG GTCGTATCAT 200
 15 GAACGTACTG GGCCAACCGG TAGACATGAA AGGCGACATC GGCGAAGAAG 250
 AGCGTTGGGC GATTCACCGC GCAGCGCCTT CCTACGAAGA GTTGTCAAAC 300
 TCTCAGGAAC TGCTGGAAAC CGGCATCAAA GTTATCGACC TGATGTGTCC 350
 GTTTGCGAAG GGCGGTAAAG TTGGTCTGTT CGGTGGTGCG GGTGTAGGTA 400
 AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC 450
 20 GGTTACTCCG TGTTTGCGGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA 500
 CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGATAAA GTATCCCTGG 550
 TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCGCTG 600
 ACCGGCCTGA CCATGGCTGA GAAGTTCCGT GACGAAGGTC GTGACGTTCT 650
 GCTGTTCGTC GATAACATCT ATCGTTACAC CCTGGCCGGT ACTGAAGTAT 700
 25 CCGCACTGCT GGGTCGTATG CCTTCAGCGG TAGGTTACCA GCCGACTCTG 750
 GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CCAAAACGGG 800
 TTCTATCACT TCC 813

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2) INFORMATION FOR SEQ ID NO: 316

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: ATCC 33531

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316

GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTACAGA ATGGTAATGA 50
 GAGCCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGTGGT ATCGTACGTG 100
 CTATCGCCAT GGGTTCTTCT GACGGTCTGC GTCGTGGTCT GGAAGTTAAA 150
 50 GACCTTGAGC ACCCGATCGA AGTCCCGGTT GGTAAGCAA CGCTGGGTCG 200
 TATCATGAAC GTGCTGGGTC AGCCGATCGA TATGAAAGGC GACATCGGCG 250
 AAGAAGAGCG TTGGGCTATT CACCGCGCAG CTCCGTCTTA TGAAGAGCTG 300
 TCCAGTTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT 350
 GTGTCCGTTT GCTAAGGGCG GTAAAGTAGG TCTGTTCCGT GGTGCGGGCG 400
 55 TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
 CACTCCGGTT ACTCCGTGTT TGCGGGCGTC GGTGAACGTA CTCGTGAGGG 500
 TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTCTG GATAAAGTAT 550
 CCCTGGTTTA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
 GCTCTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA 650
 60 CGTTCTGCTG TTCGTCGATA ACATCTATCG TTATACCCTG GCCGGTACTG 700

AAGTATCCGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTAGG	TTATCAGCCG	750
ACCCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
AACCGGTTCT	ATCACTTCCG	TA			822

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2) INFORMATION FOR SEQ ID NO: 317

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317

AGAATGGTAA	TGAAGTTCTG	GTGCTGGAAG	TTCAGCAGCA	GCTGGGCGGC	50
GGTATCGTAC	GTACCATCGC	CATGGGTTCT	TCTGATGGTC	TGCGCCGCGG	100
25 TCTGGATGTA	AAAGACCTCG	AGCACCCGAT	CGAAGTCCCG	GTAGGTAAAG	150
CAACGCTGGG	TCGTATCATG	AACGTACTGG	GTCAACCGGT	TGACATGAAA	200
GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGCG	CGGCACCGTC	250
CTATGAAGAG	CTGTCCAGCT	CTCAGGAACT	GCTGGAAACC	GGCATCAAAG	300
TTATCGACCT	GATGTGTCCG	TTCGCCAAGG	GCGGTAAAGT	TGGTCTGTTC	350
30 GGCGGTGCGG	GTGTAGGTAA	AACTGTAAAC	ATGATGGAGC	TGATCCGTAA	400
CATCGCGATC	GAGCACTCCG	GTTACTCTGT	GTTTGCGGGC	GTAGGTGAGC	450
GTACTCGTGA	GGGTAATGAC	TTCTACCACG	AAATGACCGA	CTCCAACGTT	500
ATCGATAAAG	TATCCCTGGT	GTACGGCCAG	ATGAACGAGC	CGCCGGGAAA	550
CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAATTCCGTG	600
35 ACGAAGGTCG	TGACGTACTG	CTGTTCTGTCG	ATAACATCTA	TCGTTACACC	650
CTGGCCGGTA	CTGAAGTATC	CGCACTGCTG	GGTCGTATGC	CTTCAGCGGT	700
AGGTTATCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	750
TCACCTCCAC	CAAACCGGT	TCTATCACCT	CCGTA		785

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2) INFORMATION FOR SEQ ID NO: 318

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 759 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
 (B) STRAIN: ATCC 33433

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318

CTGGTGCTGG	AAGTTCAGCA	GCAGCTCGGC	GGCGGTATCG	TACGTWCCAT	50
CGCTATGGGT	TCTTCCGACG	GTCTGCGTCG	CGGTCTGGAT	GTTAAAGATC	100
50 TCGAGCACCC	AATCGAAGTT	CCGGTMGGTA	AAGCAACMCT	GGGTCGTATC	150

	ATGAACGTAC	TGGGTCACCC	AGTMGACATG	AAAGGCGACA	TCGGTGAAAG	200
	AGAGCGTTGG	GCTATCCACC	GCGCTGCACC	TTCCTACGAA	GAGCTGTCTA	250
	GCTCTCAGGA	ATTGCTGGAA	ACCGGTATCA	AAGTTATCGA	CCTGATGTGT	300
	CCGTTTCGCTA	AGGGCGGTAA	AGTCGGTCTG	TTCGGTGGTG	CSGGTGTGG	350
5	TAAAACCGTA	AACATGATGG	AGCTGATCCG	TAACATCGCG	ATCGAGCACT	400
	CCGGTTACTC	CGTGTTTGCG	GGCGTAGGTG	AACGTACTCG	TGAGGGTAAC	450
	GACTTCTACC	ACGAAATGAC	CGACTCCAAC	GTTATCGATA	AAGTATCCCT	500
	GGTATATGGC	CAGATGAACG	AGCCACCGGG	AAACCGTCTG	CGCGTTGCTC	550
	TGACCGGTCT	GACCATGGCT	GAGAAATTCC	GTGACGAAGG	TCGTGACGTA	600
10	CTGCTGTTTCG	TCGATAACAT	CTATCGTTAC	ACCCTGGCCG	GTACTGAAGT	650
	ATCTGCWCTG	CTGGGTCGTA	TGCCTTCAGC	GGTAGGTTAC	CAGCCGACCC	700
	TGGCGGAAGA	GATGGGCGTT	CTGCAGGAAC	GTATCACCTC	CACCAAGACC	750
	GGTTCTATC					759

15

2) INFORMATION FOR SEQ ID NO: 319

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Kluyvera cryocrescens*
- (B) STRAIN: ATCC 33435

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319

	TTCCTCAGG	ATGCCGTACC	GCGTGTGTAC	GAAGCCCTTG	AGGTTTCAGAA	50
	TGGTAATGAA	GTGCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
35	TCGTACGTAC	CATCGCTATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GATGTAAAAG	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	ACTGGGTCGT	ATCATGAACG	TACTGGGCCA	ACCGGTAGAC	ATGAAAGGCG	250
	ACATCGGTGA	AGAAGAACGT	TGGGCTATCC	ACCGTGCAGC	ACCTTCCTAC	300
	GAAGAGCTGT	CAAGCTCTCA	GGAAGTGTCTG	GAAACCGGCA	TCAAAGTTAT	350
40	CGACCTGATG	TGTCCGTTTG	CGAAGGGCGG	TAAAGTTGGT	CTGTTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	450
	GCGATTGAGC	ACTCCGGTTA	TTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTTTC	CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	AGGAAACCGT	600
45	CTGCGCGTTG	CGCTGACTGG	TCTGACTATG	GCTGAGAAGT	TCCGTGACGA	650
	AGGTCGCGAC	GTACTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACAGA	AGTATCTGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

50

2) INFORMATION FOR SEQ ID NO: 320

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Kluyvera georgiana*
(B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320

10	GCCGTACCGC	GCGTGTACGA	AGCCCTTGAG	GTACAGAATG	GTAATGAAGT	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	TGGCGGTATC	GTGCGTACCA	100
	TCGCCATGGG	TTCCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	AGTTAAAGAT	150
	CTCGAGCACC	CGATCGAAGT	TCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	CTGGGTCACC	CGGTAGACAT	GAAAGGCGAC	ATCGGTGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCTGCGC	CTTCCTACGA	AGAGCTGTCC	300
15	AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTCGCG	AAGGGCGGTA	AAGTCGGTCT	GTTCGGCGGT	GCGGGTGTG	400
	GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
20	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAGAC	800
25	CGGTTCTATC					810

2) INFORMATION FOR SEQ ID NO: 321

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Lactobacillus acidophilus*
(B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321

45	TCGATAAGAA	TTTACCTGAT	ATTAACAACG	CCTTACGTGT	AATCAAGTCC	50
	GAAGATGAAA	GCATCGTTCT	TGAAGTTACA	CTTGAACTCG	GTGATGGTGT	100
	TTTAAGAACA	ATCGCCATGG	AATCTACCGA	TGGTCTTCGT	CGTGGTATGA	150
	AAGTCGAAGA	TACTGGCGCT	CCAATTTCAG	TTCCAGTTGG	AGAAGACACT	200
	TTAGGTCGTG	TGTTTAACGT	TTTAGGACAG	CCTATTGATG	GTGGTCCAGC	250
50	CTTTCCAAAG	GATCACCCAC	GTGAGGGTAT	CCACAAGGAA	GCACCTAAAT	300
	ATGAAGATTT	AACTACTAGT	CGTGAAATTC	TTGAAACTGG	TATCAAGGTT	350
	ATCGACCTTC	TTGAACCATA	TGTTCTGTGG	GGTAAAGTTG	GTTTGTTTGG	400
	TGGTGCCGGT	GTTGGTAAAA	CTACTATTAT	TCAAGAATTA	ATTCACAACA	450
	TCGCTCAAGA	ACACGGTGGT	ATTTCCGTAT	TTACTGGTGT	TGGTGAAAGA	500
55	ACTCGTGAAG	GTAATGACCT	TTACTTTGAA	ATGAAAGCTT	CAGGCGTTTT	550
	AAGTAAGACT	GCCATGGTAT	TTGGTCAGAT	GAACGAGCCG	CCTGGTGCCA	600
	GAATGCGTGT	TGCATTAACC	GGTTTGACAC	TTGCTGAATA	CTTTAGAGAT	650
	GTTGAAGGTC	AAGACGTATT	GCTCTTTATT	GACAATATCT	TTAGATTTAC	700
	TCAGGCTGGT	TCAGAGGTAT	CTGCTTTGCT	TGGTCGTATG	CCAAGTGCCG	750
60	TAGGTTATCA	GCCAACTTTG	GCAACAGAAA	TGGGTCAATT	GCAGGAAAGA	800

ATTACTTCTA CTAAGAAGGG TTCAATTACT TCAA

5 2) INFORMATION FOR SEQ ID NO: 322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322

20 TTCCTCGTGA TAGCGTGCCT AAAGTCAATG ATGCGTTAAA GCTTGTTGAT 50
 AGTGATCTGG TTTTGAAGT GCAGCAGCAA CTTGGAGACG GAGTTGTGCG 100
 TACTATTGCC ATGGGAACAA CCGATGGTTT AAAGCGAGGA TTAAAAGCAG 150
 AAAATACAGG CCATCCTATT CAAGTGCCAG TAGGTAAGAA AACTTTGGGA 200
 25 CGCATTATGG ATGTTCTTGG GCGTCCTGTA GATGATGCTG GGCCTATCGA 250
 TGCTGAAGAG ACTTGGGCTA TTCATCGTAA AGCACCAAGT TATGAAGAGC 300
 AAGCTGGCAG CCAGGAATTA TTGGAAACTG GTATTAAAGT AATTGATTTG 350
 CTTTGCCCTT TTGCCAAGGG AGGTAAAGTT GGTCTATTCG GTGGTGCCGG 400
 TGTAGGCAAA ACCGTAAACA TGATGGAATT AATACGAAAC ATTGCAATTG 450
 30 AGCATAGCGG TTATTCAGTG TTTGCAGGGG TTGGTGAACG TACCCGTGAA 500
 GGAAACGACT TCTATCATGA GATGAAAGAC TCTAATGTAT TGGATAAAGT 550
 ATCGCTTGTT TATGGTCAGA TGAATGAGCC GCCAGGAAAC CGTTTGCGTG 600
 TTGCTCTAAC CGGTTTGACT ATGGCTGAAA AATTCGGGGA TGAAGGGCGA 650
 GACGTTCTTT TGTTTATCGA TAATATTTAT CGTTATACCT TGGCTGGGGT 700
 35 TGAAGTATCT GCGCTGTTAG GCCGTATGCC TTCTGCAGTA GGATATCAGC 750
 CGACATTAGC AGAGGAAATG GGTATGCTGC AAGAGCGCAT TACCTCCACA 800
 AAAACAGGTT CTATTACTTC CATA 824

40

2) INFORMATION FOR SEQ ID NO: 323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimontii*
 (B) STRAIN: ATCC 33999

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323

GACGCCGTAC CGAAAGTGTA CGATGCGCTT GAAGTTCAAA TTGATGCCAA 50
 GCTGGTTCTG GAAGTTCAAC AGCAGCTCGG CGGCGGCGTT GTTCGCTGCA 100
 TCGCGATGGG TACTTCAGAC GGCTTAAGCC GCGGTCTGGA CGTGCTCGAT 150
 60 CTGGAACACC CGATTGAAGT ACCGGTGGGC AAAGCGACGC TGGGCCGCAT 200

	CATGAACGTG	CTTGGTCACC	CTATCGACAT	GAAGGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATTCAC	CGCGCAGCGC	CGAGCTACGA	AGACCTGTCG	300
	GGCGCAACCG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	TCCGTTTCGCC	AAGGGCGGTA	AAGTCGGCCT	GTTTCGGCGGC	GCCGGCGTAG	400
5	GTAAAACCGT	AAACATGATG	GAGCTCATTC	GCAACATTGC	GACCGAGCAC	450
	TCCGGTTACT	CCGTGTTTGC	AGGCGTAGGT	GAACGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CTGAATCCAA	CGTATTGGAC	AAGGTGTTCG	550
	TGGTATACGG	TCAGATGAAC	GAGCCGCCTG	GAAACCGTCT	GCGCGTAGCG	600
	TTAACGGGCT	TGACCATGGC	GGAGAAGTTC	CGTGATGAAG	GCCGTGACGT	650
10	TCTGCTGTTT	ATCGACAACA	TTTACCGCTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CCGTAGGCTA	CCAGCCGACT	750
	CTGGCTGAGG	AAATGGGCGT	GCTTCAAGAG	CGTATTACCT	CTACCAAGAC	800
	GGGGTCTATC	ACCTCCGT				818

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2) INFORMATION FOR SEQ ID NO: 324

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 835 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324

	GTGGAAACTT	ACCTGAAATC	TACAATGCCC	TAGTTATTGA	ATATAAATCT	50
	GATGCAGAAG	AAGCACCAAC	TAGCCAACTT	ACTTTAGAAG	TAGCCATCCA	100
	ATTAGGTGAT	GATGTTGTAC	GTACAATCGC	AATGGCATCA	ACAGATGGTG	150
35	TTCAAAGAGG	TATGGAAGTT	ATTGATACTG	GGAGCCCAAT	TACAGTTCCT	200
	GTAGGTACAG	TAACCTCTTG	TCGTGTATTT	AATGTATTAG	GAAACACCAT	250
	CGATTTGGAC	GAACCACTTC	CAAGCGATAT	TAAACGTAAT	AAAATTCACC	300
	GCGAAGCTCC	AACTTTTCGAT	CAATTAGCAA	CGACAACAGA	AATTCTTGAA	350
	ACAGGAATTA	AAGTAGTTGA	CTTGCTAGCT	CCTTACTTAA	AAGGTGGTAA	400
40	AATCGGATTG	TTCGGTGGTG	CCGGTGTTGG	TAAAACCGTT	CTAATTCAAG	450
	AGCTTATCCA	TAATATCGCA	CAAGAACATG	GTGGTATTTT	TGTGTTTCGCT	500
	GGCGTTGGAG	AACGTACTCG	TGAAGGTAAC	GACCTTTACT	TCGAAATGAA	550
	AGATTCAGGC	GTTATTGAAA	AAACAGCGAT	GGTATTCGGT	CAAATGAACG	600
	AGCCACCAGG	TGCGCGTATG	CGTGTTGCCT	TAACTGGTCT	AACAATTGCT	650
45	GAATATTTCC	GTGATGAAGA	ACATCAAGAT	GTACTTTTAT	TCATTGATAA	700
	CATTTTCCGT	TTCACACAAG	CTGGTTCAGA	GGTTTCGGCT	TTACTAGGTC	750
	GTATGCCATC	TGCGGTAGGT	TACCAACCAA	CCCTAGCTAC	TGAAATGGGT	800
	CAACTACAAG	AACGTATTAC	ATCTACTAAC	GTTGG		835

50

2) INFORMATION FOR SEQ ID NO: 325

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 828 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Micrococcus lylae*

(B) STRAIN: ATCC 27566

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325

	CCCGCGTGGC	GAGTTGCCGG	CACTGTTCAA	CGCGCTGACT	GTCGAGGTCA	50
	CCCTCGAAGC	AGTCGCTAAA	ACCATTACCC	TTGAGGTTGC	TCAGCACCTC	100
10	GGCGACAACT	TGGTTCGTGC	CGTGTCCATG	GCACCGACCG	ACGGTCTCGT	150
	CCGTGGCGCT	GCTGTGATCG	ACAGCGGTAA	GCCGATCTCA	GTTCCCGTTG	200
	GTGACGTAGT	CAAGGGACAC	GTCCTTCAACG	CTCTGGGTGA	TTGCCTCGAT	250
	GAGCCAGGTC	TTGGCCGTGA	CGGTGAGCAG	TGGGGCATCC	ACCGCGATCC	300
	GCCACCTTTT	GACCAGCTTG	AGGGTAAGAC	CGAGATTCTG	GAAACCGGTA	350
15	TTAAGGTCAT	CGACCTGCTG	ACCCCGTATG	TTAAGGGCGG	CAAGATCGGC	400
	CTGTTTCGGTG	GTGCTGGTGT	GGGTAAGACC	GTTCTTATCC	AGGAAATGAT	450
	CACCCGTATC	GCTCGCGAGT	TCTCCGGTAC	CTCGGTGTTC	GCAGGCGTGG	500
	GTGAGCGTAC	CCGTGAGGGC	ACCGACCTCT	TCCTGGAAAT	GGAAGAGATG	550
	GGCGTTCTCC	AGGACACCGC	TCTTGTGTTC	GGCCAGATGG	ACGAGCCTCC	600
20	AGGAGTTCGT	ATGCGCGTGG	CGCTGTCCGG	CCTGACCATG	GCGGAGTACT	650
	TCCGCGATGT	GCAGCACCAG	GACGTGCTTC	TGTTTCATCGA	CAACATCTTC	700
	CGTTTCACCC	AGGCAGGTTC	CGAGGTTTCC	ACCCTCCTAG	GCCGCATGCC	750
	TTCTGCCGTG	GGTTACCAGC	CAACGCTGGC	AGACGAGATG	GGTGTTCCTGC	800
	AGGAGCGTAT	TACCTCCACA	AAGGGTAA			828

25

2) INFORMATION FOR SEQ ID NO: 326

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moellerella wisconsensis*

40

(B) STRAIN: ATCC 35017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326

	GATGCCGTAC	CAAAAGTGTA	CGATGCTCTT	GAGGTTCTTA	ACGGTAAAGA	50
45	AAAATTGGTG	CTGGAAGTTC	AGCAACAATT	AGGCGGTGGT	GTTGTTTCGT	100
	GTATCGCAAT	GGGTACATCA	GATGGTTTAA	GCCGCGGTTT	AGAAGTTAAA	150
	AATACAGATC	ATCCGATCGA	AGTTCCTGTC	GGTGTTAAAA	CGCTTGGCCG	200
	TATCATGAAC	GTGCTGGGTG	ACCCAATCGA	CATGAAAGGT	GATATCGGCG	250
	AAGAAGAACG	CTGGTCAATT	CACCGCGCAG	CACCAAGCTA	TGAAGATCTG	300
50	GCTAACTCAA	CAGAACTTCT	AGAAACAGGT	ATCAAAGTTA	TGGACCTGAT	350
	TTGCCCATTC	GCTAAAGGGG	GTAAAGTGGG	TCTGTTCCGT	GGTGCGGGTG	400
	TCGGTAAAC	AGTTAACATG	ATGGAGCTTA	TTCGTAATAT	CGCGATTGAG	450
	CACTCAGGTT	ATTCTGTATT	CGCGGGTGTT	GGTGAACGTA	CTCGTGAAGG	500
	TAACGATTTT	TACCATGAAA	TGACAGACTC	AAACGTTCTG	GATAAAGTTT	550
55	CATTGGTTTA	TGGCCAGATG	AATGAGCCAC	CAGGAAACCG	TCTGCGTGTT	600
	GCTCTGACTG	GTCTGACTAT	GGCAGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTACTGTTA	TTCGTAGATA	ATATTTATCG	TTATACCTTA	GCAGGGACAG	700
	AAGTATCTGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTGGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	TGTTCTGCAA	GAACGTATCA	CCTCGACTAA	800
50	GACCGGCTCT	ATCACTTCCG	TA			822

2) INFORMATION FOR SEQ ID NO: 327

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Branhamella catarrhalis*
 (B) STRAIN: ATCC 43628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327

20	CCGTGGCGAT	GTCCCCCAA	TCTTTGATGC	ACTTCATGTT	GATGGTACTG	50
	AAACCACCCT	TGAAGTCCAA	CAACAGTTAG	GTGATGGTGT	GGTGCGTACC	100
	ATTGCCATGG	GTTCTACCGA	AGGCTTAAAG	CGTGGCTTGC	CTGTCTCTAA	150
	TTCAGGTGCA	CCCATTTCGG	TACCAGTCGG	TCAAGCAACA	CTGGGTCGCA	200
	TTATGGATGT	CCTAGGTCGC	CCAATCGATG	AAGCAGGTCC	GGTAAATGCT	250
25	GAACAAAAAT	GGTCCATTCA	TCGTGAAGCA	CCAAGTTATG	ATGAACAGTC	300
	AAATAGTACA	GAACTTTTAG	AAACAGGCAT	CAAAGTGATT	GATTTGCTTT	350
	GTCCATTTGC	CAAAGGTGGT	AAAGTCGGTC	TGTTCCGGTG	TGCTGGTGTT	400
	GGTAAGACCG	TTAACATGAT	GGAGCTTATC	AATAATATCG	CCCTAAAACA	450
	CTCAGGTCTG	TCGGTTTTTG	CTGGTGTGGG	TGAGCGTACT	CGTGAGGGTA	500
30	ATGACTTCTA	CCATGAAATG	CAAGAAGCAG	GCGTTGTAA	TACCGAAGAT	550
	TTTACTCAGT	CAAAAGTTGC	CATGGTTTAT	GGTCAGATGA	ATGAGCCACC	600
	AGGAAACCGT	CTGCGTGTTG	CCTTAACCTG	TTTGACCATG	GCAGAGTATT	650
	TCCGTGATGA	AAAAGACGAA	GCAACGGGCA	AAGGCCGTGA	TGTTCTGCTG	700
	TTCGTTGATA	ATATTTATCG	TTACACATTG	GCAGGTACTG	AGGTATCAGC	750
35	ACTTTTAGGT	CGTATGCCAT	CTGCGGTAGG	TTATCAGCCG	ACTTTGGCCG	800
	AAGAGATGGG	CTTGCTACAA	GAGCGTATCA	CCTCCACCCA	ATCAGGCTCA	850
	ATTA					854

40

2) INFORMATION FOR SEQ ID NO: 328

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella osloensis*
 (B) STRAIN: ATCC 19976

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328

	CCGTCAAAGC	GTACCAAGAA	TTTATGATGC	CTTAAAAGTT	GAAGGCACAG	50
	AAACTACATT	AGAAGTACAA	CAACAATTGG	GTGATGGTAT	CGTACGTACT	100
	ATTGCCATGG	GTTCTACTGA	AGGTCTAAAA	CGTGGTCTAC	CAGTTAGCAA	150
50	CACTGGCGCA	CCAATCTCTG	TACCTGTGGG	TAAAGGTACA	CTAGGTCGTA	200

	TCATGGACGT	TTTAGGACAC	CCAATCGATG	AGGCAGGTCC	GGTAGAGCAT	250
	AGTAACACTT	GGGCGATTCA	CCGTGAAGCG	CCAAGCTATG	ATGAACAATC	300
	AAACTCTACT	GAAC TTTTAG	AAACCGGTAT	TAAAGTAATT	GACTTACTAT	350
	GCCCATTTGC	TAAAGGTGGT	AAAGTCGGTC	TGTTCCGGTGG	CGCGGGTGTT	400
5	GGTAAAACCG	TTAACATGAT	GGAAC TTATC	AATAACATCG	CAAAAGCACA	450
	CTCAGGTTTA	TCGGTATTTG	CTGGTGTAGG	TGAGCGTACT	CGTGAAGGTA	500
	ATGACTTCTA	CCACGAGATG	AAAGACTCAA	ACGTACTTGA	TAAAGTTGCG	550
	ATGGTGTATG	GTCAGATGAA	TGAGCCACCA	GGAAACCGTT	TACGTGTTGC	600
	CCTGACAGGT	TTAACCATGG	CAGAATACTT	CCGTGACGAA	AAAGATGAAA	650
10	ACGGTAAAGG	TCGTGACGTA	TTATTGTTCG	TTGACAATAT	TTATCGTTAC	700
	ACGCTAGCGG	GTACCGAAGT	ATCAGCATTA	TTAGGTCGTA	TGCCATCTGC	750
	AGTAGGGTAT	CAGCCAACGC	TTGCAGAAGA	GATGGGTGTA	CTACAAGAAC	800
	GTATTACTTC	AACCCAATCA	GGCTCTATTA	C		831

15

2) INFORMATION FOR SEQ ID NO: 329

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 835 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Morganella morganii* subsp. *morganii*

(B) STRAIN: ATCC 25830

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329

	CGAATTTCTT	CAGGATGCAG	TACCGAAAGT	GTACGATGCG	CTTGAGGTAA	50
	CAAATGGTAA	AGAAAAACTG	GTGCTGGAAG	TTCAGCAGCA	GTTAGGCGGC	100
35	GGGGTTGTCC	GTTGTATCGC	TATGGGTACA	TCTGATGGTC	TGAGCCGTAA	150
	TCTGGAAGTA	ACCGATTTAG	GCCACCCGAT	CGAAGTCCCT	GTCGGCGTGA	200
	AAACCTTAGG	ACGTATCATG	AACGTTCTGG	GTGATCCGAT	CGATATGAAA	250
	GGTGACATCG	GCGCAGAAGA	AAAATGGTCT	ATTCACCGTG	CTGCACCAAC	300
	ATACGAAGAA	CTGTCTAACT	CCCAGGAACT	GCTGGAAACA	GGTATCAAAG	350
40	TAATGGACCT	GATCTGCCCC	TTCGCGAAGG	GTGGTAAAGT	CGGTCTGTTC	400
	GGTGGTGCGG	GTGTGGGTAA	AACCGTAAAC	ATGATGGAAC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCTGT	ATTCGCAGGG	GTCGGTGAGC	500
	GTACCCGTGA	AGGTAACGAC	TTCTATCATG	AAATGACAGA	CTCCAACGTT	550
	CTGGACAAAG	TATCACTCGT	GTACGGCCAG	ATGAACGAGC	CACCGGGAAA	600
45	CCGTCTGCGC	GTTGCTCTGA	CCGGTCTGAC	CATGGCGGAA	AAATTCCGTG	650
	ATGAAGGCCG	CGATGTACTG	CTGTTCTGTT	ATAACATCTA	CCGTTATACC	700
	CTGGCCGGTA	CTGAAGTATC	CGCGCTGTTA	GGCCGTATGC	CTTCAGCGGT	750
	AGGTTACCAG	CCGACACTGG	CGGAAGAAAT	GGGTGTGCTT	CAGGAACGTA	800
50	TCACATCGAC	CAAAACAGGC	TCTATCACGT	CTGTA		835

50

2) INFORMATION FOR SEQ ID NO: 330

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 824 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Pantoea agglomerans*
(B) STRAIN: ATCC 27155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330

	GACGCGGTAC	CGCAAGTGTA	CAGCGCCCTC	GAGGTTATGA	ATGGTGATGC	50
10	GCGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGCGGCGGC	GTAGTACGTA	100
	CCATCGCAAT	GGGTACGTCT	GACGGCCTGA	AGCGTGGTCT	GAGCGTCAAC	150
	GACCTGCAGA	AACCGATTCA	GGTACCCGTC	GGTAAAGCGA	CCCTGGGCCG	200
	TATCATGAAC	GTTCTCGGCG	AGCCAATCGA	TATGAAAGGC	GAGCTGAAAG	250
	AAGAAGATGG	CAGCGCAGTA	GAGATCGCCT	CTATTCACCG	CGCAGCCCCCT	300
15	TCTTATGAAG	ATCAGTCTAA	CTCGCAGGAA	CTGCTGGAAA	CCGGCATCAA	350
	GGTTATCGAC	CTGATGTGTC	CGTTTGCTAA	AGGCGGTAAA	GTCGGTCTGT	400
	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTCA	ACATGATGGA	ACTGATCCGT	450
	AACATCGCGG	CTGAACACTC	AGGTTACTCA	GTGTTTGCCG	GTGTGGGTGA	500
	GCGTACTCGT	GAGGGTAACG	ACTTCTACCA	CGAAATGACT	GACTCTAACG	550
20	TTATCGATAA	AGTTGCACTG	GTCTATGGCC	AGATGAACGA	GCCGCCGGGT	600
	AACCGTCTGC	GCGTAGCACT	GACCGGTCTG	ACCATGGCGG	AAAAATTCCG	650
	TGATGAAGGT	CGCGACGTTC	TGCTGTTCAT	CGATAACATC	TACCGTTATA	700
	CCCTGGCCGG	TACAGAAGTT	TCTGCACTGC	TGGGTCGTAT	GCCATCTGCG	750
	GTAGGTTACC	AGCCAACGCT	GGCAGAAGAG	ATGGGTGTGT	TGCAGGAGCG	800
25	TATTACCTCC	ACCAAGACCG	GTTC			824

2) INFORMATION FOR SEQ ID NO: 331

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Pantoea dispersa*
(B) STRAIN: ATCC 14589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331

45	TATACAGCGC	TCTCGAGGTA	AAAAATGGTG	ATGCTCGTCT	GGTGCTGGAA	50
	GTACAGCAGC	AGCTGGGCGG	TGGCGTGGTG	CGTACCATCG	CCATGGGTTC	100
	TTCTGACGGC	CTGAAGCGCG	GTCTGGAAGT	CACCGACCTG	AAAAAACCTA	150
	TCCAGGTTCC	GGTTGGTAAA	GCAACACTCG	GCCGTATCAT	GAACGTGCTG	200
	GGTGAGCCAA	TCGACATGAA	AGGCGACCTG	AAAGAAGAAG	ACGGCAGCGC	250
50	TGTAGAGGTT	TCCTCTATTG	ATCGCGCAGC	GCCTTCTTAT	GAAGATCAGT	300
	CAAACCTCGA	GGAACCTGCTG	GAAACCGGCA	TCAAGGTTAT	CGACCTGATG	350
	TGTCCGTTCC	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGGCTGAGC	450
	ACTCAGGTTA	TTCGGTCTTT	GCCGGCGTGG	GTGAGCGTAC	TCGTGAGGGT	500
55	AACGACTTCT	ACCACGAAAT	GACGGACTCC	AACGTTATCG	ATAAAGTAGC	550
	GCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGTAACCGT	CTGCGCGTAG	600
	CACTGACCGG	TCTGACCATG	GCGGAAAAAT	TCCGTGATGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCATCGACAA	CATCTACCGT	TACACCCTGG	CCGGTACAGA	700
	GGTTTCTGCA	CTGCTGGGTC	GTATGCCATC	GGCGGTAGGT	TATCAGCCAA	750
60	CGCTGGCTGA	AGAGATGGGT	GTGCTGCAGG	AGCGTATTAC	CTCCACCAAG	800

5 2) INFORMATION FOR SEQ ID NO: 332

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Pasteurella multocida*
 (B) STRAIN: NCTC 10322

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332

20	GATGCAGTAC	CAAAAGTATA	TGATGCCTTA	AATGTTGAAA	CAGGTTTAGT	50
	ACTTGAAGTT	CAACAACAAT	TAGGTGGTGG	TGTAGTTCGC	TGTATCGCAA	100
	TGGGATCATC	TGATGGATTA	AAACGCGGTT	TAAGCGTAAC	AAATACGAAT	150
	AACCCAATTT	CTGTTCCAGT	GGGAACGAAA	ACATTGGGTC	GTATCATGAA	200
25	CGTATTGGGT	GAACCAATCG	ATGAGCAAGG	TGAAATCGGT	GCAGAAGAGA	250
	ATTGGTCTAT	TCACCGTGCG	CCACCAAGTT	ATGAAGAACA	ATCTAACAGT	300
	ACTGAACTTT	TAGAAACGGG	AATTAAAGTT	ATCGACTTAG	TTTGTCCGTT	350
	TGCGAAAGGG	GGTAAAGTAG	GTTTATTCGG	TGGTGCGGGT	GTCGGTAAAA	400
	CCGTCAATAT	GATGGAATTA	ATCCGTAAAC	TCGCAATTGA	GCACTCAGGT	450
30	TACTCTGTCT	TTGCGGGGGT	AGGTGAGCGT	ACGCGTGAAG	GTAACGACTT	500
	CTATCATGAG	ATGAAAGACT	CTAACGTATT	AGATAAAGTG	TCTCTTGTTT	550
	ATGGTCAAAT	GAACGAGCCA	CCAGGTAACC	GTTTACGTGT	GGCATTAAAC	600
	GGCTTAACTA	TGGCGGAAAA	ATTCCGTGAT	GAAGGTCGTG	ATGTCTTATT	650
	CTTCGTTGAT	AATATTTATC	GTTATACTCT	TGCTGGTACA	GAAGTTTCTG	700
35	CATTATTAGG	TCGTATGCCA	TCTGCGGTAG	GTTATCAACC	AACCCTTGCA	750
	GAAGAAATGG	GTGTTCTGCA	AGAGCGTATT	ACCTCAACCA	AAACAGGTTC	800
	TATTA					805

10 2) INFORMATION FOR SEQ ID NO: 333

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 828 bases
15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 50 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Pragia fontium*
 (B) STRAIN: ATCC 49100

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333

	TTTCCTCAAG	ACGCCGTACC	AAAAGTGTAC	GACGCGCTTG	AAGTTCAGAA	50
	CGATGCCAAG	CTGGTGCTGG	AAGTTCAACA	ACAGCTCGGT	GGTGGTGTCG	100
	TTCGTTGTAT	CGCAATGGGT	ACTTCCGATG	GCTTAAGCCG	CGGTTTAAAA	150
50	GTGCTTGATT	TAGAACATCC	TATCGAAGTA	CCGGTTGGTA	CTGCGACGCT	200

	GGGCCGTATT	ATGAACGTGC	TCGGTCAGCC	AATCGATATG	AAAGGCGATA	250
	TTGGTGAAGA	AGAGCGTTGG	GCTATTCACC	GTGAAGCACC	AAGTTATGAA	300
	GATTTATCTG	GCGCCAATGA	ACTGCTGGAA	ACGGGTATCA	AGGTTATCGA	350
	CCTGATTTGT	CCGTTTGCTA	AAGGTGGTAA	AGTTGGTCTG	TTTGGTGGTG	400
5	CGGGTGTAGG	TAAAACCGTA	AACATGATGG	AGCTGATTCG	TAACATTGCG	450
	ACTGAGCACT	CAGGTTACTC	CGTATTCGCC	GGTGTAGGGG	AACGTACCCG	500
	TGAAGGTAAT	GACTTCTACC	ACGAAATGAC	CGAATCAAAC	GTACTGGATA	550
	AAGTATCTCT	GGTTTATGGC	CAGATGAACG	AGCCACCAGG	AAACCGTCTG	600
	CGCGTGGCGT	TAACGGGTTT	GACCATGGCT	GAAAAATTCC	GTGATGAAGG	650
10	TCGTGACGTT	CTGTTATTTA	TCGATAACAT	TTATCGCTAT	ACCTTAGCCG	700
	GTACCGAAGT	ATCAGCACTG	TTGGGGCGTA	TGCCATCAGC	GGTAGGTTAT	750
	CAGCCAACGT	TAGCAGAAGA	GATGGGTGTG	TTGCAGGAAC	GTATTACTTC	800
	AACCAAAC	GGTTCAATCA	CTTCTGTA			828

15

2) INFORMATION FOR SEQ ID NO: 334

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 807 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334

	GTCCCTAAAG	TATACGACGC	TCTTGAGGTT	ATGAATGGTA	AAGAAAAACT	50
	GGTGCTGGAA	G TTCAGCAAC	AGTTAGGCGG	TGGTATCGTT	CGTTGTATCG	100
35	CAATGGGTAC	ATCAGACGGT	TTAAGCCGTG	GCTTAAAGGT	TGAAGATTTA	150
	GGCCACCCAA	TTGAAGTACC	AGTAGGTAAA	GCGACTTTAG	GACGTATCAT	200
	GAACGTTCTG	GGTACACCTA	TTGATATGAA	AGGTGAGATT	GAAACCGAAG	250
	AGCGTTGGTC	AATCCACCGT	GAAGCACCAA	CTTACGAAGA	GTTATCAAAC	300
	TCTCAAGAAC	TGCTTGAAAC	CGGTATCAAA	GTTATGGACT	TAATCTGTCC	350
40	ATTTGCTAAA	GGTGGTAAAG	TCGGTCTGTT	CGGTGGTGCG	GGTGTGTTGGTA	400
	AAACAGTTAA	CATGATGGAA	TTGATCCGTA	ATATCGCGAT	CGAGCACTCA	450
	GGTTACTCTG	TATTTGCTGG	TGTTGGTGAG	CGTACTCGTG	AGGGTAACGA	500
	CTTCTATCAT	GAAATGACAG	ATTCTAACGT	TCTTGACAAA	GTATCGTTAG	550
	TTTACGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTGCG	TGTTGCACTG	600
45	ACTGGTCTGA	CTATGGCTGA	GAAATTCCGT	GATGAAGGCC	GTGACGTACT	650
	GTTATTCGTC	GATAACATCT	ATCGTTACAC	CTTAGCCGGT	ACAGAAGTAT	700
	CAGCACTGTT	AGGTCGTATG	CCATCAGCGG	TAGGTTACCA	ACCAACATTG	750
	GCTGAAGAGA	TGGGTGTTCT	GCAAGAGCGT	ATCACTTCAA	CCAAAACAGG	800
	TTCTATC					807

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2) INFORMATION FOR SEQ ID NO: 335

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 811 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 5 (B) STRAIN: ATCC 13315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335

	CCCTAAAGTA	TACGACGCTC	TTGAGGTTAT	GAATGGTAAA	GAGAAACTGG	50
10	TGCTAGAAGT	TCAGCAACAG	TTAGGCGGTG	GTATCGTTCG	TTGTATCGCA	100
	ATGGGTACAT	CAGACGGTTT	AAGCCGTGGC	TTAAAAGTTG	AAAACCTTAGG	150
	CCACCCAATT	GAAGTACCAG	TAGGTAAAGC	AACACTGGGA	CGTATCATGA	200
	ACGTTCTGGG	TACACCTATC	GATATGAAAG	GTGATATTGC	AACTGAAGAA	250
	CGTTGGTCTA	TTCACCGCGA	AGCGCCAACC	TATGAAGAGT	TATCAAGCTC	300
15	TCAAGAACTA	CTAGAAACCG	GTATCAAAGT	AATGGACTTA	ATCTGTCCGT	350
	TTGCTAAAGG	TGGTAAAGTA	GGTCTCTTCG	GTGGTGCGGG	TGTTGGTAAA	400
	ACAGTTAACA	TGATGGAATT	GATCCGTAAC	ATCGCGATTG	AGCACTCAGG	450
	TTATTCTGTA	TTTGCAGGTG	TTGGTGAGCG	TACTCGTGAG	GGTAACGACT	500
	TCTATCATGA	AATGACAGAT	TCTAACGTTT	TTGACAAAGT	ATCGTTAGTT	550
20	TATGGTCAGA	TGAATGAGCC	ACCAGGAAAC	CGTCTACGTG	TAGCACTGAC	600
	GGGTTTAACC	ATGGCGGAAA	AATTCCGTGA	TGAAGGCCGT	GACGTACTGT	650
	TATTCGTCGA	TAACATCTAT	CGTTACACCT	TAGCCGGTAC	CGAAGTATCA	700
	GCACTGTTAG	GCCGTATGCC	ATCAGCAGTA	GGTTACCAAC	CAACATTGGC	750
	TGAAGAGATG	GGTGTCTGTC	AAGAACGTAT	CACTTCAACC	AAAACAGGTT	800
25	CAATCACCTC	T				811

2) INFORMATION FOR SEQ ID NO: 336

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Providencia alcalifaciens*
 (B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336

45	TCAAGATAAC	GTACCAAAG	TGTACGATGC	TCTTGAGGTT	ATTAACGGTA	50
	AAGAAAAACT	GGTGTGGA	GTTCAACAAC	AGTTAGGTGG	TGGTGTGTC	100
	CGTTGTATCG	CAATGGGTAC	ATCAGATGGT	CTGAGCCGTG	GTTTAGAAGT	150
	TGTAAACTTA	GAGCACCCAA	TCGAAGTACC	AGTCGGTAAA	GCAACTCTGG	200
	GACGTATCAT	GAACGTTCTG	GGTGAACCAA	TCGACATGAA	AGGTGATATC	250
50	GGCGAAGAAG	AGCGCTGGTC	TATTCACCGT	GCTGCACCAA	GCTACGAAGA	300
	ATTAGCTAAC	TCAACTGAAC	TGCTGGAAAC	CGGTATCAAA	GTAATGGACT	350
	TAATCTGTCC	ATTCGCGAAA	GGTGGTAAAG	TAGGTCTGTT	CGGTGGTGCG	400
	GGTGTGGA	AAACCGTAAA	CATGATGGAA	CTGATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTTACTCAG	TGTTGCTGAG	TGTTGGTGAG	CGTACCCGTG	500
55	AAGGTAACGA	CTTCTATCAT	GAAATGACAG	ACTCAAACGT	TCTGGATAAA	550
	GTATCACTGG	TTTATGGCCA	GATGAACGAG	CCACCAGGAA	ACCGTCTGCG	600
	TGTTGCGCTG	ACTGGTCTGA	CTATGGCTGA	AAAATTCCGT	GACGAAGGTC	650
	GTGACGTACT	GCTGTTTCGTT	GACAACATTT	ATCGTTATAC	ACTGGCAGGT	700
	ACTGAAGTAT	CAGCACTGTT	AGGTCGTATG	CCATCAGCGG	TAGGTTACCA	750
50	ACCAACGCTG	GCGGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATTACCTCAA	800

5 2) INFORMATION FOR SEQ ID NO: 337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
(B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337

20 TTCCCTCAAG ATGACGTACC AAAAGTGTAC GACGCTCTTG AGGTTGTTAA 50
CGGTAAAGAA ACACTGGTGC TGGAAAGTTCA GCAACAGTTA GGCGGTGGTG 100
TTGTCCGTTG TATCGCAATG GGTACATCAG ATGGCCTGAG CCGTGGTTTA 150
GAAGTTGTAA ACTTAGAGCA CCCAATTGAA GTACCAGTAG GTAAAGCAAC 200
25 TTTAGGACGT ATCATGAACG TTCTGGGTCA GCCTATTGAT ATGAAAGGTG 250
ATATCGGCGA AGAAGAGCGC TGGTCAATTC ACCGTGCTGC ACCTAGCTAC 300
GAAGAGTTAG CTAACCTAAC AGAGCTGCTG GAAACCGGTA TCAAAGTAAT 350
GGACTTAATC TGTCCATTCT CGAAAGGTGG TAAAGTTGGT CTGTTCCGGT 400
GTGCGGGTGT TGGTAAAACA GTAAACATGA TGGAACTGAT CCGTAACATC 450
30 GCGATTGAGC ACTCAGGTTA CTCAGTATTC GCTGGTGTG GTGAGCGTAC 500
TCGTGAAGGG AACGACTTCT ATCATGAAAT GACTGACTCA AACGTTCTGG 550
ATAAAGTATC ACTGGTTTAT GGCCAGATGA ATGAGCCACC AGGAAACCGT 600
CTGCGCGTTG CGTTGACTGG TCTGACTATG GCTGAAAAAT TCCGTGACGA 650
AGGTCGTGAC GTACTACTGT TCGTTGACAA CATCTATCGT TATACTACTG 700
35 CAGGTACTGA AGTATCAGCA CTGTTAGGTC GTATGCCTTC AGCGGTAGGT 750
TATCAGCCAA CGCTGGCGGA AGAGATGGGT GTTCTGCAAG AACGTATTAC 800
CTCAACTCAA ACGGGTTCTA TCACTTCCGT 830

10 2) INFORMATION FOR SEQ ID NO: 338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*
(B) STRAIN: ATCC 33673

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338

AGCGTACCAA AAGTGTACGA TGCTCTTGAG GTTATTAACG GTAAAGAAAA 50
ACTGGTGTG GAAGTTCAGC AGCAGTTAGG CGGTGGTGTG GTCCGTTGTA 100
TCGCAATGGG TACATCAGAT GGTCTGAGCC GTGGTTTAGA AGTTGTAAAC 150
50 TTAGAACACC CAATTGAAGT ACCAGTAGGT AAAGCAACTC TGGGACGTAT 200

	CATGAACGTT	CTGGGTGACC	CTATTGATAT	GAAAGGTGAT	ATCGGCGAAG	250
	AAGAGCGCTG	GTCTATTCAC	CGTTCAGCGC	CAAGCTATGA	AGAATTAGCT	300
	AACTCAACAG	AACTGCTAGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
	TCCATTCGCG	AAAGGTGGTA	AAGTTGGTCT	GTTCCGGTGGT	GCGGGTGTG	400
5	GTAAAACAGT	AAACATGATG	GAACGTATCC	GTAACATCGC	GATTGAGCAC	450
	TCAGGTTACT	CAGTATTCGC	TGGTGTTGGT	GAGCGTACCC	GTGAAGGTAA	500
	CGACTTCTAT	CATGAAATGA	CTGATTCTAA	CGTTCTGGAT	AAAGTATCAC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGTGTTGCG	600
	CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGACGAAG	GTCGTGACGT	650
10	ACTGCTGTTC	GTTGACAACA	TTTATCGTTA	TACACTGGCA	GGTACTGAAG	700
	TATCAGCACT	GTTAGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCAACA	750
	TTGGCAGAAG	AGATGGGTGT	TCTACAAGAA	CGTATCACTT	CTACCAAAAC	800
	CGGTTCTATC	AC				812

15

2) INFORMATION FOR SEQ ID NO: 339

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 819 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia stuartii*

(B) STRAIN: ATCC 33672

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339

	TCAAGATGCA	GTACCAAAAG	TGTACGATGC	GCTTGAGGTT	GTTAACGGTA	50
	AAGAAAAACT	GGTGCTGGAA	GTTTCAGCAAC	AGTTAGGCCG	TGGTGTTGTC	100
35	CGTTGTATCG	CAATGGGTAC	ATCAGATGGC	CTAAGCCGTG	GTTTAGAAGT	150
	TAAAAATTTA	GAACACCCAA	TTGAAGTACC	AGTAGGTAAA	GCAACACTCG	200
	GACGTATCAT	GAACGTTCTG	GGTGACCCTA	TTGATATGAA	AGGTGATATC	250
	GGCGAAGAAG	AGCGTTGGTC	TATTCACCGC	GCTGCACCAA	GCTACGAAGA	300
	GCTATCGAGC	TCAACTGAAC	TGCTAGAGAC	AGGTATCAAA	GTCATGGACT	350
10	TGATCTGTCC	ATTCGCGAAA	GGTGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	400
	GGTGTTGGTA	AAACGGTAAA	CATGATGGAA	CTTATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTACTCAG	TATTCGCAGG	TGTTGGTGAG	CGTACCCGTG	500
	AAGGTAAACGA	CTTCTATCAT	GAAATGACAG	ATTCAAACGT	TCTTGACAAA	550
	GTATCACTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTACG	600
15	CGTAGCATTG	ACTGGTTTGA	CTATGGCTGA	GAAATTCCGT	GACGAAGGCC	650
	GTGATGTTCT	GTTGTTTCGTG	GATAACATCT	ATCGTTATAC	ACTGGCAGGT	700
	ACAGAAGTAT	CGGCTCTGTT	AGGTCGTATG	CCATCAGCAG	TAGGTTATCA	750
	GCCAACATTG	GCAGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATCACTTCTA	800
	CTAAGACAGG	TTCTATCAC				819

50

2) INFORMATION FOR SEQ ID NO: 340

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 907 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Psychrobacter phenylpyruvici*
 5 (B) STRAIN: ATCC 23333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340

	AACCGCACTG	ACGTGCCTCA	AATTTATGAC	GCGTTAGTTG	TAGATGGTAC	50
10	CGAAACCACC	CTAGAAGTTC	AGCAGCAGCT	GGGCGATGGT	GTGGTACGTA	100
	CTATTGCAAT	GGGATCTACT	GAAGGTCTTA	AGCGTGGTTT	ACCAGTAACA	150
	AACACTGGTG	CCCCAATTAC	AGTTCCAGTA	GGTGATGCGA	CTTTAGGTCG	200
	TATTATGGAC	GTTTTAGGTC	GTCCAATTGA	CGAACAAGGT	CCAGTTAATT	250
	CTGAAGACCA	TTGGTCAATC	CACCGTCAAG	CGCCATCATA	TGATGAGCAA	300
15	GCTAACAGTA	CTGACCTATT	AGAGACAGGT	ATTAAAGTAA	TTGACTTACT	350
	TTGTCCGTTT	GCTAAAGGGG	GTAAAGTTGG	TCTGTTCCGT	GGTGCCGGTG	400
	TTGGTAAAC	CGTAAACATG	ATGGAATTGA	TTAATAACAT	CGCTCTTAAG	450
	CACTCAGGTT	TATCAGTATT	CGCTGGTGTG	GGTGAGCGTA	CTCGTGAAGG	500
	TAACGACTTC	TACCACGAGA	TGCAAGAAGC	GGGTGTTGTT	GACGTTGAAA	550
20	ACTTCACCAA	CTCAAAAGTT	GCGATGGTTT	ATGGTCAGAT	GAATGAGCCA	600
	CCAGGTAACC	GTTTACGTGT	TGCGTTAACC	GGTCTGACTA	TGGCTGAGTA	650
	CTTCCGTGAT	CAAAAAGATG	AAAACGGTAA	AGGTAAAGAC	GTTCTATTAT	700
	TCGTTGATAA	CATCTACCGC	TACACGCTAG	CCGGTACTGA	AGTATCAGCA	750
	CTTCTAGGTC	GTATGCCATC	AGCAGTAGGT	TATCAGCCAA	CACTAGCGGA	800
25	AGAGATGGGT	GTACTACAAG	AGCGTATTAC	TTCAACTCAG	ACTGGTTCTA	850
	TTACTTC					907

30 2) INFORMATION FOR SEQ ID NO: 341

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rahnella aquatilis*
 (B) STRAIN: DSM 4594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341

45	GTTCCCTCAG	GATGCAGTAC	CGAACGTGTA	CAATGCTCTT	GAGGTAGAAA	50
	ACGGTACCTC	CAAACCTGGT	CTGGAAGTTC	AGCAACAGTT	AGGCGGCGGC	100
	GTTGTTTCGT	GTATCGCAAT	GGGTACCTCA	GACGGCCTGC	GTCGCGGTCT	150
	GAAAGTGAAC	AACCTGGAAC	ACCCAATTGA	AGTACCGGTA	GGTAAAGCGA	200
50	CTCTGGGTCG	TATCATGAAC	GTATTGGGTG	AACCAATCGA	CATGAAAGGT	250
	GAAATCGGCG	AAGAAGAACG	TCGTGCTATT	CACCGTGCTG	CGCCTTCTTA	300
	TGAAGAGCTG	GCAAACCTCC	AGGAATTGCT	GGAAACCGGT	ATCAAAGTTA	350
	TGGACCTGAT	GTGTCCGTTC	GCTAAGGGCG	GTAAAGTTGG	TCTGTTCCGT	400
	GGTGCGGGTG	TAGGTAAAAC	TGTGAACATG	ATGGAGCTGA	TCCGTAACAT	450
55	TGCGATCGAG	CACTCCGGTT	ATTCTGTGTT	TGCAGGCGTG	GGTGAACGTA	500
	CTCGTGAGGG	TAACGACTTC	TACCACGAAA	TGACTGATTC	CAACGTTATC	550
	GACAAAGTTT	CCCTGGTGTA	TGGCCAGATG	AATGAGCCAC	CAGGTAACCG	600
	TCTGCGCGTT	GCACTGACCG	GCCTGACCAT	GGCGGAAAAA	TTCCGTGATG	650
	AAGGTCGTGA	CGTACTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	700
60	GCCGGTACCG	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	750

TTATCAGCCA ACGCTGGCGG AAGAGATGGG CGCTCTGCAA GAACGTATCA' 800
 CCTCGACCAA AAGTGGTTCT ATCACCTCCG TA 832

5

2) INFORMATION FOR SEQ ID NO: 342

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342

TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTGGTGC TGAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
 TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTT 150
 25 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200
 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCGA AGAAGAGCGT TGGGCTATTC ACCGCGCGGC GCCGTCCTAC 300
 GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TAAAAGTTAT 350
 CGACCTGATG TGTCCGTTTC CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
 30 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550
 ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAACCGT 600
 CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
 35 AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCCTCG 700
 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
 TAYCASCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAAA ACCGGTTCTA TCAC 824

40

2) INFORMATION FOR SEQ ID NO: 343

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *Choleraesuis*
 55 (B) STRAIN: ATCC 7001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343

GATGCCGTAC CACGCGTGTA CGATGCCCTT GAGGTGCAGA ATGGTAATGA 50
 60 GAAGCTGGTG CTGGAAGTTC AGCAGCAGCT TGGCGGCGGT ATCGTGCGTA 100

	CCATCGCGAT	GGGGTCTTCT	GACGGTCTGC	GTCGCGGTCT	GGATGTAAAA	150
	GATCTCGAAC	ACCCGATCGA	AGTCCC GGTA	GGTAAAGCCA	CGCTGGGTCG	200
	TATCATGAAC	GTCCTGGGCG	AACCGGTCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGCGCAG	CACCTTCCTA	CGAAGAGTTG	300
5	TCAAAC TCTC	AGGAACTGCT	GGAAACCGGT	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTTCGGT	GGTGCGGGTG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTTA	TTCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCAGTGTT	TGCGGGCGTA	GGGGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	GATAAAGTAT	550
10	CCCTGGTGTA	TGGCCAGATG	AACGAGCCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCACTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	TGTACTGCTG	TTCGTCGATA	ACATCTATCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CCGCAGTAGG	TTACCAGCCG	750
	ACTCTGGCGG	AAGAGATGGG	CGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
15	AACCGGTTCT	ATCACCTCCG				820

2) INFORMATION FOR SEQ ID NO: 344

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*
 (B) STRAIN: ATCC 43973

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344

35	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCTCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTT	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCC GGTA	GTAAAGCAAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGTGA	ACCGGTCGAT	ATGAAAGGCG	250
40	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCGGC	GCCGTCCTAC	300
	GAAGAGTTGT	CAAAC TCTCA	GGAAC TGTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTC	CGAAGGGCGG	TAAAGTCGGT	CTGTTTCGGTG	400
	GCGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
45	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCT	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCACC	GGGAAACCGT	600
	CTGCGCGTTG	CATTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGATGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTGACAA	CATCTACCGT	TATACCCTCG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
50	TATCAGCCGA	CTCTGGCTGA	AGAAATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

55 2) INFORMATION FOR SEQ ID NO: 345

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*

(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345

10
 TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTGGTGC TGGAAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
 TCGTACGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG 150
 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCTAC 200
 15 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCTGC GCCGTCCTAC 300
 GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT 350
 CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 20 GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG 550
 ATAAAGTATC CCTGGTGTAT GGTGAGATGA ACGAGCCGCC GGGAAACCGT 600
 CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGACGA 650
 AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG 700
 25 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
 TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAAG ACCGGTTCTA TCACCTCCGT A 831

30

2) INFORMATION FOR SEQ ID NO: 346

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*

(B) STRAIN: ATCC 43974

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346

TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTCGTGC TGGAAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
 TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG 150
 50 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200
 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCGGC GCCGTCCTAT 300
 GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT 350
 CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
 55 GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG 550
 ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT 600
 CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAGAAGT TCCGTGACGA 650
 60 AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG 700

CCGGTACGGA AGTTTCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
TATCAGCCAA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
CTCCACCAA ACCGGTTCTA TCACCTCCG 829

5

2) INFORMATION FOR SEQ ID NO: 347

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi A
- 20 (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347

25 GCCGTACCAC GCGTGTACGA TGCCCTTGAG GTGCAGAATG GTAATGAGAA 50
GCTGGTGCTG GAAGTTCAGC AGCAGCTTGG CGGCGGTATC GTGCGTACCA 100
TCGCGATGGG GTCTTCTGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAGAT 150
CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCTACGC TGGGTCGTAT 200
CATGAACGTC CTGGGCGAAC CGGTCGACAT GAAAGGCGAG ATCGGCGAAG 250
AAGAGCGTTG GGCGATTCAC CGCGCAGCGC CTCCTACGA AGAGTTGTCA 300
30 AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG 350
TCCGTTTCGG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAACCGT AAACATGATG GAGCTTATCC GTAACATCGC GATCGAGCAC 450
TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CATGAAATGA CCGACTCCAA CGTTATCGAT AAAGTATCCC 550
35 TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA 600
CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGACGAAG GTCGTGACGT 650
ACTGCTGTTC GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG 700
TATCCGCACT GCTGGGTCGT ATGCCTTCCG CGGTAGGTTA CCAGCCGACT 750
CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAGAC 800
40 CGGTTCTATC ACCTCCG 817

2) INFORMATION FOR SEQ ID NO: 348

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
- 50 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- 55 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi B
(B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATT	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTCTGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCG	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTGG	400
	GTAACACCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CGGTTC					806

20

2) INFORMATION FOR SEQ ID NO: 349

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
- (B) STRAIN: ATCC 43972

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGKGGTCTG	150
40	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	GCTGGGCCGT	ATCATGAACG	TACTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATTGGTGA	AGAAGAGCGT	TGGGCTATTC	ACCGTGCTGC	GCCGTCCTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGTG	400
45	GCGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGACGA	650
50	AGGTCGTGAC	GTAATGCTGT	TCGTGATAA	CATCTATCGT	TATACCTTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TATCAGCCGA	CGCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACTAAA	ACCGGTTCTA	TCACCTCCGT	A		831

55

2) INFORMATION FOR SEQ ID NO: 350

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 823 bases

60

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhi
 10 (B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
15	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCTAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	GCCTTCCTAC	300
20	GAAGAGTTAT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCATGAAAT	GACCGACTCC	AACGTTATCG	550
25	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTACTGCTGT	TCGTGATAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
30	CTCCACCAAG	ACCGGTTCTA	TCA			823

2) INFORMATION FOR SEQ ID NO: 351

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351

50

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TTGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCTAC	200
55	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	GCCTTCCTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
60	GCGATCGAGC	ACTCCGGTTA	CTCAGTGTTT	GCGGGCGTAG	GGGAACGTAC	500

TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC ~~AACGTTATCG~~ 511
 ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT 600
 CTGCGCGTTG CATTGACCGG TCTGACCATG GCGGAGAAAT TCCGTGACGA 650
 AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG 700
 5 CCGGTACGGA AGTATCCGCA CTGCTGGGCC GTATGCCTTC CGCAGTAGGT 750
 TACCAGCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAA ACCGGTTCTA TCACCTCCGT A 831

10

2) INFORMATION FOR SEQ ID NO: 352

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA
 20

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Virchow
 (B) STRAIN: ATCC 51955
 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352

GCCGTACCAC GCGTGTACGA TGCCCTTGAG GTGCAGAATG GTAATGAGAA 50
 GCTGGTGCTG GAAGTTCAGC AGCAGCTTGG CGGCGGTATC GTGCGTACCA 100
 30 TCGCGATGGG GTCTTCTGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAGAT 150
 CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCCACGC TGGGTCGTAT 200
 CATGAACGTC CTGGGCGAAC CGGTCGACAT GAAAGGCGAG ATCGGCGAAG 250
 AAGAGCGTTG GGCGATTCAC CGCGCAGCAC CTTCTTACGA AGAGTTGTCA 300
 AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG 350
 35 TCCGTTTCGG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400
 GTAAAACCGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC 450
 TCCGGTTACT CTGTGTTTGC GGGCGTAGGG GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTCTCCC 550
 TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA 600
 40 TTGACCGGTC TGACCATGGC GGAGAAATTC CGTGACGAAG GTCGTGACGT 650
 ACTGCTGTTC GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG 700
 TATCCGCACT GCTGGGCCGT ATGCCTTCCG CAGTAGGTTA CCAGCCGACT 750
 CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAC 800
 CGGTTCTATC 810

45

2) INFORMATION FOR SEQ ID NO: 353

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Serratia ficaria*
 60 (B) STRAIN: ATCC 33105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353

	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
5	GAAACTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTCGTTTCGCT	100
	GTATCGCAAT	GGGGACCTCT	GACGGTCTGC	GTCGCGGTCT	GAAAGTGAAC	150
	AACCTGGAAC	ACCCGATTGA	AGTGCCGGTG	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGCG	AACCAATCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGTCCTG	CGCCAAGCTA	CGAAGAGCTG	300
10	TCCAAC TCCC	AGGACCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	TTGTCCGTTT	GCCAAGGGCG	GTAAAGTCGG	TCTGTTTCGGT	GGTGCGGGCG	400
	TGGGCAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCCGTGTT	TGCGGGCGTG	GGCGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGAACGACTC	CAACGTTCTG	GACAAAGTAT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCGC	CGGGTAACCG	TCTGCGCGTT	600
	GCATTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGCCGCGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CCGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCC	ATCACCTCCG				820

2) INFORMATION FOR SEQ ID NO: 354

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia fonticola*
 (B) STRAIN: ATCC 29844

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354

40	GATGCCGTAC	CGAAAGTGTA	CAACGCTCTT	GAGGTTGCAA	ACGGCACCGA	50
	GAAATTGGTG	CTGGAAGTTC	AGCAACAGCT	GGGTGGCGGC	GTGGTTTCGCT	100
	GTATCGCAAT	GGGGACCTCA	GACGGTCTGC	GTCGTGGTCT	GGCCGTAACC	150
	GACCTGCAGC	ACCCAATTGA	AGTACCGGTA	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGTG	AACCAATCGA	CATGAAGGGC	GACATCGGCG	250
45	AAGAAGAACG	TTGGGCTATT	CACCGCCCTG	CGCCAAGCTA	CGAAGAGCTG	300
	TCCAGCTCCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	CTGCCCCTTC	GCCAAGGGTG	GTAAAGTTGG	TCTGTTTCGGT	GGTGCTGGTG	400
	TAGGTAA AAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
50	TAACGACTTC	TACCACGAAA	TGACCGATTG	CAACGTACTG	GACAAAGTTT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CAGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GCCTGACCAT	GGCTGAGAAG	TTCCGTGACG	AAGGTCGTGA	650
	CGTACTGCTG	TTCGTCGATA	ACATCTACCG	TTATACCCTG	GCCGGTACCG	700
	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
55	ACGCTGGCGG	AAGAGATGGG	TGTTCTGCAA	GAACGTATCA	CCTCTACCAA	800
	GACTGGTTCA	ATCACC				816

60 2) INFORMATION FOR SEQ ID NO: 355

212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia grimesii*
 (B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355

15 GATGCCGTAC CAAAAGTGTA CAACGCTCTT GAGGTAGAAA ACGGTGCCAA 50
 TAAGCTGGTG CTGGAAGTTC AGCAACAGTT GGGCGGTGGC GTGGTTCGCT 100
 GTATCGCAAT GGGGACCTCT GATGGTCTGC GTCGCGGTCT GAAAGTCACA 150
 GACCTGGACC ACCCAATTGA AGTACCGGTA GGTAAGCTA CTCTGGGCCG 200
 20 TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAGGGC GATATCGGCG 250
 AAGAAGAACG TTGGGCGATT CACCGTCCGG CGCCAAGCTA CGAAGATTTG 300
 GCCAACTCCC AGGATCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT 350
 CTGCCCCGTT GCCAAGGGTG GTAAAGTCGG TCTGTTTCGGT GGTGCGGGTG 400
 TTGGTAA AAC CGTAAACATG ATGGAGCTGA TCCGTAAACAT CGCGATCGAG 450
 25 CACTCCGGTT ATTCTGTGTT TCGGGCGGTG GGTGAGCGTA CTCGTGAGGG 500
 TAACGACTTC TACCACGAAA TGAACGACTC CAACGTACTG GACAAAGTAT 550
 CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT 600
 GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGCCGTGA 650
 CGTTCTGCTG TTCGTTGATA ACATCTACCG TTATACCCTG GCCGGTACCG 700
 30 AAGTGTCGCG ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA 750
 ACGCTGGCGG AAGAGATGGG TGTTCGCAA GAACGTATCA CCTCTACCAA 800
 GACTGGTTCA ATCACCTCCG TA 822

35

2) INFORMATION FOR SEQ ID NO: 356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia liquefaciens*
 (B) STRAIN: ATCC 27592

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356

ATGCCGTACC AAAAGTGTA AATGCTCTTG AGGTAGAAAA CCGTACCGAG 50
 AAGCTGGTGC TGGAAGTTCA GCAGCAGTTG GGCAGGTGGCG TAGTTCGCTG 100
 TATCGCGATG GGGACCTCAG ATGGTCTGCG CCGCGGTCTG AAAGTGAACG 150
 55 ATCTGGAACA CCCAATTGAA GTACCGGTAG GTAAAGCTAC CCTGGGCCGT 200
 ATCATGAACG TATTGGGTGA ACCAATCGAC ATGAAAGGCG ACATCGGCGA 250
 AGAAGAACGT TGGGCGATTC ACCGTCCAGC GCCAAGCTAC GAAGATTTGT 300
 CAAACTCCCA GGATCTGCTG GAAACCGGTA TCAAGGTTAT GGACCTGATT 350
 TGTCCGTTTC CTAAGGGCGG TAAAGTTGGT CTGTTTCGGTG GTGCTGGTGT 400
 60 TGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC 450

	ACTCCGGTTA	TTC CGTGT TTT	GCAGGCGTGG	GTGAGCGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GAACGACTCC	AACGTACTGG	ACAAAGTATC	550
	CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	GGGTAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGACGA	AGGCCGCGAC	650
5	GTTCTGCTGT	TCGTTGATAA	CATTTACCGT	TATACCCTGG	CCGGTACCGA	700
	AGTGTCCGCA	CTTCTGGGCC	GTATGCCATC	TGCGGTAGGT	TATCAGCCAA	750
	CGCTGGCGGA	AGAGATGGGC	GTTCTGCAAG	AACGTATCAC	CTCTACCAAG	800
	ACCGGTTCTA	TCACTTCCG				819

10

2) INFORMATION FOR SEQ ID NO: 357

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia marcescens*

(B) STRAIN: ATCC 13880

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357

	TCAGGATGCC	GTACCGAAAG	TGTACGACGC	CCTTGAGGTA	GAAAACGGCA	50
	CCGAAAAACT	GGTGTGGAA	GTT CAGCAAC	AGCTGGGCGG	TGGCGTGGTT	100
30	CGCTGTATCG	CAATGGGGAC	CTCCGACGGT	CTGCGTCGCG	GTCTGAAAGT	150
	GAACAACCTG	GACCACCCGA	TTGAAGTGCC	GGTGGGTAAA	GCTACCCTGG	200
	GTCGTATCAT	GAACGTATTG	GGTCAACCGA	TCGACATGAA	AGGCGACATC	250
	GGCGAAGAAG	AGCGTTGGGC	GATTCACCGC	GCGGCGCCAA	GCTACGAAGA	300
	GCTGTCAAGC	TCTCAGGAAC	TGCTGGAAAC	CGGTATCAAG	GTAATGGACC	350
35	TGATTTGTCC	GTT CGCCAAG	GGCGGTAAAG	TCGGTCTGTT	CGGCGGTGCG	400
	GGCGTAGGTA	AAACCGTAAA	CATGATGGAG	CTGATCCGTA	ACATCGCGAT	450
	CGAGCACTCC	GGTTATTCCG	TGTTTGCGGG	CGTGGGCGAG	CGTACTCGTG	500
	AGGGTAACGA	CTTCTACCAC	GAAATGACCG	ACTCCAACGT	TCTGGACAAA	550
	GTATCCCTGG	TTTACGGCCA	GATGAACGAG	CCACCAGGTA	ACCGTCTGCG	600
40	CGTTGCGCTG	ACCGGTCTGA	CCATGGCGGA	GAAATTCCGT	GACGAAGGCC	650
	GTGACGTTCT	GCTGTTTCGTT	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	700
	ACCGAAGTGT	CCGCACTTCT	GGGCCGTATG	CCATCCGCGG	TAGGTTATCA	750
	GCCAACGCTG	GCGGAAGAGA	TGGGCGTTCT	GCAAGAACGT	ATCACCTCGA	800
	CCAAG					805

45

2) INFORMATION FOR SEQ ID NO: 358

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia odorifera*

60 (B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358

	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
5	AACTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTGGTTCGTT	100
	GTATCGCTAT	GGGCACCTCC	GACGGTTTGC	GTCGCGGCCT	GAAAGTGAAC	150
	GATCTGCAAC	ACCCAATCGA	AGTCCCAGTT	GGCAAGGCAA	CGCTGGGTCG	200
	TATCATGAAC	GTATTGGGTC	AACCAATCGA	CATGAAAGGC	GACATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGCGCGG	CGCCAAGCTA	CGAAGAAGTG	300
10	TCCAACCTCCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTTA	TGGACCTGAT	350
	CTGCCCCTTT	GCCAAGGGTG	GTAAAGTCGG	TCTGTTTCGGT	GGTGCGGGTG	400
	TTGGTAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCAGTGTT	TGCGGGCGTG	GGTGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTACTG	GACAAGGTTT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CGGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GTCTGACCAT	GGCCGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCTGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCT	ATCACCTCCG	TA			822

2) INFORMATION FOR SEQ ID NO: 359

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia plymuthica*
 (B) STRAIN: ATCC 183

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359

40	GTGTACAACG	CTCTTGAGGT	AGAAAACGGT	GCCAATAAGC	TGGTGCTGGA	50
	AGTTCAGCAA	CAGCTGGGCG	GTGGCGTGGT	TCGCTGTATC	GCGATGGGGA	100
	CCTCTGATGG	TCTGCGTCGC	GGTCTGAAAG	TGATCGACCT	GGATCACCCG	150
	ATTGAAGTAC	CGGTAGGTAA	AGCTACCCTG	GGCCGTATCA	TGAACGTATT	200
	GGGTGAACCA	ATCGACATGA	AAGGCGACAT	CGGCGAAGAA	GAACGTTGGG	250
45	CAATTCACCG	TCCAGCGCCA	AGCTACGAAG	ATTTGGCCAA	CTCCCAGGAT	300
	CTGCTGGAAA	CCGGTATCAA	GGTTATGGAC	CTGATCTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTGGGTCTGT	TCGGCGGTGC	GGGCGTGGGT	AAAACCGTAA	400
	ACATGATGGA	GCTGATCCGT	AACATCGCGA	TCGAACACTC	CGGTTATTCC	450
	GTGTTTGCGG	GCGTGGGTGA	GCGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
50	CGAAATGAAC	GACTCCAACG	TACTGGACAA	AGTATCCCTG	GTTTACGGCC	550
	AGATGAACGA	GCCACCGGGT	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCGG	AGAAATTCCG	TGACGAAGGC	CGCGACGTTT	TGCTGTTTCG	650
	TGATAACATC	TACCGTTATA	CCCTGGCCCG	TACCGAAGTG	TCCGCACTTC	700
	TGGGCCGTAT	GCCATCTGCG	GTAGGTTATC	AGCCAACGCT	GGCGGAAGAG	750
55	ATGGGCGTTC	TGCAAGAACG	TATCACCTCT	ACCAAGACCG	GTTCTATCAC	800
	CTCCG					805

60 2) INFORMATION FOR SEQ ID NO: 360

215

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360

15 TTCCCTCAGG ATGCCGTACC AAAAGTGTAC GATGCCCTTG AGGTAGAGAA 50
 CGGTAACGAA AAACCTGGTGC TGGAAAGTTCA GCAGCAGCTG GGCGGCGGCG 100
 TTGTACGCTG TATCGCCATG GGTACTTCCG ACGGTCTGCG TCGCGGTCTG 150
 AAAGTTAACG ACCTCGAGCA CCCAATCGAA GTGCCAGTTG GTAAAGCAAC 200
 20 GCTGGGTCGT ATCATGAACG TATTGGGTCA GCCAATCGAC ATGAAAGGCG 250
 ACATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCGGC GCCAAGCTAC 300
 GAAGAGCTGT CCAGCTCCCA AGAGCTGCTG GAAACCGGTA TCAAGGTAAT 350
 GGACCTGATC TGCCCGTTTC CCAAGGGTGG TAAAGTTGGT CTGTTCTGGT 400
 GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC 450
 25 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAGCGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTACTGG 550
 ACAAAGTATC CCTGGTTTAC GGCCAGATGA ACGAGCCGCC GGGTAACCGT 600
 CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
 AGGCCGCGAC GTTCTGCTGT TCGTGGATAA CATCTACCGT TACACCCTGG 700
 30 CCGGTACCGA AGTGTCGCA CTGCTCGGCC GTATGCCATC TCGGGTAGGT 750
 TATCAGCCAA CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC 800
 CTCGACCAAG ACCGGTTCAA TCACCTCCGT A 831

35 2) INFORMATION FOR SEQ ID NO: 361

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Pseudomonas putida*
 (B) STRAIN: LCDC D7172

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361

CCGTAAACAT GATGGAAGT ATCCGTAACA TCGCCATCGA GCACAGCGGT 50
 TATTCCGTGT TCGCCGGTGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT 100
 CTACCACGAG ATGAAGGACT CCAACGTTCT CGACAAGGTA GCGCTGGTCT 150
 55 ACGGTCAGAT GAACGAGCCA CCAGGAAACC GTCTGCGCGT AGCGCTGACC 200
 GGCCTGACCA TGGCCGAGAA GTTCCGTGAC GAAGGTAACG ACGTTCTGCT 250
 GTTCGTGAC AACATCTATC GTTACACCCT GGCCGGTACC GAAGTATCCG 300
 CACTGCTGGG CCGTATGCCT TCGGCGGTAG GTTACCAGCC GACCCTGGCT 350
 GAAGAGATGG GCGTTCTGCA AGAACGTATC ACTTCGACCA AGGAAGGTTC 400
 60 GATCAC 406

2) INFORMATION FOR SEQ ID NO: 362

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Shigella boydii*
 (B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362

20	TTCCCTCAGG ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTGCAAAA	50
	TGGTAATGAG CGTCTGGTGC TGGAAAGTTCA GCAGCAGCTC GGCGGCGGTA	100
	TCGTGCGTAC CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGCGGTCTG	150
	GATGTAAAAG ACCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC	200
	TCTGGGCCGT ATCATGAACG TACTGGGTGA ACCGGTCGAC ATGAAAGGCG	250
25	AGATCGGTGA AGAAGAGCGT TGGGCGATTC ACCGCGCAGC ACCTTCCTAC	300
	GAAGAGCTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT	350
	CGACCTGATG TGTCCGTTCG CTAAGGGCGG TAAAGTTGGT CTGTTCGGTG	400
	GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTCAT TCGTAACATC	450
	GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC	500
30	TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG	550
	ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT	600
	CTGCGCGTTG CTCTGACCGG TCTGACCATG GCTGAGAAAT TCCGTGACGA	650
	AGGTCGTGAC GTTCTGCTGT TCGTTGACAA CATCTATCGT TACACCCTGG	700
	CCGGTACGGA AGTATCCGCA CTGCTGGGCC GTATGCCTTC AGCGGTAGGT	750
35	TATCAGCCGA CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC	800
	CTCCACCAAA ACTGGTTCTA TCACCTCCGT A	831

40 2) INFORMATION FOR SEQ ID NO: 363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363

55

	GCCGTACCGC GCGTGTACGA TGCTCTTGCG GTGCAAAATG GTAATGAGCG	50
	TCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA	100
	TCGCAATGGG TTCCTCCGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAGAC	150
	CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCGACTC TGGGCCGTAT	200
60	CATGAACGTA CTGGGTGAAC CGGTCGACAT GAAAGGCGAG ATCGGTGAAG	250

	AAGAGCGTTG	GGCTATTCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCT	AAGGGCGGTA	AAGTTGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTCATTC	GTAACATCGC	GATCGAGCAC	450
5	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTAATC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCT	600
	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTC	GTTGACAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
10	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CG					802

15

2) INFORMATION FOR SEQ ID NO: 364

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 819 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Shigella flexneri</i>
(B)	STRAIN: ATCC 12022

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364

	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
35	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGTG	GTGCGGGTGT	400
40	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
45	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAA	800
	ACTGGTTCTA	TCACCTCCG				819

50

2) INFORMATION FOR SEQ ID NO: 365

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 802 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella sonnei*
 (B) STRAIN: ATCC 29930

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365

	GTACCGCGCG	TGTACGATGC	TCTTGAGGTG	CAAAATGGTA	ATGAGCGTCT	50
	GGTGCTGGAA	G TTCAGCAGC	AGCTCGGCGG	CGGTATCGTG	CGTACCATCG	100
10	CAATGGGTTC	CTCCGACGGT	CTGCGTCGCG	GTCTGGATGT	AAAAGACCTC	150
	GAACACCCGA	TCGAAGTCCC	GGTAGGTAAA	GCGACTCTGG	GCCGTATCAT	200
	GAACGTACTG	GGTGAACCGG	TCGACATGAA	AGGCGAGATC	GGTGAAGAAG	250
	AGCGTTGGGC	GATTCACCGC	GCAGCACCTT	CCTACGAAGA	GCTGTCAAAC	300
	TCTCAGGAAC	TGCTGGAAAC	CGGTATCAAA	GTTATCGACC	TGATGTGTCC	350
15	GTTCGCTAAG	GGCGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	GGTGTAGGTA	400
	AAACCGTAAA	CATGATGGAG	CTCATTCGTA	ACATCGCGAT	CGAGCACTCC	450
	GGTTACTCTG	TGTTTGCGGG	CGTAGGTGAA	CGTACTCGTG	AGGGTAACGA	500
	CTTCTACCAC	GAAATGACCG	ACTCCAACGT	TATCGACAAA	GTATCCCTGG	550
	TGTATGGCCA	GATGAACGAG	CCGCCGGGAA	ACCGTCTGCG	CGTTGCTCTG	600
20	ACCGGTCTGA	CCATGGCTGA	GAAATTCCGT	GACGAAGGTC	GTGACGTTCT	650
	GCTGTTTCGT	GACAACATCT	ATCGTTACAC	CCTGGCCGGT	ACGGAAGTAT	700
	CCGCACTGCT	GGGCCGTATG	CCTTCAGCGG	TAGGTTATCA	GCCGACCCTG	750
	GCGGAAGAGA	TGGGCGTTCT	GCAGGAACGT	ATCACCTCCA	CCAAACTGG	800
	TT					802

25

2) INFORMATION FOR SEQ ID NO: 366

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366

	TAACGCCTTG	GTTATTGATG	TGCCTAAAGA	AGAAGGTACA	ATACAACTAA	50
	CATTAGAAGT	TGCGCTGCAA	TTAGGTGACG	ACGTTGTTCG	TACAATTGCG	100
45	ATGGATTCAA	CTGATGGTGT	CCAAAGAGGC	ATGGATGTAA	AAGATACAGG	150
	CAAAGAAATT	AGTGACCTG	TTGGTGATGA	AACATTAGGT	CGTGTATTTA	200
	ATGTACTAGG	TGAAACAATT	GACCTTAAAG	AAGAAATTAG	TGATTCTGTT	250
	CGCCGCGATC	CTATCCATCG	TCAAGCACCA	GCATTCGATG	AACTTTCAAC	300
	AGAAGTTCAA	ATTTTAGAAA	CAGGTATTAA	AGTAGTAGAT	TTACTAGCAC	350
50	CTTATATTAA	AGGTGGTAAA	ATCGGATTGT	TCGGTGGTGC	CGGTGTAGGT	400
	AAAACAGTAT	TAATCCAAGA	ATTAATTAAC	AACATCGCTC	AAGAGCACGG	450
	TGGTATTTCT	GTATTCGCCG	GTGTAGGTGA	ACGTACTCGT	GAAGGTAACG	500
	ATTTATACTT	CGAAATGAGT	GATAGTGGTG	TAATTAAGAA	AACAGCCATG	550
	GTATTCGGGC	AAATGAATGA	GCCACCTGGT	GCACGTATGC	GTGTTGCATT	600
55	ATCTGGTTTA	ACAATGGCTG	AATATTTCCG	TGACGAACAA	GGTCAAGACG	650
	TATTATTATT	CATCGATAAC	ATTTTCAGAT	TTACACAAGC	TGGTTCTGAG	700
	GTATCTGCAT	TATTAGGTCG	TATGCCTTCT	GCAGTAGGTT	ACCAACCAAC	750
	ACTTGCTACT	GAAATGGGAC	AATTACAAGA	ACGTA		785

60

2) INFORMATION FOR SEQ ID NO: 367

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
 (B) STRAIN: ATCC 33753

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367

GAACATAACG AAGTGCCTAA TATTAATAAC GCCTTAGTAC TCGATGTTGA 50
 AAGAGAAGAC GGAACAGTGT CTTTAACTTT AGAAGTAGCT TTACAATTAG 100
 20 GCGATGACGT TGTTCGTACC ATTGCAATGG ATTCAACTGA TGGTGTGTTAAA 150
 CGTGGTAACG AAGTCAAAGA TACTGGTAAT AGCATTAGCG TACCAGTCGG 200
 AGACGAAACT TTAGGACGTG TCTTCAACGT TCTAGGTGAA ACAATTGATT 250
 TAGAAGATAA ACTTGATGAT TCTGCGCGAC GTGACCCTAT ACATAGAGAA 300
 GCGCCAGCGT TTGATCAATT ATCAACTCAA GTTGAAATTT TAGAAACAGG 350
 25 AATTAAAGTT GTTGACTTAT TAGCACCTTA TATTAAAGGT GGTAAAGTTG 400
 GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTTTAAT CCAAGAATTA 450
 ATCAACAACA TCGCTCAAGA ACACGGTGGT ATTTCACTCT TTGCCGGTGT 500
 AGGTGAACGT ACACGTGAAG GTAACGACTT GTACTATGAA ATGAGCGACA 550
 GTGGTGTAAT CAAGAAAACA GCCATGGTCT TCGGACAAAT GAACGAACCA 600
 30 CCTGGCGCAC GTATGCGTGT TGCTTTATCT GGTTTAACAA TGGCTGAATA 650
 TTTCCGTGAT GAACAAGGAC AAGACGTATT GTTATTCATC GACAATATTT 700
 TCCGTTTCAC ACAAGCCGGT TCAGAAGTTT CTGCCTTACT AGGTCGTTTA 750
 CCATCAGCCG TTGGTTATCA ACCTACATTA GCAACAGAAA TGGGACAATT 800
 ACAAGAACGT ATTACTTCAA CAACAAAAGG ATCAGTTACT TCA 843

35

2) INFORMATION FOR SEQ ID NO: 368

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*
 50 (B) STRAIN: ATCC 27840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368

GCTTTGAACA TAATGAAGTT CCTGATATTA ACAATGCCTT ACACATCGAA 50
 55 GTTCCTAAAG AAGATAGCAC ACTTCATTTA ACTTTAGAAG TTGCACTTCA 100
 ATTAGGTGAC GATGTAGTAC GTACAATCGC AATGGACTCA ACTGACGGCG 150
 TTCAAAGAGG TATGGAAGTT AAAGATACAG GTAAAGATAT TAGCGTACCT 200
 GTTGGTGATG CAACTTTAGG AAGAGTATTT AACGTATTAG GAGAAACAAT 250
 CGATTTAGAT GAAAAGATTG ATGATTCACT ACGTCGTGAT CCTATTCATA 300
 60 GACAGGCACC TGGCTTCGAT GAATTATCTA CTAAAGTAGA AATCTTAGAA 350

220

	ACAGGTATCA	AAGTAGTAGA	CTTATTAGCA	CCTTACATTA	AAGGTGGTAA	400
	AATTGGATTA	TTCGGTGGTG	CCGGTGTG	TAAGACAGTT	TTAATCCAAG	450
	AACTTATCAA	TAATATCGCT	CAAGAGCATG	GTGGTATTTC	AGTATTGCGC	500
	GGTGTGGTG	AACGTACACG	TGAAGGTAAC	GACCTTTACT	ATGAAATGAG	550
5	CGATAGTGGT	GTAATTAAGA	AAACAGCGAT	GGTATTCGGT	CAGATGAACG	600
	AGCCACCTGG	TGCTCGTATG	CGTGTTGCAT	TATCAGGTTT	AACAATGGCA	650
	GAATATTTCC	GTGATGAAGA	AGGCCAAGAC	GTATTATTAT	TCATTGATAA	700
	TATCTTCAGA	TTCACACAAG	CTGGTTCCTGA	AGTTTCAGCA	TTACTTGGAC	750
	GTATGCCTTC	AGCCGTTGGT	TATCAACCAA	CACTTGCTAC	TGAAATGGGT	800
10	CAATTACAAG	AACGTATTAG	TTCAACTAAT	AAAGGTTCTG	TTACTTCAA	849

2) INFORMATION FOR SEQ ID NO: 369

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Staphylococcus cohnii*
 (B) STRAIN: DSM 20260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369

30	GAAGTTCCAG	AAATTAATAA	TGCCTTAGTT	CTCGATATAG	AAAGAGAAGA	50
	AGGTACTGTT	GAATTAACGT	TAGAAGTTGC	ATTACAACCTT	GGTGATGACG	100
	TAGTACGAAC	AATCGCAATG	GATTCAACTG	ATGGTGTTAA	ACGTGGTACA	150
	GAAGTTAGAG	ATAGCGGAAA	TAGTATCAGC	GTACCAGTTG	GTAATGAAAC	200
	ATTAGGTAGA	GTATTTAATG	TATTAGGTGA	TACGATAGAT	TTAGATGAAG	250
35	ACATAGATGA	CTCAGTGCGT	CGTGACCCAA	TTCATAGAGA	AGCACCTGCA	300
	TTTGATCAGT	TATCTACTAA	AGTTGAAATT	TTAGAAACAG	GTATCAAAGT	350
	CATTGATTTA	TTAGCACCAT	ATATCAAAGG	TGGTAAAGTT	GGATTATTCTG	400
	GTGGTGCCGG	TGTTGGTAAA	ACTGTATTAA	TTCAAGAATT	AATCAATAAT	450
	ATCGCTCAAG	AGCATGGTGG	TATATCCGTA	TTTGCTGGTG	TAGGTGAGCG	500
40	TACGCGTGAA	GGTAATGACC	TATACTTTGA	AATGAGTGAT	AGTGGTGTTA	550
	TTAAAAAGAC	AGCTATGGTA	TTTGGACAAA	TGAACGAACC	ACCTGGTGCG	600
	CGTATGCGAG	TAGCACTTTC	TGGTTTAAACA	ATGGCTGAAT	ATTTCCGGGA	650
	TGAACAAGGA	CAAGATGTTC	TATTATTTCAT	AGATAACATC	TTTAGATTTA	700
	CTCAAGCTGG	TTCAGAAGTT	TCTGCGTTAT	TAGGTCGTAT	GCCTTCAGCT	750
45	GTTGGTTACC	AACCAACGTT	AGCAACTGAA	ATGGGACAAT	TACAAGAACG	800
	TATTACTTCT	ACAACATAAG	GTTTCAGTAAC			830

50 2) INFORMATION FOR SEQ ID NO: 370

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370

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5      AATAATGCAT TACACATCGA AGTTCCTAAA GAAGATGGAG CGCTTCAATT      50
      AACATTAGAA GTTGCACTTC AACTAGGTGA CGATGTAGTT CGTACAATTG      100
      CAATGGACTC AACTGACGGC GTTCAAAGAG GAATGGAAGT TAAAGATACA      150
      GGTAGAGACA TAAGTGTACC TGTCGGTGAC GTAACCTAG GAAGAGTGTT      200
10     TAACGTACTA GGAGAAACTA TTGACTTAGA TGAAAAAATT GATGATTCAG      250
      TACGACGTGA CCTATCCAT AGACAAGCTC CAGGATTCGA CGAATTATCA      300
      ACAAAGTAG AAATCTTAGA AACTGGTATT AAAGTAGTAG ACTTATTAGC      350
      ACCTTACATA AAAGGTGGTA AAATTGGATT ATTTGGTGGT GCCGGTGTAG      400
      GTAAAACCGT ACTAATCCAA GAACTTATTA ATAACATCGC TCAAGAACAC      450
15     GGTGGTATCT CAGTATTCGC TGGTGTGGT GAACGTACAC GTGAAGGTAA      500
      TGATCTTTAC TATGAAATGA GTGACAGTGG TGTATCAAG AAAACTGCAA      550
      TGGTCTTTGG TCAAATGAAT GAGCCACCTG GTGCACGTAT GCGTGTAGCA      600
      TTATCCGGAT TAACAATGGC CGAATATTTT CGAGATGAAG AAGGCCAAGA      650
      TGTGTTATTA TTCATTGATA ACATTTTCAG ATTCACTCAA GCTGGTTCAG      700
20     AAGTTTCTGC GTTATTAGGT CGTATGCCAT CAGCTGTTGG TTATCAACCT      750
      ACACTTGCTA CAGAAATGGG TCAATTACAA GAACGTA      787
  
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25 2) INFORMATION FOR SEQ ID NO: 371

(i) SEQUENCE CHARACTERISTICS:

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      (A) LENGTH: 830 bases
      (B) TYPE: Nucleic acid
30     (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371

```

40     GAAGTACCTG AAATTAATAA CGCCTTAATC ATCGAAGTTC CCAAAGAAGA      50
      TGGTACTTTT GAATTAACGC TTGAAGTTGC ATTACAATA GGTGATGACG      100
      TTGTTTCGTAC AATTGCTATG GATTCAACAG ATGGTGTTCA ACGTGGTATG      150
      GAAGTTCAGA ACACTGGAAA AGACATTTCA GTACCAGTTG GCGAAGTAAC      200
45     TTTAGGACGT GTATTTAACG TATTAGGTGA CACAATTGAT TTAGAAGATA      250
      AATTAGATGG TTCAGTAAGA CGTGATCCAA TTCATAGACA ATCACCTAAC      300
      TTTGACGAAT TATCTACTGA AGTAGAAATT CTTGAAACTG GAATCAAAGT      350
      TGTAGACTTA TTAGCACCAT ACATCAAAGG TGGTAAAATC GGTCTATTTG      400
      GTGGTGCCGG TGTTGGTAAA ACCGTTTTAA TCCAAGAATT GATTAATAAT      450
50     ATCGCACAAG AACATGGTGG TATCTCAGTA TTTGCTGGTG TAGGTGAACG      500
      TACACGTGAA GGTAACGACC TATATTATGA AATGAGAGAT AGTGGTGTTA      550
      TTAAGAAAAC AGCAATGGTA TTTGGTCAAA TGAACGAGCC ACCTGGTGCA      600
      CGTATGCGTG TGGCACTTTC TGCATTGACA ATGGCTGAGT ATTTCCGTGA      650
      TGAACAAGGA CAAGACGTTC TGTTATTCAT CGATAACATT TTCAGATTTA      700
55     CTCAAGCAGG TTCAGAAGTA TCAGCATTAT TGGGACGTAT GCCTTCAGCT      750
      GTAGGTTATC AACCTACTTT AGCTACAGAA ATGGGTCAAT TACAAGAACG      800
      TATTACATCA ACGAATAAAG GTTCAGTAAC      830
  
```

60

2) INFORMATION FOR SEQ ID NO: 372

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372

	TCGAACATAA	TGAAGTCCCT	GAAATTAATA	ATGCCCTAAT	TATTGAAGTA	50
	CCCAAAAATG	ATGGCACATT	TAAATTAACA	TTAGAAGTTG	CATTGCAACT	100
	AGGTGATGAT	GTTGTTTCGTA	CTATTGCAAT	GGATTCAACT	GATGGTGTTC	150
20	AACGTGGTAT	GCAAGTTGTG	AATACTGGTA	AAGATATTAG	TGTTCCCTGTA	200
	GGTGAAGAAA	CACTTGGACG	TGTGTTTAAC	GTTT TAGGAG	AAACAATAGA	250
	TTTAAACGAA	AAAATAGATA	GTTCTGT TAG	ACGTGATCCA	ATTCATCGTC	300
	GTCAACCTAA	TTTTGATGAA	TTATCTACTG	AAGTAGAAAT	TCTTGAAACA	350
	GGTATTAAAG	TTGTAGACTT	ATTAGCACCT	TATATTAAAG	GTGGTAAGAT	400
25	TGGTTTATTC	GGTGGTGCCG	GCGTAGGTAA	AACTGTATTA	ATTCAAGAAT	450
	TAATCAATAA	TATCGCTCAA	GAACATGGTG	GTATTTCTGT	ATTCGCTGGT	500
	GTAGGTGAAC	GTACTCGTGA	AGGTAACGAT	TTATACTATG	AAATGAGCGA	550
	TAGTGGCGTT	ATCAATAAAA	CAGCCATGGT	ATTTGGGCAA	ATGAATGAGC	600
	CGCCAGGTGC	GCGTATGCGT	GTTGCTTTAT	CAGCATTGAC	AATGGCTGAA	650
30	TATTTCCGTG	ATGAACAAGG	TCAAGATGTA	CTTTTATTCA	TTGACAATAT	700
	TTTCCGCTTT	ACTCAAGCTG	GTTCTGAAGT	TTCAGCATT	TTAGGACGTA	750
	TGCCTTCAGC	TGTAGGTTAT	CAACCTACAT	TAGCAACTGA	AATGGGTCAA	800
	TTACAAGAAC	GTATTACATC	TACTAATAAA	GGTTCAGTCA	CTTCAA	846

35

2) INFORMATION FOR SEQ ID NO: 373

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 175

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373

	TCGAACATAA	TGAAGTCCCT	GAAATTAATA	ATGCCCTAAT	TATTGAAGTA	50
	CCCAAAAATG	ATGGCACATT	CAAATTAACA	TTAGAAGTTG	CATTGCAACT	100
55	AGGTGATGAT	GTTGTTTCGTA	CTATTGCAAT	GGATTCAACT	GATGGTGTTC	150
	AACGTGGTAT	GCAAGTTGTG	AATACTGGTA	AAGATATTAG	TGTTCCCTGTA	200
	GGTGAAGAAA	CACTTGGACG	TGTGTTTAAC	GTTT TAGGAG	AAACAATAGA	250
	TTTAAACGAA	AAAATAGATA	GTTCTGT TAG	ACGTGATCCA	ATTCATCGTC	300
	GTCAACCTAA	TTTTGATGAA	TTATCTACTG	AAGTAGAAAT	TCTTGAAACA	350
60	GGTATTAAAG	TTGTAGACTT	ATTAGCACCT	TATATTAAAG	GTGGTAAGAT	400

TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT 450
 TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT 500
 GTAGGTGAAC GTACTCGTGA AGGTAACGAT TTATACTATG AAATGAGCGA 550
 TAGTGGCGTT ATCAATAAAA CAGCCATGGT ATTTGGGCAA ATGAATGAGC 600
 5 CGCCAGGTGC GCGTATGCGT GTTGCTTTAT CAGCATTGAC AATGGCTGAA 650
 TATTTCCGTG ATGAACAAGG TCAAGATGTA CTTTTATTCA TTGACAATAT 700
 TTTCCGCTTT ACTCAAGCTG GTTCTGAAGT TTCAGCATTA TTAGGACGTA 750
 TGCCTTCAGC TGTAGGTTAT CAACCTACAT TAGCAACTGA AATGGGTCAA 800
 TTACAAGAAC GTATTACATC TACTAATAAA GGTTCAGTCA CTTCAA 846
 10

2) INFORMATION FOR SEQ ID NO: 374

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus lugdunensis*
 25 (B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374

30 ATAATGAAGT GCCTGAAATA AATAATGCGC TCATTGTTGA AATTCCTAAA 50
 AGTGATACAA CAATCAGTTT AACACTTGAA GTTGCTTTGC AATTAGGTGA 100
 CGATGTTGTA CGTACTATTG CAATGGATTC AACTGATGGC GTTCAACGTG 150
 GTATGGAAGT TCAAAACACA GGTAAAGACA TCAGTGTACC TGTGAGAGAT 200
 GAAACATTAG GAAGAGTATT TAACGTTTTA GGAGAATCTA TTGATTTAGA 250
 AGAAAAGCTA GATGACTCTG TGCCTAGAGA TCCAATTCAT AGACTAGCAC 300
 35 CTAAATTTGA TGAATTATCT ACAGAAGTAG AAATTCTTGA AACTGGTATT 350
 AAAGTTGTTG ATTTATTAGC ACCATATATT AAAGGTGGTA AAGTTGGATT 400
 GTTTGGTGGT GCCGGAGTAG GTAAAACGGT ATTAATTCAA GAATTAATCA 450
 ACAATATTGC TCAAGAACAT GGTGGTATTT CTGTGTTTGC CGGAGTAGGT 500
 GAACGTACAC GTGAAGGTAA TGAATTATAT TATGAAATGA GCGATAGTGG 550
 40 CGTAATTAAG AAAACAGCGA TGGTATTTGG CCAAATGAAT GAACCACCTG 600
 GTGCACGTAT GAGAGTTGCG TTATCTGCCT TAACAATGGC TGAATATTTT 650
 CGTGACGAGC AAGGACAAGA CGTATTGCTG TTTATCGATA ATATATTCCG 700
 TTTTACACAA GCAGGTTTCAG AAGTATCTGC ATTACTTGGA CGTATGCCAT 750
 CTGCCGTTGG TTATCAACCA ACATTGGCTA CAGAAATGGG ACAATTGCAA 800
 45 GAAAGAATTA CATCTACAAA TAAAGGTTCT GTAAC 835

2) INFORMATION FOR SEQ ID NO: 375

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 842 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375

5	GAGCACAATG	AAGTTCCAGA	AATTAACAAT	GCCTTAGTCG	TAGACGTTGA	50
	AAGAGATGAA	GGTACAGTAT	CTCTTACATT	AGAAGTGGCA	TTACAACCTG	100
	GCGATGATGT	CGTACGTACA	ATTGCAATGG	ATTCTACTGA	TGGTGTTAAA	150
	CGTGGTACAG	AAGTTCGAGA	TAGCGGAGAT	AGCATCAGTG	TTCCAGTTGG	200
	TGATGCTACG	TTAGGACGTG	TGTTTAATGT	TCTTGGTGAT	ACAATTGACT	250
10	TAGACGAGAA	GCTTGATACT	TCTGTCAAAC	GTGATCCAAT	TCATAGAGAA	300
	GCACCTGCAT	TCGATCAATT	ATCAACAAAA	GTTGAAATCT	TAGAAACAGG	350
	TATTAAAGTA	ATTGATTTAC	TTGCACCATA	TATTAAAGGT	GGTAAAATCG	400
	GTTTATTTCGG	TGGCGCTGGT	GTAGGTAAAA	CAGTATTAAT	TCAAGAATTA	450
	ATTAATAATA	TAGCTCAAGA	ACATGGTGGT	ATTTCAGTAT	TTGCCGGCGT	500
15	AGGTGAACGT	ACGCGTGAAG	GTAATGACTT	ATACTACGAA	ATGAGTGATA	550
	GTGGTGTTAT	TAAGAAAACA	GCTATGGTCT	TCGGACAAAT	GAATGAGCCA	600
	CCTGGTGCGC	GTATGCGTGT	TGCTTTATCA	GGCTTAACAA	TGGCTGAACA	650
	CTTCCGTGAT	GTACAAGGAC	AAGATGTTTT	ACTATTTATT	GATAACATAT	700
	TCAGATTTAC	GCAAGCTGGT	TCAGAAGTAT	CAGCACTATT	AGGTCGTATG	750
20	CCATCAGCCG	TTGGTTATCA	ACCTACCCTT	GCTACTGAAA	TGGGTCAATT	800
	ACAAGAACGT	ATTACATCAA	CAACTAAAGG	ATCTGTAACG	TC	842

25 2) INFORMATION FOR SEQ ID NO: 376

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 842 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Staphylococcus simulans</i>
	(B)	STRAIN: ATCC 27848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376

40	TGATGAACTG	CCTAAGATTA	ATAACGCATT	AGTGCTAGAT	GTACCTAAGA	50
	AAGATGGCAC	GACTGAATCT	CTTACATTAG	AAGTAGCACT	TGAATTAGGC	100
	GACGACGTAG	TTAGAACTAT	CGCCATGGAC	TCTACAGACG	GAATTAAACG	150
	TGGTGACGAC	GTAAAGACA	CTGGTCGTCC	AATCAGTGTA	CCTGTCGGTG	200
45	AAGATACGTT	AGGAAGAGTA	TTTAACGTTT	TAGGTGATCC	AATCGATAAT	250
	GATGGACCGA	TTTCTGAATC	AGTTCCACGT	GAACCAATTC	ATAGACAACC	300
	ACCTAAATTT	GATGAATTAT	CAACAAAAGT	TGAACTACTT	GAAACTGGTA	350
	TCAAAGTAGT	AGACTTATTA	GCACCATATA	TCAAAGGTGG	TAAAGTTGGT	400
	TTATTCGGTG	GTGCCGGAGT	AGGTAAAAC	GTATTAATCC	AAGAATTAAT	450
50	TAATAACATC	GCTCAAGAAC	ACGGCGGTAT	TTCAGTATTC	GCAGGTGTTG	500
	GTGAACGTAC	ACGTGAAGGT	AACGACTTGT	ACTTCGAAAT	GAGCGACAGT	550
	GGTGTTATCA	AGAAAACAGC	GATGGTATTC	GGACAAATGA	ACGAACCACC	600
	TGGTGACAGT	ATGCGTGTAG	CTTTATCAGG	TTTAACAATG	GCTGAATACT	650
	TCCGTGATGT	TAAAGGACAA	GACGTTCTTT	TATTCATCGA	TAACATTTTC	700
55	CGCTTCACAC	AAGCAGGTTT	TGAGGTATCA	GCATTGCTTG	GCCGTATGCC	750
	ATCAGCCGTT	GGTTACCAAC	CAACATTGGC	AACAGAAATG	GGTCAATTAC	800
	AAGAACGTAT	CACTTCTACA	ATGAAAGGTT	CTATCACATC	TA	842

60

2) INFORMATION FOR SEQ ID NO: 377

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377

CATAACGAAG TCCCTGATAT TAATAATGCC CTTATTATTG AAGTTCCAAA 50
 AGAAGATGGA ACGTTAAACT TAACATTAGA AGTTGCACTA CAATTAGGTG 100
 ATGATGTTGT ACGTACAATT GCAATGGATT CAACTGATGG TGTTCAAAGA 150
 20 GGCATGGATG TTAAAGACAC AGGTAAAGAT ATTAGTGTAC CTGTAGGCGA 200
 TGAAACGCTT GGAAGAGTGT TTAATGTACT AGGTGAAACA ATTGACTTGG 250
 AAGAGAAAAT TGATGATTCC GTACGTCGTG ATCCAATCCA TAGACAATCA 300
 CCAGGTTTCG ATGAATTATC TACTGAAGTA GAAATCTTAG AAACAGGTAT 350
 TAAAGTAGTA GACTTATTAG CACCTTACAT TAAAGGTGGT AAAGTTGGAC 400
 25 TATTCGGTGG TGCCGGAGTA GGTAACCCG TTTTAATCCA AGAATTAATT 450
 AACAATATTG CACAAGAACA TGGTGGTATT TCAGTATTCG CGGGTGTAGG 500
 TGAACGTACT CGTGAAGGTA ATGATTTATA CTATGAAATG AGTGATAGTG 550
 GTGTAATTAA GAAAACAGCG ATGGTATTTG GACAAATGAA TGAACCACT 600
 GGCGCACGTA TCGGTGTAGC TTTATCTGGT TTAACATATG CTGAATACTT 650
 30 CCGTGATGAA CAAGGACAAG ACGTACTTTT ATTCATCGAT AATATTTTCA 700
 GATTTACACA AGCTGGTTCT GAAGTTTCTG CATTACTTGG TCGTATGCCT 750
 TCAGCCGTTG GTTACCAACC AACATTAGCA ACTGAAATGG GTCAATTACA 800
 AGAACGAATT ACATCTACAA ATAAAGGTTC TGTAACATCT A 841

35

2) INFORMATION FOR SEQ ID NO: 378

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378

TTTAACACGA ATGAACCGCT TCCTGAGATA AATAATGCAC TTGTTGTTTA 50
 CAAAGACAGT GAGAAAAAAC ATAAAATCGT TCTTGAAGTA GCTCTTGAAC 100
 55 TTGGTGAAGG CCTCGTTCGT ACCATTGCTA TGGAATCAAC TGATGGTTTG 150
 ACACGTGGTC TAGAAGTTCT TGATACAGGC CGTGCAATCA GTGTACCAGT 200
 TGGTAAAGAA ACGCTTGGAC GTGTCTTCAA CGTTCCTTGGT GATGCTATCG 250
 ATCTTGAAGA ACCATTTGGA GAAGATGCAG AACGTCACCC CATTATAAG 300
 AGTGCCCCAA CTTTTGATGA ATTATCAACG TCAACAGAAA TCCTTGAAAC 350
 60 AGGGATTAAA GTTATCGACC TACTTGCCCC TTAATTAAAA GGAGGGAAGG 400

	TTGGACTTTT	CGGTGGTGCC	GGAGTTGGTA	AGACCGTTCT	TATCCAAGAG	450
	TTGATTCATA	ACATTGCTCA	AGAGCATGGT	GGTATTTTCAG	TATTTACCGG	500
	AGTTGGTGAA	CGTACACGTG	AAGGTAATGA	CCTCTATTGG	GAAATGAAAG	550
	AATCAGGCGT	TATTGAAAAA	ACAGCTATGG	TATTTGGTCA	GATGAATGAG	600
5	CCACCTGGTG	CACGTATGCG	TGTAGCCCTT	ACTGGTTTGA	CAATCGCTGA	650
	ATATTTCCGT	GATGTTGAAG	GACAGGACGT	GCTTCTCTTT	ATTGATAACA	700
	TTTTTCGTTT	CACACAAGCA	GGTTCTGAAG	TTTCAGCTCT	TCTTGGACGT	750
	ATGCCATCAG	CCGTTGGTTA	TCAACCAACC	TTGGCAACTG	AAATGGGTCA	800
10	ATTGCAAGAA	CGTATCACGT	CAACTAAAAA	AGGTTCTGTT	ACATCA	846

2) INFORMATION FOR SEQ ID NO: 379

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 25 (B) STRAIN: ATCC 12403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379

	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
30	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTA	CTCTTGAACT	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GCGCAATTAG	TGTGCCGGTT	200
	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
	CCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
35	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACA	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCAG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
	GTAGGAGAAC	GTACTCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
40	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
45	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCAA	846

2) INFORMATION FOR SEQ ID NO: 380

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(B) STRAIN: ATCC 13813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380

5	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTG	CTCTTGAACT	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GCGCAATTAG	TGTGCCGGTT	200
	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
10	TCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACT	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCGG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
15	GTAGGAGAAC	GTAATCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
20	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCAA	846

25 2) INFORMATION FOR SEQ ID NO: 381

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 845 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Streptococcus agalactiae</i>
	(B)	STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381

40	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTG	CTCTTGAACT	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GTGCAATTAG	TGTGCCGGTT	200
45	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
	CCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCACCATC	ATTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACA	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCGG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
50	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
	GTAGGAGAAC	GTAATCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
55	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCA	845

60

2) INFORMATION FOR SEQ ID NO: 382

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 27591

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT 50
 AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT 100
 TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
 20 CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT 200
 GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA 250
 CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA 300
 AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT 350
 GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT 400
 25 TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
 TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT 500
 GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
 ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
 CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
 30 TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
 CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA 750
 TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
 TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CATCA 845

35

2) INFORMATION FOR SEQ ID NO: 383

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: CDC ss1073

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT 50
 AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT 100
 55 TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
 CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT 200
 GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA 250
 CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA 300
 AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT 350
 60 GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT 400

TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
 TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT 500
 GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
 ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
 5 CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
 TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
 CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA 750
 TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
 TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCGTGTA CATCA 845
 10

2) INFORMATION FOR SEQ ID NO: 384

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus dysgalactiae*
 25 (B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384

TTGCTAGTGG GGACAAACTT CCAGAGATTA ATAATGCATT GATTGTTTAT 50
 30 AAAGATAGTG ATAAAAAGCA AAAAATCGTC CTTGAAGTTG CTCTGGAAC 100
 TGGTGACGGT ATGGTGCGAA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
 CACGTGGGTT AGAAGTTCTT GACACTGGTC GTGCGATTAG TGTACCAGTA 200
 GGTAAGAAA CTTTGGGACG CGTCTTTAAT GTACTTGGAG AAACCATTGA 250
 CTTGGAAGAA CCATTTGCAG AAGACGTTGA CCGTCAGCCA ATCCATAAAA 300
 35 AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT TCTTGAAACT 350
 GGTATCAAGG TAATTGACCT TCTTGCCCCT TACCTTAAAG GTGGTAAAGT 400
 TGGACTTTTC GGGGGTGCCG GAGTTGGTAA GACTGTCCTT ATCCAAGAAT 450
 TAATCCACAA TATCGCCCAA GAACACGGAG GTATTTTCAGT ATTTACCGGT 500
 GTTGGTGAGC GAACACGTGA AGGAAATGAC CTTTACTGGG AAATGAAAGA 550
 40 ATCAGGCGTT ATTGAGAAAA CTGCCATGGT TTTTGGTCAG ATGAATGAGC 600
 CGCCTGGGGC ACGTATGCGT GTAGCCCTTA CTGGTTTAAAC CATTGCTGAG 650
 TATTTCCGTG ATGTAGAAGG CCAAGATGTT TTGCTCTTTA TTGATAATAT 700
 CTTCCGTTTC ACTCAGGCAG GTTCAGAAGT ATCAGCCCTC TTAGGCCGTA 750
 TGCCTTCTGC TGTTGGTTAC CAACCGACCC TTGCTACTGA AATGGGACAA 800
 45 TTGCAAGAAC GTATTACGTC AACTCAAAAA GGATCTGTTA CTTCT 845

2) INFORMATION FOR SEQ ID NO: 385

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Streptococcus equi* subsp. *equi*

(B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385

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5  TTGCGAGTGG GGACAAACTA CCAGAGATTA ATAATGCGTT GATAGTTTAT      50
   AAAGATGGCG ATAAAAAGCA AAAAATCGTT CTCGAGGTTG CCCTAGAGCT      100
   TGGAGACGGT ATGGTACGTA CAATTGCTAT GGAATCAACC GATGGGCTTA      150
   CACGTGGATT AGAGGTTCTT GATACTGGTC GTGCCATTAG TGTACCAGTT      200
   GGTAAGAGA CTCTAGGTCG TGTTCCTAAC GTTCTTGGTG AAACCATCGA      250
10 CCTAGAAGCA CCATTGTCAG ATGATGTTAA TCGTGAACCG ATCCATAAAA      300
   AAGCACCAGC CTTTGATGAA TTGTCAACAT CATCAGAAAT TCTTGAAACA      350
   GGTATCAAGG TTATTGACCT GCTTGCCCTT TACTTAAAGG GTGGTAAGGT      400
   CGGTCTTTTC GGTGGTGCCG GAGTTGGTAA AACCGTTCTT ATCCAAGAAT      450
   TAATCCACAA TATCGCTCAA GAGCATGGTG GGATCTCGGT ATTTACCGGT      500
15 GTTGGTGAGC GTACGCGTGA AGGAAATGAC CTTTACTGGG AAATGAAGGA      550
   ATCAGGCGTT ATTGAAAAAA CAGCCATGGT TTTTGGTCAG ATGAATGAAC      600
   CACCAGGAGC CCGTATGCGT GTTGCCTTGA CCGGCTTGAC AATTGCTGAA      650
   TATTTCCGCG ATGTTGAAGG CCAAGACGTC CTGCTCTTCA TTGACAATAT      700
   TTTCCGCTTT ACTCAAGCAG GCTCAGAGGT ATCAGCCCTT CTAGGTCGTA      750
20 TGCCTTCAGC CGTTGGTTAC CAGCCAACAC TTGCCACTGA AATGGGACAA      800
   TTGCAAGAGC GTATCACCTC AACGAAAAAA GGCTCTGTTA CCTCTA      846

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25 2) INFORMATION FOR SEQ ID NO: 386

(i) SEQUENCE CHARACTERISTICS:

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30  (A) LENGTH: 846 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Streptococcus anginosus
    (B) STRAIN: ATCC 27335

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386

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40  TTGCAGCTGG TGATAAATTA CCTGAGATAA ATAATGCACT TGTAGTCTAT      50
   AAAAATGACG AAAATAAATC AAAAATCGTC CTTGAAGTAG CTCTTGAGCT      100
   TGGTGATGGA GTGGTTCGAA CTATTGCCAT GGAATCCACT GATGGGTTGA      150
   CTCGTGGCAT GGAAGTTCTA GATACTGGTC GACCAATTTT TGTTCAGTT      200
45 GGGAAAGAAA CACTTGGTCG CGTCTTTAAC GTTTTAGGCG ATACCATTGA      250
   TTTGGATACT CCATTCGGCG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
   AAGCTCCAAC TTTTGATGAG TTATCTACTT CATCAGAAAT CTTAGAAACA      350
   GGAATAAAGG TTATTGACCT TTTAGCCCCC TACCTCAAAG GTGGGAAAGT      400
   CGGCCTCTTC GGTGGTGCTG GCGTTGGGAA AACTGTCTTG ATTCAAGAGT      450
50 TGATTCATAA TATCGCCCAA GAACACGGCG GGATTTTCAGT CTTTACTGGT      500
   GTTGGGGAAC GAACTCGTGA AGGGAATGAC CTGTACTGGG AAATGAAAGA      550
   ATCTGGTGTT ATCGAAAAGA CGGCTATGGT CTTTGGGCAA ATGAATGAAC      600
   CGCCTGGAGC ACGTATGCGT GTAGCTTTGA CTGGGTAAAC GATTGCAGAG      650
   TATTTCCGTG ATGTGGAAGG TCAAGATGTT CTTTGTGTTA TTGATAATAT      700
55 TTTCCGTTTC ACTCAAGCTG GTTCTGAAGT GTCAGCCCTT CTTGGTCGTA      750
   TGCCATCAGC TGTGTTGTTAC CAACCAACCT TGGCTACTGA AATGGGGCAA      800
   TTACAAGAAC GTATTACATC AACGAAAAAA GGTTCGTGTA CCTCAA      846

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60

2) INFORMATION FOR SEQ ID NO: 387

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Streptococcus salivarius*
 (B) STRAIN: ATCC 7073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387

15 GCAGCTGGTG ATAAACTTCC TGAGATTAAC AATGCATTGG TCGTTTATAC 50
 TGATGAACAA AAGTCTAAAC GTATCGTGCT CGAAGTAGCT CTTGAACTTG 100
 GAGAAGGTGT GGTTCGTACC ATTGCCATGG AATCTACTGA TGGATTGACT 150
 20 CGTGGACTAG AAGTTCTGGA CACTGGTCGT CCAATCAGCG TTCCTGTTGG 200
 TAAAGATACC CTTGGACGTG TCTTTAACGT TCTTGGTGAT ACCATTGACT 250
 TGAAGCACC TTTTGCAGAC GATGCAGAGC GTGAACCAAT TCACAAAAAA 300
 GCACCAACTT TCGATGAATT GTCAACATCT ACTGAAATCC TTGAAACAGG 350
 GATTAAAGTT ATCGACTTGC TAGCCCCTTA CCTTAAGGGT GGTAAAGTCG 400
 25 GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTCTTAT TCAAGAGTTG 450
 ATTCACAACA TTGCCAAGA GCACGGTGGT ATTTCCGTGT TTACAGGTGT 500
 TGGTGAACGT ACACGTGAAG GTAATGACCT TTACTGGGAA ATGAAAGAAT 550
 CTGGCGTTAT CGAGAAAACA GCCATGGTCT TCGGTCAAAT GAACGAACCA 600
 CCTGGAGCAC GTATGCGTGT TGCCCTTACT GGTTTGACAA TTGCGGAATA 650
 30 CTTCCGTGAT GTCGAGGGTC AAGACGTTCT TCTCTTCATC GATAACATCT 700
 TCCGTTTCAC TCAAGCAGGT TCTGAGGTTT CTGCCCTTCT TGGTCGTATG 750
 CCATCAGCCG TTGGTTACCA ACCTACACTT GCTACTGAAA TGGGTCAATT 800
 GCAAGAACGT ATCACATCAA CTAAAAAAGG TTCTGTTACA TCT 843

35

2) INFORMATION FOR SEQ ID NO: 388

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Streptococcus suis*
 (B) STRAIN: ATCC 43765

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388

TTGCAGCAGA AGATAAACTT CCTGAGATTA ACAACGCACT CGTTGTATAT 50
 AAAAATGATG ATTCCAAACA AAAAGTCGTG CTTGAAGTGG CTTTGGAAC 100
 55 TGGTGATGGC GTTGTACGGA CCATTGCCAT GGAATCAACG GATGGATTGA 150
 CACGTGGGAT GGAAGTTCTC GATACAGGTC GTCCCATCTC TGTTCCAGTC 200
 GGTAAGAAA CGCTGGGTCG TGTCTTCAAT GTGTTGGGAG ATACCATTGA 250
 CCTTGAAGAG TCTTTTCCGG CAGATTTTGA ACGTGAGCCT ATCCATAAGA 300
 AAGCGCCGGC TTTTGACGAA TTATCTACTT CAAGCGAAAT TTTGGAAACA 350
 60 GGGATTAAGG TTATCGACCT CCTAGCACCT TATCTAAAAG GTGGTAAGGT 400

	TGGTCTCTTC	GGTGGTGCTG	GTGTTGGTAA	AACCGTTCTT	ATCCAAGAAT	450
	TGATTCACAA	TATTGCCCAA	GAACACGGTG	GTATCTCTGT	ATTTACCGGA	500
	GTTGGCGAGC	GTACCCGTGA	AGGGAACGAT	CTTTACTGGG	AAATGAAAGA	550
	ATCAGGTGTT	ATTGAAAAAA	CGGCCATGGT	ATTTGGTCAG	ATGAATGAGC	600
5	CACCAGGAGC	CCGTATGCGT	GTTGCTCTTA	CTGGTTTGAC	TATTGCGGAA	650
	TACTTCCGTG	ATGTGGAAGG	GCAGGATGTT	CTTCTGTTCA	TCGATAATAT	700
	CTTCCGTTTC	ACACAGGCTG	GTTCAGAAGT	GTCTGCCCTC	TTGGGTCGTA	750
	TGCCATCAGC	CGTTGGTTAT	CAGCCAACAC	TTGCGACGGA	GATGGGACAA	800
	TTGCAGGAGC	GTATTACCTC	AACCAAGAAG	GGTTCTGTTA	C	841

10

2) INFORMATION FOR SEQ ID NO: 389

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 844 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus uberis*

25 (B) STRAIN: ATCC 19436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389

	GCAAACGGTG	AAAAATTACC	AGAGATTAAT	AATGCATTGA	TAGTTTATAA	50
30	AGGTAGCGAT	AAAAAACAAA	AGATTGTTCT	TGAAGTTGCT	TTGGAACTTG	100
	GGGACGGAAT	GGTTCGTACA	ATCGCTATGG	AATCAACTGA	TGGGCTTACA	150
	CGTGGATTAG	AAGTTTTAGA	TACTGGCCGT	GCCATTAGTG	TACCAGTCGG	200
	AAAAGAACT	TTGGGTCGTG	TTTTCAATGT	GCTTGGTGAA	ACCATTGATT	250
	TGGATGAACC	ATTTGCCGCT	GATGCTGCAA	GAGAACCCAT	CCATAAAAAA	300
35	GCCCCAGCAT	TTGATGAACT	ATCAACGTCT	TCAGAAATTC	TTGAAACCGG	350
	AATAAAAGTT	ATTGACTTAT	TAGCCCCCTTA	TCTCAAAGGT	GGTAAAGTTG	400
	GTTTATTTGG	TGGTGCCGGA	GTAGGTAAAA	CGGTTTTAAT	TCAAGAATTA	450
	ATTCATAATA	TTGCACAAGA	ACATGGTGGT	ATTTCAGTAT	TTACCGGTGT	500
	TGGTGAAAGA	ACTCGTGAAG	GTAATGACCT	TTATTGGGAA	ATGAAAGAAT	550
40	CTGGCGTTAT	TGAAAAAACA	GCCATGGTAT	TTGGACAAAT	GAACGAACCA	600
	CCAGGAGCAC	GTATGCGCGT	TGCTTTAACA	GGTTTAACCA	TTGCTGAATA	650
	TTTCCGGGAT	GTTGAAGGTC	AAGATGTTTT	GCTCTTTATT	GACAACATTT	700
	TCCGTTTCAC	GCAAGCTGGT	TCAGAAGTTT	CAGCCCTATT	GGGTCGTATG	750
	CCTTCAGCGG	TAGGATACCA	ACCAACACTT	GCTACCGAAA	TGGGACAATT	800
45	GCAAGAAAGA	ATTACCTCAA	CTAACAAGGG	ATCTGTACT	TCTA	844

2) INFORMATION FOR SEQ ID NO: 390

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 896 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Tatumella ptyseos*

(B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390

5	TTCCCTCAGG	ACGCTGTACC	ACAGGTGTAC	AACGCTCTTG	AGGTTGAAAA	50
	TGGTGATACC	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTG	GGCGGTGGTG	100
	TCGTTCGTAC	GATTGCAATG	GGAACCTCTG	ACGGCCTGAA	ACGTGGCCTT	150
	AAGGTGACCG	ATCTGCAAAA	ACCGATTGAG	GTACCGGTCTG	GTAAAGCGAC	200
	GCTGGGCCGT	ATCATGAACG	TACTGGGTCA	GCCAATCGAT	ATGAAAGGCG	250
10	ACCTGAAGAA	CGAAGATGGT	AGCAATGTTG	AGGTGAACTC	TATTCACCGT	300
	GCAGCGCCAA	GCTACGAAGA	ACTGGCTAAC	TCTACTGAGC	TGCTGGAAAC	350
	GGGTATCAAG	GTTATCGACC	TGATCTGTCC	GTTTGCAAAA	GGCGGTAAAG	400
	TGGGTCTGTT	CGGTGGTGCG	GGTGTAGGTA	AGACCGTCAA	CATGATGGAA	450
	CTGATCCGTA	ACATCGCTAT	CGAGCACTCT	GGTTACTCTG	TATTTGCAGG	500
15	GGTGGGTGAG	CGTACCCGTG	AAGGTAACGA	CTTCTACCAC	GAAATGACCG	550
	AGTCTAACGT	TCTGGATAAA	GTTGCTCTGG	TTTATGGCCA	GATGAACGAG	600
	CCACCAGGAA	ACCGTCTGCG	CGTTGCGCTG	ACCGGTCTGA	CTATGGCTGA	650
	AAAATTCCGT	GACGAAGGCC	GTGACGTACT	GCTGTTTCGT	GATAACATCT	700
	ATCGTTATAC	CCTGGCCGGT	ACTGAAGTTT	CAGCACTGCT	GGGTCGTATG	750
20	CCTTCTGCGG	TAGGTTATCA	GCCAACACTG	GCCGAAGAAA	TGGGTGTTCT	800
	TCAGGAACGT	ATCACGTCAA	CCAAAACCGG	TCAATCACT	TCCGTA	896

25 2) INFORMATION FOR SEQ ID NO: 391

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 829 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Trabulsiella guamensis</i>
	(B)	STRAIN: ATCC 49490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391

40	TTCCCTCAGG	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTTATGAA	50
	TGGTAGTGAG	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGTGGTGGTA	100
	TCGTACGTAC	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GATGTAAAG	ATCTCGAGCA	TCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
45	GCTGGGTCGT	ATCATGAACG	TGCTGGGTCA	GCCGATCGAT	ATGAAAGGCG	250
	ACATCGGCGA	AGAAGAGCGT	TGGGCTATCC	ACCGCGCAGC	ACCGTCCTAC	300
	GAAGAGCTGT	CCAGCTCTCA	GGAAGTGTG	GAAACCGGCA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGT	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTGAT	TCGTAACATC	450
50	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTGG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTCTGG	550
	ACAAAGTATC	CCTGGTGTAT	GGACAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	TCTGACCATG	GCTGAGAAGT	TCCGTGACGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTCGATAA	CATCTACCGT	TACACCCTGG	700
55	CGGGTACTGA	AGTATCTGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	750
	TACCAGCCGA	CCCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	800
	CTCAACCAAA	ACCGGTTCTA	TCACCTCCG			829

60

2) INFORMATION FOR SEQ ID NO: 392

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia bercovieri*
(B) STRAIN: ATCC 43970

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392

CGAATTCCCC CAAGACGCTG TACCAAAAGT GTACAACGCC CTTGAGGTTG 50
AAGGCACAGC TCAGAAGCTG GTGCTGGAAG TTCAGCAACA GCTGGGCGGT 100
GGTGTGTGTC GTTGTATCGC AATGGGCTCT TCCGATGGTC TGAGCCGCGG 150
20 GTTGAAAGTC ATCAACCTGG AACACCCAAT TGAAGTGCCG GTGGGTAAAT 200
CAACTCTGGG CCGTATCATG AACGTATTGG GTGACCCAAT CGACATGAAA 250
GGTCCTATCG GTGAAGAAGA GCGTTGGGCA ATCCACCGCG AAGCGCCTTC 300
TTACGAAGAG CTTGCCAGCT CGCAAGATCT GTTAGAAACC GGTATCAAGG 350
TAATGGATCT GATTTGTCCG TTCGCTAAGG GCGGTAAAGT CCGTCTGTTC 400
25 GGTGGTGCGG GTGTGGGTAA AACAGTCAAC ATGATGGAGC TGATTCGTAA 450
TATTGCGATT GAGCACTCAG GTTATTCTGT ATTTGCCGGT GTGGGTGAGC 500
GTACTCGTGA GGGTAACGAC TTCTACCACG AGATGACTGA CTCCAACGTT 550
CTGGACAAAG TATCCTTGGT TTATGGCCAG ATGAATGAGC CACCAGGTAA 600
CCGTCTGCGC GTTGCCTGTA CCGGCTTGAC CATGGCGGAG AAATTCCGTG 650
30 ATGAAGGTCG TGATGTACTG TTATTCATCG ATAACATCTA TCGTTATACC 700
CTGGCCGGTA CAGAGGTATC TGCCTGCTA GGTCTGTATG CATCAGCGGT 750
AGGCTATCAG CCAACGCTGG CAGAAGAGAT GGGTGTGTTG CAGGAACGTA 800
TCACTTCCAC CAAGACGGGT TCAATCACCT CCGTA 835

35

2) INFORMATION FOR SEQ ID NO: 393

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 812 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
(B) STRAIN: ATCC 9610

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393

GCTGTACCAA AAGTGTACAA CGCCCTTGAG GTTGAAGGCG CAGCTGAGAA 50
GCTGGTGCTG GAAGTTCAGC AACAGCTGGG CCGTGGTGTT GTTCGTTGTA 100
55 TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GTGGGTGTA AGTCATCAAC 150
CTGGAACACC CAATTGAAGT GCCTGTGGGC AAGTCAACTC TGGGCCGTAT 200
CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGGCGAAG 250
AAGAGCGTTG GGCAATCCAT CGTGAAGCGC CTTCTTACGA AGATCTTGCC 300
AGCTCGCAAG ACTTGTTAGA AACCGGTATC AAGGTAATGG ACTTGATTTG 350
60 TCCGTTTCGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400

235

GTAAAACGGT AAACATGATG GAGCTTATTC GTAACATTGC GATTGAGCAC 450
 TCAGGTTATT CCGTATTTGC TGGCGTGGGT GAGCGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAGATGA CTGACTCCAA CGTTCTGGAC AAAGTATCCT 550
 TGGTTTATGG CCAAATGAAT GAGCCACCAG GTAACCGTCT GCGCGTTGCA 600
 5 CTGACCGGCT TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT 650
 ATTGCTGTTC ATCGATAACA TCTATCGCTA TACCTTAGCC GGTACGGAAG 700
 TTTCCGCACT GCTGGGTCGT ATGCCATCTG CCGTAGGTTA CCAGCCAACG 750
 CTGGCAGAAG AGATGGGTGT GTTGCAGGAA CGTATTACTT CCACCAAGAC 800
 GGGTTCAATC AC 812
 10

2) INFORMATION FOR SEQ ID NO: 394

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Yersinia frederiksenii*
 25 (B) STRAIN: ATCC 33641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394

AAAGTGTACA ACGCCCTTGA GGTGAAGGT ACTGCTGAGA AGTTAGTACT 50
 30 GGAAGTTCAG CAACAGCTGG GCGGTGGTGT TGCTCGTTGT ATCGCCATGG 100
 GCTCTTCCGA TGGTTTGAGC CGCGGGTTGA AAGTTGTCAA CCTGGAACAC 150
 CCAATTGAAG TACCGGTTGG TAAATCAACT CTGGGCCGTA TCATGAACGT 200
 ATTGGGTGAC CCAATCGACA TGAAAGGTCC TATCGGTGAA GAAGAGCGTT 250
 GGGCAATCCA CCGCGAAGCG CCTTCTTACG AAGAGCTTGC CAGCTCGCAA 300
 35 GATCTGTTAG AAACCGGTAT CAAGGTAATG GATCTGATTT GCCCGTTTCGC 350
 TAAAGGCGGT AAAGTCGGTC TGTTCCGGTGG TGCGGGTGTA GGTAACACGG 400
 TAAACATGAT GGAGCTGATC CGTAATATCG CGATCGAGCA CTCAGGTTAT 450
 TCCGTATTTG CGGGTGTTGG TGAACGTACC CGTGAGGGTA ACGACTTCTA 500
 CCACGAGATG ACTGACTCCA ACGTTCTGGA CAAAGTATCC TTGGTTTATG 550
 40 GCCAGATGAA TGAGCCACCA GGTAACCGTC TTCGCGTTGC ACTGACCGGT 600
 CTGACCATGG CGGAGAAATT CCGTGATGAA GGTCGTGACG TATTGCTGTT 650
 CATCGATAAC ATCTATCGTT ATACCTTGGC CCGTACGGAA GTATCCGCAC 700
 TGCTGGGTCG TATGCCATCT GCGGTAGGCT ATCAGCCAAC GCTGGCAGAA 750
 GAGATGGGTG TGTTGCAGGA ACGTATTACT TCCACCAAGA CGGGTTCAAT 800
 45 CA 802

2) INFORMATION FOR SEQ ID NO: 395

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Yersinia intermedia*

(B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395

5	GCTGTACCAA	GAGTGTACAA	CGCCCTTGAG	GTTGAAGGCA	CTGCTGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AACAGCTAGG	CGGTGGTGTT	GTTCGTTGTA	100
	TCGCAATGGG	CTCTTCCGAT	GGTCTGAGCC	GCGGGTTGAA	AGTCATCAAC	150
	CTGGAACACC	CAATTGAAGT	GCCGGTTGGT	AAATCAACTC	TGGGCCGTAT	200
	CATGAACGTA	TTGGGTGACC	CAATCGACAT	GAAAGGTCCT	ATCGGTGAAG	250
10	AAGAGCGTTG	GGCAATCCAC	CGCGAAGCGC	CTTCTTACGA	AGAGCTTGCC	300
	AGCTCACAAAG	ATTTGTTAGA	AACCGGTATC	AAAGTAATGG	ACTTGATTTG	350
	CCCGTTTCGCT	AAGGGCGGTA	AAGTGGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAACACAGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATTGAGCAC	450
	TCAGGTTATT	CTGTATTTGC	TGGTGTGGGT	GAGCGTACTC	GTGAGGGTAA	500
15	CGACTTCTAC	CACGAGATGA	CTGACTCCAA	CGTTCTGGAC	AAAGTATCCT	550
	TGGTGTATGG	CCAGATGAAT	GAGCCACCAG	GTAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGTGACGT	650
	ACTGTTGTTC	ATCGATAACA	TCTATCGCTA	TACCTTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCAACG	750
20	CTGGCAGAAG	AGATGGGTGT	GTTGCAGGAA	CGTATTACGT	CCACCAAGAC	800
	GGGTTC					806

25 2) INFORMATION FOR SEQ ID NO: 396

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 806 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Yersinia pseudotuberculosis</i>
	(B)	STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396

40	GCTGTACCAA	AAGTGTACAA	CGCCCTTGAG	GTAGAAGGCA	CAACTGAAAA	50
	GTTAGTGCTG	GAAGTTCAGC	AACAGTTGGG	CGGTGGTGTT	GTTCGTTGTA	100
	TCGCAATGGG	CTCTTCCGAT	GGTCTGAGCC	GTGGGTTGAA	AGTAACCAAC	150
	CTGGAACACC	CGATCGAAGT	ACCGGTGTTG	AAAGCGACCC	TTGGCCGTAT	200
45	CATGAACGTA	TTGGGTGAAC	CAATCGACAT	GAAAGGTCCT	ATCGGTGAAG	250
	AAGAGCGTTG	GGCAATCCAT	CGCGAAGCGC	CTTCTTATGA	AGAGCTTGCT	300
	AGCTCACAAAG	ATCTGTTAGA	AACCGGTATC	AAGGTTATGG	ACCTGATTTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAACACAGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
50	TCTGGGTATT	CTGTATTTGC	CGGTGTAGGT	GAGCGTACCC	GTGAGGGTAA	500
	TGACTTCTAC	CATGAAATGA	CTGACTCCAA	CGTTTTGGAC	AAAGTATCCT	550
	TGGTTTACGG	CCAGATGAAT	GAGCCACCAG	GTAACCGTCT	ACGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGTGACGT	650
	ACTGCTGTTC	ATCGATAATA	TCTATCGTTA	TACCCTAGCT	GGTACGGAAG	700
55	TATCCGCATT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGTTA	TCAGCCAACA	750
	CTGGCTGAAG	AGATGGGTGT	GTTGCAGGAA	CGTATTACTT	CCACTAAGAC	800
	GGGTTC					806

60

2) INFORMATION FOR SEQ ID NO: 397

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia rohdei*
 (B) STRAIN: ATCC 43380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397

15 TTCCCCCAAG ACGCTGTACC AAAAGTGTAC AACGCCCTTG AGGTTGAAGG 50
 TGCAGCTGAG AAGCTTGTGC TGGAAAGTTCA GCAGCAGCTG GGCGGTGGTG 100
 TTGTTTCGTTG TATCGCAATG GGCTCTTCCG ATGGTTTGAG CCGTGGGTTG 150
 20 AAAGTTATCA ACCTGGAACA CCCAATTGAA GTGCCAGTTG GTAAATCAAC 200
 TCTGGGCCGT ATCATGAACG TATTGGGTGA CCCAATCGAC ATGAAAGGCC 250
 CTATCGGTGA AGAAGAGCGT TGGGCAATCC ACCGTGAAGC GCCTTCTTAC 300
 GAAGAGCTTG CCAGCTCGCA AGATCTGTTA GAAACCGGTA TCAAGGTAAT 350
 GGATCTGATT TGTCCGTTTCG CTAAGGGCGG TAAAGTCGGT CTGTTCCGGT 400
 25 GTGCGGGTGT TGGTAAAACA GTAAACATGA TGGAGCTTAT TCGTAACATC 450
 GCGATTGAGC ACTCAGGTTA TTCTGTATTT GCCGGGGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAGAT GACTGACTCC AACGTTCTGG 550
 ACAAAGTATC CTTGGTTTAT GGCCAGATGA ATGAGCCACC AGGTAACCGT 600
 CTGCGCGTTG CACTGACCGG CTTGACCATG GCGGAAAAAT TCCGTGATGA 650
 30 AGGCCGTGAC GTATTGCTGT TCATCGATAA CATTTATCGT TATACCCTAG 700
 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCATC TGCGGTAGGC 750
 TATCAGCCAA CACTGGCAGA AGAGATGGGT GTGTTGCAGG AACGTATTAC 800
 TTCCACTAAG ACGGGTTCAA TCACCTCCG 829

35

2) INFORMATION FOR SEQ ID NO: 398

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yokenella regensburgei*
 (B) STRAIN: ATCC 35313

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398

ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTACAAAA TGGTAACGAG 50
 AAAGTGGTGC TGGAAAGCTCA GCAGCAGCTC GGCGGCGGTA TCGTGCGTAC 100
 55 TATCGCCATG GGTTCTTCCG ACGGTCTGCG TCGTGGTCTG GAAGTTAAAG 150
 ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC CCTGGGCCGT 200
 ATCATGAACG TCCTGGGTCA GCCGATCGAC ATGAAAGGCG ACATCGGTGA 250
 AGAAGAGCGT TGGGCTATCC ACCGCGCAGC ACCTTCCTAT GAAGAGCTGT 300
 CCAGCTCTCA GGAAGTCTG GAAACCGGTA TCAAAGTAAT GGATCTGATC 350
 60 TGCCCGTTTCG CTAAGGGTGG TAAAGTCGGT CTGTTCCGGT GTGCGGGTGT 400

	AGGTAAAACT	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	GCGATTGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCAGGCGTGG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTACTGG	ATAAAGTATC	550
	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
5	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCGTCGATAA	CATCTACCGT	TATACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	TGCGGTAGGT	TATCAGCCAA	750
	CTCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	CTCTACCAAA	800
	ACCGGTTCTA	TCACCTCCG				819

10

2) INFORMATION FOR SEQ ID NO: 399

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1097 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yarrowia lipolytica*
 (B) STRAIN: ATCC 38295

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399

	AAGCTTAAGG	CTGAGCGAGA	GCGAGGTATC	ACCATTGATA	TCGCTCTCTG	50
30	GAAGTTCCAG	ACCCCTAAGT	ACTACGTCAC	CGTTATTGAT	GCTCCCGGTC	100
	ACCGAGATTT	CATCAAGAAC	ATGATTACCG	GTACTTCCCA	GGCTGACTGC	150
	GCCATCCTCA	TCATTGCTGG	TGGTGTGGT	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGT	CAGACCCGAG	AGCACGCCCT	GCTCGCTTTC	ACCCTCGGTG	250
	TTAAGCAGCT	CATTGTTGCT	ATCAACAAGA	TGGACTCCGT	CAAGTGGTCT	300
35	CAGGATCGAT	ACCTCGAGAT	TTGCAAGGAG	ACTGCCAACT	TCGTCAAGAA	350
	GGTCGGTTAC	AACCCCAAGG	CTGTCCCCTT	CGTCCCCATT	TCCGGATGGA	400
	ACGGTGACAA	CATGATCGAG	CCCTCTACCA	ACTGTGACTG	GTACAAGGGA	450
	TGGACCAAGG	AGACCAAGGC	CGGCGAGATC	AAGGGTAAGA	CCCTCCTCGA	500
	GGCCATTGAT	GCCATTGAGC	CCCCCGTGCG	ACCCACGAC	AAGCCCCCTCC	550
40	GACTTCCCCT	CCAGGATGTC	TACAAGATCG	GTGGTATCGG	CACAGTGCCC	600
	GTTGGCCGAG	TCGAGACCGG	TGTTATCAAG	GCCGGTATGG	KTGTTACCTT	650
	CGCTCCCGCC	AACGTGACCA	CTGAGGTCAA	GTCTGTCGAG	ATGCACCACG	700
	AGATCCTCCC	CGATGGAGGT	TTCCCCGGTG	ACAACGTCGG	TTTCAACGTC	750
	AAGAACGTTT	CCGTCAAGGA	TATCCGACGA	GGTAACGTTG	CTGGTGACTC	800
45	CAAGAACGAC	CCCCCAAGG	GCTGCGACTC	TTTCAACGCT	CAGGTCATTG	850
	TTCTTAACCA	CCCCGGTCAG	ATCGGTGCTG	GTTACGCTCC	CGTCCTTGAT	900
	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	GACACCCTGA	TCGAGAAGAT	950
	CGACCGACGA	ACCGGTAAGA	AGATGGAGGA	CTCCCCCAAG	TTCATCAAGT	1000
	CTGGTGATGC	TGCCATTGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGTGTC	1050
50	GAGGCCTTCA	CTGAGTACCC	CCCTCTTGGT	CGATTCGCCG	TCCGAGA	1097

2) INFORMATION FOR SEQ ID NO: 400

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1233 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Absidia corymbifera*
(B) STRAIN: ATCC 46775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400

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10 CAAGCTTAAG GCTGAACGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT      50
   GGAAGTTCGA GACTCCCAAG TACCACGTTA CCGTCATTGA TGCCCCTGGC      100
   CATCGTGATT TCATCAAGAA CATGATTACT GGTACTTCCC AAGCTGACTG      150
   CGGTATCTTG ATTATTGCTG CTGGTACTGG TGAATTCGAA GCTGGTATCT      200
   CCAAGGATGG TCAAACCCGT GAACACGCTT TGCTTGCTTT CACCCTTGGT      250
15 GTCCGTCAAT TGATTGTCGC TATCAACAAG ATGGATTCCA CCAAGTACTC      300
   TGAGGCCCGT TACAACGAAA TTGTCAAGGA AGTCTCCACC TTCATCAAGA      350
   AGATTGGTTT CAACCCCAAG TCCGTTCCCT TCGTCCCTAT CTCTGGCTGG      400
   AACGGTGACA ACATGTTGGA GGARTCCACC AACATGCCTT GGTTCAGGG      450
   ATGGAACAAG GAGACTAAGG CTGGTGCCAA GACYGGCAAG ACCCTTCTTG      500
20 AAGCCATTGA CAACATTGAT CCCCTGTTC GTCCTTCCGA CAAGCCCCTT      550
   CGTCTTCCCC TTCAAGATGT CTACAAGATC GGTGGTATTG GTACAGTTCC      600
   TGTCGGTCGT GTTGAGACTG GTGTCATCAA GCCTGGTATG GTTGTCACCT      650
   TCGCTCCCGC TAACGTCACC ACTGAAGTCA AGTCCGTYGA AATGCACCAC      700
   GAGCAACTTG CTGAAGGTGT TCCCGGTGAC AACGTCGGTT TCAACGTCAA      750
25 GAACGTTTCC GTCAAGGATA TCCGCCGTGG TAACGTYTGC TCTGACTCCA      800
   AGAACGACCC CGCCAAGGAA TCCGCTTCCT TCACCGCTCA AGTTATTGTC      850
   TTGAACCACC CTGGTCARAT TGGTGCTGGT TACTCTCCTG TCTTGGATTG      900
   CCACACTGCT CACATTGCAT GCAAGTTCTY TKAGCTTCTT KAGAAGATCG      950
   ATYGTCGTTT CGGTAAGTAA ATANTTTGGT TTRGGATATG GGTATTGGGC      1000
30 TTAATCTYTG GATTTTGCCT CAATTGCTCC TTCCTTGATC TTTCTCGATT      1050
   ACTTTTGTGAT CATTTGCTAA TCCAAACCCT TTCCATTTYA TTGAAAACAG      1100
   GTAAGAAGTT GGAAGACTCC CCCAAGTTCG TCAAGWSYGG TGA CTCTGCTG      1150
   ATCGTCAAGA TGGTTCCTTC CAAGCCCATG TCGGTTGAAG CCTACACTGA      1200
   ATATCCTCCT CTTGGTCGTT TCGGTGTCCG TGA                        1233
35

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2) INFORMATION FOR SEQ ID NO: 401

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Alternaria alternata*
(B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401

```

55 CAAGTTGAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTCT      50
   GGAAGTTCGA GACTCCCAAG GTTAGTACCC CTCTGCCTAC TACATCAAGT      100
   TCTTTACAAT GCTAACATGT TGTACTCAGT ACTATGTCAC CGTCATTGAC      150
   GCCCCCGGTC ACCGTGATTT CATCAAGAAC ATGATCACTG GTACCTCCCA      200
   GGCCGACTGC GCTATTCTCA TCATTGCCGC CGGTACTGGT GAGTTCGAGG      250
   CTGGTATCTC CAAGGATGGC CAGACTCGTG AGCACGCTCT CCTCGCTTAC      300
60 ACCCTCGGTG TCAAGCAGCT CATCGTTGCC ATCAACAAGA TGGACACCAC      350

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	CAAGTGGTCC	GAGGAGCGTT	ACCAGGAGAT	CATCAAGGAG	ACCTCCAAC T'	400
	TCATCAAGAA	GGTCGGCTAC	AACCCCAAGC	ACGTTCCCTT	CGTCCCCATC	450
	TCCGGTTTCA	ACGGTGACAA	CATGATTGAG	GCCTCATCCA	ACTGCCCCTG	500
	GTACAAGGGT	TGGGAGAAGG	AGACCAAGGC	CAAGGCCACT	GGTAAGACCC	550
5	TCCTCGAGGC	CATCGACGCC	ATCGACCCTY	CCAGCCGTCC	CACCGACAAG	600
	CCCCTCCGTC	TTCCCCTYCA	GGATGTTTAC	AAGATTGGTG	GTATTGGCAC	650
	GGTGCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATCAAGGCC	GGTATGGTCG	700
	TCACCTTCGC	CCCCGCTGGT	GTCACCACTG	AAGTCAAGTC	CGTCGAGATG	750
	CACCACGAGC	AGCTCACCGA	GGGTGTCCCC	GGTGACAACG	TCGGCTTCAA	800
10	CGTCAAGAAC	GTCTCCGTCA	AGGAGATCCG	TCGTGGTAAC	GTTGCCGGTG	850
	ACTCCAAGAA	CGACCCCCCC	AAGGGTGCCG	AGTCCTTCAA	CGCCCAGGTC	900
	ATCGTCCTCA	ACCACCCTGG	TCAGGTCGGT	GCTGGTTACG	CCCCAGTCCT	950
	CGACTGCCAC	ACCGCCCACA	TTGCTTGCAA	GTTCTCTGAG	CTCCTCGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AGAACTCTCC	CAAGFTCATC	1050
15	AAGTCCGGTG	ACGCCGCCAT	CGTCAAGATG	GTTCCCTCCA	AGCCCATGTG	1100
	CGTTGAGGCT	TTCACTGACT	ACCCTCCTCT	CGGTCGTTTC	GCTGTCCGTG	1150
	A					1151

20

2) INFORMATION FOR SEQ ID NO: 402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402

	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	50
	GGAAGTTCCA	GACCTCCAAG	TATGAGGTCA	CCGTCATTGG	TAAGCATTTG	100
	AGTTCCAACC	TACGTTGCCC	AACATTTACA	GTCATCTAAC	AAAGTTCAAT	150
40	AGATGCCCCC	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACTT	200
	CCCAGGCTGA	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAATTC	250
	GAGGCTGGTA	TCTCCAAGGA	TGGTCAGACC	CGTGAGCACG	CTCTGCTCGC	300
	TTTCACCCTC	GGTGTCCGTC	AGCTCATCGT	TGCCCTCAAC	AAGATGGACA	350
	CCTGCAAGTG	GTCTCAGGAT	CGTTACAACG	AAATCGTTAA	GGAGACTTCC	400
45	AACTTCATCA	AGAAGGTCGG	ATACAACCCC	AAGAGCGTTC	CTTTCGTCCC	450
	CATCTCCGGT	TTCAACGGTG	ACAACATGAT	TGAGGCCTCC	ACCAACTGCC	500
	CCTGGTACAA	GGGTTGGGAG	AAGGAGACCA	AGGCTGGCAA	GTCCACCGGT	550
	AAGACCCTTC	TCGAGGCCAT	CGATGCCATC	GAGCCCCCCG	TCCGTCCCAC	600
	CGACAAGCCT	CTCCGTCTTC	CCCTYCAGGA	TGTCTACAAG	ATCTCTGGTA	650
50	TCGGTACTGT	GCCCGTCGGT	CGTGTCGAGA	CTGGTGTGAT	CAAGCCTGGT	700
	ATGGTCGTTA	CTTTCGCTCC	TGCCAACGTG	ACCACTGAAG	TCAAGTCCGT	750
	TGAAATGCAC	CACCAGCAGC	TCCAGGCCGG	TAACCCCGGT	GACAACGTTG	800
	GTTTCAACGT	CAAGAACGTC	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTT	850
	GCCGGTGACT	CCAAGAACGA	CCCCCCTGCT	GGCTGCGATT	CCTTCAACGC	900
55	CCAGGTCATC	GTCCTTAACC	ACCCCGGTCA	GGTCGGCAAC	GGTTACGCTC	950
	CCGTCCTGGA	CTGCCACACC	GCTCACATTG	CTTGCAAGTT	CGCTGAGCTC	1000
	CTTGAGAAGA	TTGACCGCCG	TACCGGTAAA	TCTGTTGAGG	ACAAGCCCAA	1050
	GTTTCATCAAG	TCTGGTGATG	CTGCCATCGT	CAAGATGATT	CCCTCCAAGC	1100
	CCATGTGTGT	GGAGTCTTTC	ACTGACTTCC	CCCCTCTTGG	TCGTTTCGCT	1150
60	GTCCGTGACG	TAAGTTTTTC	CCTCTTGACT	ATCTTCACAA	TTTTTCACAT	1200

ATTTTCACGC CTCGTCCCAC TCTTTTTCCT CCCTTCCTCT TTGGTTCCCC 1250
TTTTTGCCTG CAAGTTCTCT ATAGCTAACA TGA 1283

5

2) INFORMATION FOR SEQ ID NO: 403

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1103 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: DAL95

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403

TCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT GGAAGTTCCA 50
GACTCCCAAG TATGAGGTCA CTGTCATCGG TAAGCTCGAC TCGCCCCGAT 100
ATGTTTTGGT GCTGTAGCTA ACACGATCTG AAGATGCCCC CGGTCACCGT 150
25 GACTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCTG ACTGCGCTAT 200
CCTCATCATT GCCTCCGGTA CTGGTGAGTT CGAGGCTGGT ATCTCCAAGG 250
ATGGCCAGAC CCGTGAGCAC GCTCTGCTGG CTTTCACCCT CGGTGTCAAG 300
CAGCTCATCG TCGCCCTCAA CAAGATGGAC ACCTGCAAGT GGTCCGAGGA 350
TCGTTACAAC GAAATTGTCA AGGAAACCTC CAACTTCATC AAGAAGGTCG 400
30 GCTACAACCC CAAGGCCGTT CCCTTCGTCC CCATCTCTGG CTTC AACGGT 450
GACAACATGC TTGAGCCCTC CTCCAAC TGC CCCTGGTACA AGGGATGGGA 500
GAAGGAGACC AAGGCCGGCA AGGTCAC TGG TAAGACCCTC ATCGAGGCCA 550
TCGACGCCAT TGAGCCCCCT GTCCGTCCCT CCAACAAGCC CCTCCGTCTT 600
CCCCTCCAGG ATGTCTACAA GATCTCTGGT ATCGGAACGG TCCCTGTTCGG 650
35 CCGTGTTCGAG ACCGGTATCA TCAAGCCCGG CATGGTTCGTC ACCTTCGCCC 700
CCGCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA CCACCAGCAG 750
CTCCAGGAGG GTGTCCCCGG TGACAACGTC GGTTC AACG TCAAGAACGT 800
TTCCGTCAAG GAAGTCCGCC GTGGTAACGT CTGCGGTGAC TCCAAGAACG 850
ATCCCCCTCA GGGTGCTGCC TCCTTCAACG CCCAGGTCAT CGTCCTCAAC 900
40 CACCCCGGTC AGGTCGGCGC TGGTTACGCC CCCGTCCTCG ACTGCCACAC 950
TGCCACATT GCTTGCAAGT TCTCTGAGCT GCTTGAGAAG ATTGACCGCC 1000
GTACCGGCAA GTCTGTTGAG AACAAACCCA AGTTCATCAA GTCCGGTGAT 1050
GCCGCCATCG TGAAGATGGT TCCTTCCAAG CCCATGTGTG TCGAGTCCTT 1100
CAC 1103

45

2) INFORMATION FOR SEQ ID NO: 404

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1149 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: WSA-172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
5	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
10	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTC	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAACCTGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
15	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	600
	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTGCGC	CGTGTCGAGA	CCGGTATCAT	CAAGCCCGGC	ATGGTCGTCA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
20	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	950
	CTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
25	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
	CGAGTCCTTC	ACTGACTACC	CCCCTCTGGG	TCGTTTCGCC	GTCCGTGAC	1149

30 2) INFORMATION FOR SEQ ID NO: 405

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus niger*
 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405

45	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCCCTCT	50
	GGAAGTTCCA	GACTGGCAAG	TATGAGGTCA	CCGTCATTGG	TATGTACTCA	100
	CAGAGTTCTC	TTTTCATCAA	AGCAATATAC	TAACGTCCAT	CATAGACGCC	150
	CCCGGTCACC	GTGACTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	200
50	TGACTGCGCT	ATCCTCATCA	TTGCCTCCGG	TACTGGTGAG	TTCGAGGCTG	250
	GTATCTCCAA	GGATGGCCAG	ACTCGTGAGC	ACGCTCTGCT	TGCTTTCACC	300
	CTCGGTGTCC	GCCAGCTCAT	CGTTGCCCTC	AACAAGATGG	ACACCTGCAA	350
	GTGGTCCGAG	GACCGTTACA	ACGAAATCGT	TAAGGAGACC	TCCAACCTTCA	400
	TCAAGAAGGT	CGGATACAAC	CCCAAGGGTG	TTCCTTTCGT	CCCCATCTCC	450
55	GGTTTCAACG	GTGACAACAT	GCTCGAGCCC	TCCCCCAACT	GCCCCCTGGTA	500
	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	CAAGGTCACC	GGTAAGACCC	550
	TCCTTGAGGC	CATCGACGCC	ATCGAGCCCC	CCGTCCGTCC	CTCCAACAAG	600
	CCCCTCCGTC	TTCCCCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGAAC	650
	TGTTCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATTGCCCTT	GGTATGGTCG	700
60	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAGATG	750

CACCACCAGC AGCTCAAGGA AGGTGTCCCC GGTGACAACG TTGGTTTCAA 800
 CGTCAAGAAC GTTTCCTGCA AGGAGGTTTCG CCGTGGTAAC GTTGCCGGTG 850
 ACTCCAAGAA CGACCCCCCT CTTGGCTGTG AGAGCTTCAC CGCCCAGGTC 900
 ATCGTCCTCA ACCACCCCGG TCAGGTCGGC GCTGGTTACG CTCCCGTCCT 950
 5 GGA CTGCCAC ACTGCTCACA TTGCTTGCAA GTTCGCTGAG CTCCTTGAGA 1000
 AGATTGACCG CCGTACCGGA AAGTCTGTTG AATCTTCCCC CAAGTTCATC 1050
 AAGTCCGGTG ACGCTGCCAT CGTCAAGATG ATTCCCTCCA AGCCCATGTG 1100
 TGTGAGGCT TTCCTGACT ACCCCCCTCT TGGTCGTTTC GCCGTCCGCG 1150
 A 1151

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2) INFORMATION FOR SEQ ID NO: 406

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastoschizomyces capitatus*
 25 (B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406

GCTTAAAGCT GAACGTGAAC GTGGTATCAC CATTGATATC GCTCTCTGGA 50
 30 AGTTCGAAAC TCCTAAGTAC TACGTTACTG TTATTGATGC TCCAGGTCAC 100
 CGTGATTTCA TCAAGAACAT GATTACTGGT ACTTCCCAAG CCGATTGCGC 150
 CATTCTTATC ATTGCTGCCG GTGTCGGTGA ATTCGAAGCT GGTATCTCCA 200
 AGGAAGGTCA AACCAGAGAA CACGCTCTTC TCGCTTTCAC CCTTGGTGTC 250
 AGACAACCTA TCATTGCCAT CAACAAGATG GACTCTGTCA AGTGGGACCA 300
 35 AAAGAGATAC GAAGAAATCG TCAAGGAGGC TTCCAACCTC GTCAAGAAGG 350
 TTGGTTACAA CCCCAAGTCT GTTCCATTCG TTCCTATCTC TGGTTGGAAC 400
 GGTGACAACA TGTGGAACC TACCACCAAC GCCCATGGT ACAAGGGATG 450
 GACCAAGGAA ACCAAGGCTG GTGCCACTAA GGGTATGACT CTTATTGAAG 500
 CCATTGACGC CATTGAACCA CCAGTAAGAC CATCCGACAA GCCACTCCGT 550
 40 CTCCCACTCC AAGATGTTTA CAAGATTGGT GGTATCGGAA CTGTGCCAGT 600
 CGGCCGTGTC GAAACCGGTA TCATCAAGGC CGGTATGGTC GTTACCTTTG 650
 CTCCACCAAT GGTCACAAC GAAGTTAAGT CCGTTGAAAT GCACCACGAA 700
 CAACTTGCTC AAGGTAACCC AGGTGACAAC GTTGGTTTCA ACGTCAAGAA 750
 CGTTTCCGTT AAGGAAATCA GACGTGGTAA CGTCTGTGGT GACTCCAAGA 800
 45 ACGATCCACC AAAGGGCTGC GAATCTTTCA ACGCTCAAGT TATCGTCTTG 850
 AACCACCCTG GTCAAATCTC TGCTGGTTAC TCTCCAGTTC TCGATTGCCA 900
 CACTGCCCAC ATTGCCTGCA GATTCGACGA ACTCCTTGAA AAGATCGACC 950
 GTCGTTCTGG TAAGAAGATT GAAGACTCTC CAAAGTTTGT CAAGTCTGGT 1000
 GATGCCGCTA TCGTCAAGAT GATCCCAACC AAGCCAATGT GCGTTGAAAC 1050
 50 CTTCACTGAA TACCCACCAC TTGGTCGTTT CGCCGTCCGT GAT 1093

2) INFORMATION FOR SEQ ID NO: 407

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 10231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407

10	CTTGGACAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTCAT	CAAGAATATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
15	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTYGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
20	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
	TTACTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
25	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
30	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	A					1101

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2) INFORMATION FOR SEQ ID NO: 408

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1089 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 18804

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408

	GAAGGCTGAA	AGAGAAAGAG	GTATCACCAT	TGATATCGCT	TTGTGGAAAT	50
	TCGAAACTCC	AAAATACCAC	GTTACCGTCA	TTGATGCTCC	AGGTCACAGA	100
	GATTTTCATCA	AGAATATGAT	CACTGGTACT	TCTCAAGCTG	ATTGTGCTAT	150
55	TTTGATTATT	GCTGGTGGTA	CTGGTGAATT	CGAAGCCGGT	ATTTCTAAGG	200
	ATGGTCAAAC	CAGAGAACAC	GCTTTGTTGG	CTTACACTTT	GGGTGTCAAA	250
	CAATTGATTG	TTGCTGTCAA	CAAGATGGAC	TCTGTCAAAT	GGGACAAAAA	300
	CAGATTTGAA	GAAATCATCA	AGGAAACCTC	CAACTTCGTC	AAGAAGGTTG	350
	GTTACAACCC	AAAGACTGTT	CCATTCGTTC	CAATCTCTGG	TTGGAATGGT	400
60	GACAACATGA	TTGAACCATC	CACCAACTGT	CCATGGTACA	AGGGTTGGGA	450

	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	TTAGAAGCTA	500
	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	CCGACAAACC	ATTGAGATTG	550
	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	ATTGGTACTG	TGCCAGTCGG	600
	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	TATGGTTGTT	ACTTTCGCCC	650
5	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	TTGAAATGCA	TCACGAACAA	700
	TTGGCTGAAG	GTGTTCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	750
	TTCCGTTAAA	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	800
	ATCCACCAAA	GGGTTGTGAC	TCTTTCAATG	CCCAAGTCAT	TGTTTTGAAC	850
	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTCTTGG	ATTGTCACAC	900
10	TGCCCACATT	GCTTGTAAT	TCGACACTTT	GGTTGAAAAG	ATTGACAGAA	950
	GAACTGGTAA	GAAATTGGAA	GAAAATCCAA	AATTCGTCAA	ATCCGGTGAT	1000
	GCTGCTATCG	TCAAGATGGT	CCCAACCAAA	CCAATGTGTG	TTGAAGCTTT	1050
	CACTGACTAC	CCACCATTAG	GTAGATTTCG	TGTCAGAGA		1089

15

2) INFORMATION FOR SEQ ID NO: 409

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 56884

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409

	CTTGGACAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
35	CCAGGTCACA	GAGATTTTCAT	CAAGAATATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
40	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
45	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
	TTACTTTTCG	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
50	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
55	A					1101

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2) INFORMATION FOR SEQ ID NO: 410

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 60193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410

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15  CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CCAAATACC  ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
    TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
    GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
20  TTGGGTGTCA AACAATTGAT TGTGCTGTC AACAAGATGG ACTCTGTCAA      300
    ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCCAACCTCG      350
    TCAAGAAGGT TGGTTACAAC CCAAGACTG TTCCATTCGT TCCAATCTCT      400
    GGTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
    CAAGGGTTGG GAAAAGGAAA CCAATCCGG TAAAGTTACT GGTAAGACCT      500
25  TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
    CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
    TGTGCCAGTC GGTAGAGTTG AAAGTGGTAT CATCAAAGCC GGTATGGTTG      650
    TTAAGTTTCG CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG      700
    CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
30  CGTTAAGAAC GTTTCGGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG      800
    ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC      850
    ATTGTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT      900
    GGATTGTCAC ACTGCCCACA TTGCTTGTA AATCGACACT TTGGTTGAAA      950
    AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC     1000
35  AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG     1050
    TGTGTAAGCT TTCCTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG     1100
    AT                                     1102
  
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2) INFORMATION FOR SEQ ID NO: 411

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 90028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411

```

    CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CCAAATACC  ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
60  TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
  
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	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
5	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
10	TTACTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
15	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
20						

2) INFORMATION FOR SEQ ID NO: 412

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 35 (B) STRAIN: NCPF 3108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
40	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
45	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
50	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAA	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
55	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
60	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100

5 2) INFORMATION FOR SEQ ID NO: 413

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1098 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida catenulata*
(B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413

20 GGACAAGCTT AAGGCTGAGC GTGAGAGAGG TATCACCATT GACATTGCCT 50
TGTGGAAGTT CGAGACTCCC AAGTACCACG TCACTGTCAT TGACGCCCCC 100
GGTCACAGAG ATTTTCATCAA GAACATGATC ACTGGTACCT CGCAGGCTGA 150
CTGTGCTATC TTGATCATTG CTTCCGGTGT CCGTGAGTTC GAGGCTGGTA 200
25 TCTCCAAGGA CGGTCAGACC CGTGAGCACG CCTTGTTGGC CTACACCTTG 250
GGTGTCAAGC AGTTGATCGT TGCCATCAAC AAGATGGACT CCGTCAAGTG 300
GGACAAGAAC AGATTCGAGG AGATTGTCAA GGAGACCACC AACTTCGTCA 350
AGAAGGTTGG TTACAACCCC AAGGCTGTCC CCTTCGTCCC CATCTCTGGC 400
TGGAACGGTG ACAACATGAT TGAGGCCTCC ACCAACTGCC CCTGGTACAA 450
30 GGGCTGGGAG AAGGAGACCA AGGCCGGTAA GTCTACCGGT AAGACCTTGT 500
TGGAGGCCAT TGACGCCATT GAGCCCCCTA CCAGACCCAC CGACAAGCCC 550
TTGAGATTGC CCTTGCAGGA TGTCTACAAG ATCGGTGGTA TTGGTACGGT 600
GCCCCGTCGGC CGTGTGCGA CCGGTGTCAT CAAGCCCGGT ATGGTCGTCA 650
CCTTCGCCCC CGCTGGTGTC ACCACTGAAG TCAAGTCCGT CGAGATGCAC 700
35 CACGAGCAGT TGTCCGAGGG TGTCCCCGGT GACAACGTTG GTTTCAACGT 750
CAAGAACGTC TCTGTTAAGG AGATCAGACG TGGTAACGTC TGCGGTGACT 800
CCAAGAACGA CCCCCCATG GGTGCTCTT CTTTCAACGC CCAGGTTATC 850
GTGTTGAACC ACCCCGGTCA GATCTCTGCC GGTTACTCTC CCGTCTTGGA 900
CTGCCACACC GCCACATTG CTTGCAAGTT CGCCGAGTTG ATCGAGAAGA 950
40 TTGACAGACG TACCGGTAAG TCCATGGAGG CTAACCCCAA GTTCGTCAAG 1000
TCTGGTGACG CCGCCATCGT CAAGATGGAG CCCACTAAGC CCATGTGTGT 1050
TGAGGCCTTC ACTGACTTCC CTCCTTTGGG TAGATTCGCC GTCAGAGA 1098

45

2) INFORMATION FOR SEQ ID NO: 414

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1102 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
(B) STRAIN: NCPF 3949

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414

249

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
5	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTCTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCTG	TCCAATCTCT	400
10	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
15	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTAYT	CTCCAGTCTT	900
20	GGATTGTCAC	ACTGCCACCA	TTGCTTGTA	ATTGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
25						

2) INFORMATION FOR SEQ ID NO: 415

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1102 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida dubliniensis*
 - (B) STRAIN: CBS 7987
- 40
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
45	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
50	ATGGGACAAA	AACAGATTCTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCTG	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
55	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
60	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850

	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTAYT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
5	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102

10 2) INFORMATION FOR SEQ ID NO: 416

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida famata*
 (B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416

25	AATTGAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATTGATAT	CGCTTTATGG	50
	AAATTCGAAA	CTCCAAAATA	CCACGTTACC	GTTATTGATG	CTCCAGGTCA	100
	CAGAGATTTC	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGATTGTG	150
	CTATTTTRAT	TATTGCTGGT	GGTGTCCGGT	AATTCGAAGC	CGGTATCTCT	200
30	AAGGATGGTC	AAACCAGAGA	ACACGCTTTA	TTGGCTTACA	CCTTAGGTGT	250
	TAGACAATTG	ATTGTTGCCG	TCAACAAGAT	GGACTCTGTT	AAATGGGACA	300
	AGGCTAGATT	CGAAGAAATC	ATCAAGGAAA	CCTCTAACTT	CGTCAAGAAG	350
	GTTGGTTACA	ACCCTAAGAC	TGTTCCTTTC	GTGCCAATTT	CTGGATGGAA	400
	CGGTGACAAC	ATGATTGAAG	CCTCCACCAA	CTGTCCATGG	TACAAGGGTT	450
35	GGGAAAAGGA	AACCAAGGCT	GGTAAATCTA	CTGGTAAGAC	TTTGTTAGAA	500
	GCCATTGATG	CCATTGAACC	ACCAACCAGA	CCAACCGAAA	AGCCATTGAG	550
	ATTACCATTA	CAAGATGTCT	ACAAGATCGG	TGGTATTGGT	ACTGTGCCAG	600
	TCGGTAGAGT	TGAAACCGGT	GTTATCAAGG	GTGGTATGGT	TGTTACCTTT	650
	GCCCCAGCCG	GTGTCACTAC	CGAAGTCAAA	TCCGTTGAAA	TGCACCACGA	700
40	ACAATTAGCT	GAAGGTGTTC	CAGGTGACAA	TGTTGGTTTC	AACGTCAAGA	750
	ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTTTGTGG	TGACTCCAAG	800
	AACGACCCAC	CAAAGGGTGC	TGAATCTTTC	ACCGCTCAAG	TTATTGTCTT	850
	GAACCACCCA	GGTCARATCT	CTGCTGGTTA	CTCTCCAGTC	TTAGATTGTC	900
	ACACCGCCCA	CATTGCTTGT	AAATTCGATG	CTTTACTCGA	AAAGATTGAC	950
45	AGAAGATCCG	GTAAGAAATT	AGAAGACGAA	CCAAAATTCG	TCAAGTCCGG	1000
	TGATGCTGCT	ATCGTCAAGA	TGGTCCCAAC	CAAACCAATG	TGTGTTGAAG	1050
	CTTTCACCTGA	ATACCCACCA	TTAGGTAGAT	TCGCTGTTAG	AGAT	1094

50

2) INFORMATION FOR SEQ ID NO: 417

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida glabrata*

(B) STRAIN: ATCC 66032

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417

	TTTGGACAAG	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATCGATATCG	50
	CTTTGTGGAA	GTTTCGAACT	CCAAAGTACC	ACGTYACCGT	TATCGATGCT	100
	CCAGGTCACA	GAGATTTCAT	CAAGAACATG	ATTACTGGTA	CTTCTCAAGC	150
10	TGACTGTGCT	ATCTTGATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCYG	200
	GTATCTCCAA	GGATGGTCAA	ACCAGAGAAC	ACGCTCTATT	GGCTTTTACC	250
	CTAGGTGTTA	GACAATTGAT	TGTYGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	GTGGGATGAA	TCCAGATTCT	CTGAAATCGT	TAAGGAAACC	TCCAACCTCA	350
	TCAAGAAGGT	CGGTTACAAC	CCAAAGACTG	TTCCATTCTG	CCCAATCTCT	400
15	GGTTGGAACG	GTGACAACAT	GATTGAAGCC	ACCACCAACG	CTTCCTGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAGGCTGG	TGTCGTCAAG	GGTAAGACCT	500
	TGTTGGAAGC	CATTGACGCT	ATCGAACCAC	CAACCAGACC	AACTGACAAG	550
	CCATTGAGAT	TGCCATTGCA	AGATGTCTAC	AAGATCGGTG	GTATCGGTAC	600
	GGTGCCAGTC	GGTAGAGTCG	AAACCGGTGT	CATCAAGCCA	GGTATGGTTG	650
20	TTACCTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCACGAAC	AATTGACTGA	AGGTTTGCCA	GGTGACAACG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AGGAAATCAG	AAGAGGTAAT	GTCTGTGGTG	800
	ACTCCAAGAA	CGACCCACCA	AAGGCTGCTG	CTTCTTTCAA	CGCTACCGTC	850
	ATTGTCTTGA	ACCACCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTTTT	900
25	GGACTGTCAC	ACCGCCACCA	TTGCTTGTA	GTTCTGAAGAA	TTGTTGGAAA	950
	AGAACGACAG	AAGATCCGGT	AAGAAGTTGG	AAGACTCTCC	AAAGTTCTTG	1000
	AAGTCCGGTG	ACGCTGCTTT	GGTTAAGTTC	GTTCCATCCA	AGCCAATGTG	1050
	TGTCGAAGCT	TTCTCCGACT	ACCCACCATT	GGGTAGATTC	GCTGTCAGAG	1100
	A					1101

2) INFORMATION FOR SEQ ID NO: 418

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1080 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida guilliermondii*

45 (B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418

	AGAGAAAGAG	GTATCACCAT	TGACATTGCT	TTGTGGAAAT	TCGAGACTCC	50
50	AAAGTACCAC	GTTACYGTCA	TTGATGCCCC	AGGTCACAGA	GATTTCATCA	100
	AGAACATGAT	CACTGGTACT	TCTCAAGCTG	ACTGTGCTAT	TTTGATTATT	150
	GCTGGTGGTA	CCGGTGAATT	CGAAGCTGGT	ATCTCTAAGG	ATGGTCAAAC	200
	CAGAGAGCAC	GCTTTGTTGG	CTTACACCTT	GGGTGTTAGA	CAATTGATTG	250
	TTGCTGTCAA	CAAGATGGAC	TCCGTCAART	GGGACAAGAA	CAGATTYAG	300
55	GAAATCATCA	AGGAAACCTC	TAACTTCGTC	AAGAAGGTTG	GTTACAACCC	350
	TAAGACTGTG	CCATTCTGTT	CTATCTCTGG	ATGGAAYGGT	GACAACATGA	400
	TTGAGGCTTC	TACCAACTGT	CCTTGGTACA	AGGGATGGGA	GAAGGAGACC	450
	AAGGCTGGTA	AGTCCACCGG	TAAGACTTTG	TTGGAGGCCA	TTGACGCCAT	500
	TGAGCCACCT	CAAAGACCAA	CCGACAAGCC	ATTGAGATTG	CCATTGCAAG	550
60	ATGTYTACAA	GATTGGTGGT	ATTGGAACGG	TGCCAGTCCG	TAGAGTTGAA	600

	ACCGGTATCA	TYAAGGCCGG	TATGGTTGTT	ACCTTTGCCC	CAGCTGGTGT	650
	YACCACTGAA	GTCAAGTCCG	TGGAAATGCA	CCACGAACAA	TTGGTTGAAG	700
	GTGTTCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	TTCCGTTAAG	750
	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	ACCCACCAAA	800
5	GGGTTGTGAC	TCTTTCACCG	CTCAAGTTAT	TGTGTTGAAC	CACCCTGGTC	850
	AAATCTCTGC	TGGTTACTCT	CCAGTTTTTG	ACTGTCACAC	CGCCCACATT	900
	GCTTGTAAT	TCGACACCTT	GTTGGAGAAG	ATTGACAGAA	GAACCGGTAA	950
	GAAGATGGAG	GACAACCCCA	AGTTTGTCAA	GTCCGGTGAC	GCTTCTATCG	1000
	TCAAGATGGT	GCCATCCAAG	CCAATGTGTG	TTGAGGCTTT	CACCGACTAC	1050
10	CCACCATTGG	GAAGATTCGC	CGTCAGAGAC			1080

2) INFORMATION FOR SEQ ID NO: 419

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Candida haemulonii*
 (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419

30	TCTGTCAAGT	GGGACAAGGC	CAGATACGAG	GAAATCGTCA	AGGAGACCTC	50
	TAACCTTCGTC	AAGAAGGTTG	GTTACAACCC	TAAGACTGTT	CCATTCGTCC	100
	CAATCTCTGG	TTGGAACGGT	GACAACATGA	TTGAGGCTTC	TACCAACTGT	150
	GACTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGTCTGGTA	AGTCCACCGG	200
	TAAGACCTTG	TTGGAGGCCA	TTGACGCCAT	TGAGCCACCA	ACCAGACCAA	250
35	CCGACAAGCC	ATTGAGATTG	CCATTGCAGG	ATGTCTACAA	GATTGGTGGT	300
	ATCGGAAGCTG	TGCCAGTCGG	CAGAGTTGAG	ACCGGTGTTA	TCAAGGCCGG	350
	TATGGTTGTC	ACCTTCGCCC	CAGCTGGTGT	CACCACTGAA	GTCAAGTCTG	400
	TCGAGATGCA	CCACGAGCAG	TTGCCAGAGG	GTGTCCCAGG	TGACAACGTT	450
	GGTTTCAACG	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	500
40	CTGTGGTGAC	TCCAAGCAGG	ACCCACCAAA	GGGCTGTGAC	TCTTTCACCG	550
	CTCAGGTTAT	TGTGTTGAAC	CACCCAGGTC	AGATCTCTTC	TGGTTACTCT	600
	CCAGTTTTTG	ACTGTCACAC	TGCCCACATT	GCTTGTAAGT	TCGACACCTT	650
	GGTTGAGAAG	ATCGACAGAA	GAACCGGTAA	GAAGTTGGAA	GATGAGCCAA	700
	AGTTCATCAA	GTCCGGTGAC	GCTGCTATCG	TCAAGATGGT	CCCAACCAAG	750
45	C					751

2) INFORMATION FOR SEQ ID NO: 420

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Candida inconspicua*

(B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420

5	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAGTATC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTCAT	TAAGAACATG	ATTACTGGTA	CTTCTCAAGC	150
	AGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATTTCCAA	GGATGGTCAA	ACTAGAGAAC	ACGCTTTATT	AGCATTCACC	250
10	TTAGGTGTTA	AGCAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCTGTAA	300
	GTGGGATGAA	AAGAGATTTG	AAGAAATTGT	CAAGGAAACC	CAAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATTTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTTCTAACT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTCAAG	GGTAAGACCT	500
15	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGATAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTAT	TATTAAGCCA	GGTATGGTTG	650
	TTGTTTTTCGC	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCATGAAC	AATTAGAAGA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
20	CGTCAAGAAC	GTCTCTGTTA	AGGATATCAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	TGACCCACCA	CAAGGTTGTG	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCCTGG	TCAAATTTCT	GCTGGTTACT	CTCCAGTTTT	900
	AGATTGTCAC	ACTGCCCACA	TTGCATGTAA	ATTGATGAA	TTAATTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
25	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCACTGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
	AT					1102

30

2) INFORMATION FOR SEQ ID NO: 421

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1099 bases
35	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Candida kefyr</i>
	(B)	STRAIN: ATCC 28838

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421

	TGGACAAGTT	AAAGGCTGAA	AGAGAAAGAG	GTATCACCAT	CGATATCGCT	50
	TTGTGGAAGT	TCGAAACTCC	AAAGTACCAA	GTTACCGTTA	TCGATGCTCC	100
	AGGTCACAGA	GATTTTCATCA	AGAACATGAT	TACTGGTACT	TCTCAAGCTG	150
50	ACTGTGCTAT	CTTGATTATT	GCTGGTGGTG	TCGGTGAATT	CGAAGCCGGT	200
	ATCTCCAAGG	ATGGTCAAAC	CAGAGAACAC	GCTTTGTTGG	CTTACACCTT	250
	GGGTGTTAGA	CAATTGATTG	TTGCTATCAA	CAAGATGGAC	TCTGTTAAGT	300
	GGGATGAATC	TCGTTACCAA	GAAATTGTTA	AGGAAACCTC	CAACTTCATC	350
	AAGAAGGTCG	GTTACAACCC	AAAGAATGTT	CCATTCGTCC	CAATCTCTGG	400
55	TTGGAACGGT	GACAACATGA	TTGAAGCCAC	CACCAACGCT	CCATGGTACA	450
	AGGGTTGGGA	AAAGGAAACC	AAGGCTGGTA	CCGTCAAGGG	TAAGACCTTG	500
	TTGGAAGCTA	TTGACGCTAT	CGAACCACCA	ACCAGACCAA	CTGACAAGCC	550
	ATTGAGATTG	CCATTGCAAG	ATGTCTACAA	GATCGGTGGT	ATTGGTACTG	600
	TGCCAGTCGG	TAGAGTCGAA	ACCGGTGTCA	TCAAGCCAGG	TATGGTTGTT	650
60	ACCTTCGCCC	CAGCCGGTGT	CACTACCGAA	GTTAAGTCCG	TCGAAATGCA	700

	CCACGAACAA	TTGGAAGAAG	GTCTACCAGG	TGACAACGTC	GGTTTCAACG	750
	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	CTGTGGTGAC	800
	TCCAAGAACG	ATCCACCAAA	GGCTGCTGCT	TCTTTCAACG	CCACTGTTAT	850
	CGTCTTGAAC	CACCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTTTGG	900
5	ATTGTCACAC	TGCTCACATT	GCTTGTAAGT	TCGACGAATT	GTTGGAAAAG	950
	AACGACAGAA	GATCCGGTAA	GAAGTTGGAA	GACTCTCCAA	AGTTCTTGAA	1000
	GTCTGGTGAC	GCTGCTTTGG	TTAAGTTCGT	TCCATCTAAG	CCAATGTGTG	1050
	TTGAAGCATT	CTCTGACTAC	CCACCATTGG	GTAGATTTCG	TGTCAGAGA	1099

10

2) INFORMATION FOR SEQ ID NO: 422

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1095 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(B) STRAIN: ATCC 34135

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422

	AAGTTAAAGG	CAGAAAGAGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
	GAAGTTYGAA	ACTCCAAART	ACCACGTTAC	CGTTATTGAT	GCTCCAGGTC	100
30	ACAGAGATTT	CATCAAGAAC	ATGATTACCG	GTAATTCTCA	AGCTGATTGT	150
	GCTATTTTGA	TTATTGCTGG	TGGTGTCTGG	GAATTCGAAG	CTGGTATCTC	200
	CAAGGATGGT	CAAAC TAGAG	AACACGCTCT	ATTGGCTTTC	ACCTTAGGTG	250
	TTAGACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAARTGGGAT	300
	GAAAACAGAT	TTGAAGAAAT	TGTCAAGGAA	ACCCAAA ACT	TCATCAAGAA	350
35	GGTTGGTTAC	AACCCAAAGA	CTGTTCCATT	CGTTCCAATY	TCTGGTTGGA	400
	ATGGTGACAA	CATGATTGAA	GCATCCACCA	ACTGTCCATG	GTACAAGGGT	450
	TGGACTAAGG	AAACCAAGGC	AGGTGTTGTT	AAGGGTAAGA	CCTTATTAGA	500
	AGCAATCGAT	GCTATTGAAC	CACCTGTCAG	ACCAACCGAA	AAGCCATTAA	550
	GATTACCATT	ACAAGATGTT	TACAAGATTG	GTGGTATTGG	TACTGTGCCA	600
40	GTCGGTAGAG	TCGAAACCGG	TGTCATTAAAG	CCAGGTATGG	TTGTCACTTT	650
	TGCTCCAGCA	GGTGTCACCA	CCGAAGTCAA	GTCCGTTGAA	ATGCACCATG	700
	AACAATTAGA	ACAAGGTGTT	CCAGGTGATA	ACGTTGGTTT	CAACGTTAAG	750
	AACGTTTCTG	TCAAGGATAT	CAAGAGAGGT	AACGTTTGTG	GTGACTCCAA	800
	GAACGACCCA	CCAATGGGTG	CAGCTTCCTT	CAATGCTCAA	GTCATTGTCT	850
45	TGAACCAACC	TGGTCAAATT	TCCGCTGGTT	ACTCTCCAGT	CTTGGATTGT	900
	CACACTGCCC	ACATTGCATG	TAAGTTCGAC	GAATTAATCG	AAAAGATTGA	950
	CAGAAGAACT	GGTAAGTCTG	TTGAAGACCA	TCCAAAGTCY	GTCAAGTCTG	1000
	GTGATGCAGC	TATCGTCAAG	ATGGTCCCAA	CCAAGCCAAT	GTGTGTTGAA	1050
	GCTTTCCTG	AATAYCCACC	ATTAGGTAGA	TTCGCAGTCA	GAGAT	1095

50

2) INFORMATION FOR SEQ ID NO: 423

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1104 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*
 5 (B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423

	CTTGGACAAG	CTTAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
10	CTTTATGGAA	GTTCGAAACT	CCAAAGTACC	ACGTTACCGT	CATTGACGCT	100
	CCAGGTCACA	GAGATTTCAT	CAAGAACATG	ATTACTGGTA	CCTCTCAAGC	150
	AGATTGTGCT	ATTTTTRATYA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATCTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTCTTCT	TGCATTCACT	250
	CTTGGTGTTA	GACAATTGAT	TGTTGCTATC	AACAAGATGG	ACTCTGTCAA	300
15	GTGGGACGAA	TCCAGATTCG	ATGAAATTTG	TAAGGAAACC	GCWAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	CCCAATCTCT	400
	GGTTGGAACG	GTGACAACAT	GATTGAACCA	TCTGCTAACT	GTCCATGGTA	450
	CAAGGGATGG	ACTAAGGAAA	CCAAGGCTTC	CGGTGTCGTC	AAGGGTAAGA	500
	CCCTTCTTGA	AGCAATTGAT	GCTATTGAGC	CACCTGTCAG	ACCAACTGAC	550
20	AAGGCTTTGA	GATTGCCATT	RCAAGATGTC	TACAAGATTG	GTGGTATTGG	600
	TACTGTGCCA	GTCGGTAGAG	TTGAAACCGG	TATCATCAAG	CCAGGTATGA	650
	TTGTCGTTTT	CGCTCCAACC	GGTGTTACTA	CTGAAGTTAA	GTCCGTTGAA	700
	ATGCACCATG	AACAATTAGA	AGAAGGTGTC	CCAGGTGACA	ATGTTGGTTT	750
	CAACGTCAAG	AACGTCTCTG	TTAAGGATAT	TAAGAGAGGT	AACGTCTGTG	800
25	GTGACTCCAA	GAACGACCCA	CCAATGGGTT	GTGCTTCCTT	CAATGCTCAA	850
	GTCATTGTTC	TTAACCACCC	AGGTCAAATT	TCTGCTGGTT	ACTCACCAGT	900
	TCTTGACTGT	CACACTGCCC	ACATTGCATG	TAAGTTCGAY	GAATTACTCG	950
	AAAAGATTGA	CAGAAGAACC	GGTAAGGCTA	CTGAAGACCA	TCCAAAGTCT	1000
	GTCAAGTCTG	GTGATGCAGC	TATCGTCAAG	ATGGTTCCAA	CCAAGCCAAT	1050
30	GTGTGTYGAA	GCTTTCCTG	ACTACCCACC	ATTAGGTAGA	TTCGCTGTYA	1100
	GAGA					1104

35 2) INFORMATION FOR SEQ ID NO: 424

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitaniae*
 (B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424

50	GGACAAGTTG	AAGGCTGAGA	GAGAAAGAGG	TATCACCATC	GATATCGCTT	50
	TGTGGAAGTT	CGAGACTCCA	AAGTACCACG	TTACCGTCAT	TGACGCTCCA	100
	GGTCACAGAG	ATTTTCATCAA	GAACATGATC	ACTGGTACTT	CCCAAGCTGA	150
	CTGTGCTATC	TTGATTATCG	CTGGTGGTGT	CGGTGAGTTC	GAAGCCGGTA	200
55	TCTCTAAGGA	CGGTCAAACC	AGAGAGCACG	CTTTGTTGGC	TTACACCTTG	250
	GGTGTCAAGC	AGTTGATTGT	TGCTGTCAAC	AAGATGGACT	CCGTCAAGTG	300
	GGACCAATCT	AGATTTCGAGG	AAATCATCAA	GGAAACCTCT	AACTTCGTCA	350
	AGAAGGTTGG	TTACAACCCT	AAGACTGTTC	CATTCGTCCC	AATCTCTGGT	400
	TGGAACGGTG	ACAACATGAT	TGAGCCATCY	ACCAACTGCC	CATGGTACAA	450
60	GGGTTGGGAG	AAGGAGACCA	AGTCYGGTAA	GTCCACCGGT	AAGACCTTGT	500

	TGGAGGCCAT	TGACGCCATT	GAGCCACCTT	CGAGACCAAC	CGACAAGCCA	550
	TTGAGATTGC	CATTGCAAGA	TGTCTACAAG	ATYGGTGGTA	TTGGTACTGT	600
	GCCAGTCGGT	AGAGTTGAGA	CCGGTGTCAT	CAAGGCCGGT	ATGGTTGTCA	650
	CCTTTGCTCC	AGCTGGTGTC	ACCACTGAAG	TCAAGTCCGT	GGAAATGCAC	700
5	CACGAACAAT	TGGCTGAGGG	TGTCCCAGGT	GACAACGTTG	GTTTCAACGT	750
	CAAGAACGTT	TCCGTCAAGG	AAATCAGAAG	AGGTAACGTC	TGTGGTGACT	800
	CCAAGAACGA	CCCACCAAAG	GCTGCTGCTT	CYTTCACCTG	TCAAGTYATY	850
	GTCTTGAACC	ACCCAGGTCA	AATCTCCTCY	GGTTACTCTC	CAGTYTTGGA	900
	CTGTCACACT	GCYCACATTG	CTTGTAAGTT	CGACACCTTG	ATTGAGAAGA	950
10	TCGACAGAAG	AACYGGTAAG	AAGTTGGAAG	AAGAGCCAAA	GTTTCATCAAG	1000
	TCYGGTGACG	CTGCTATCGT	CAAGATGGTC	CCAACCAAGC	CAATGTGYGT	1050
	YGAAGCTTTC	ACCGACTACC	CACCATTGGG	TAGATTCGCT	GTCAGAGA	1098

15

2) INFORMATION FOR SEQ ID NO: 425

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1101 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
(B) STRAIN: ATCC 22977

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425

	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	TAAGAACATG	ATTACTGGTA	CTTCCCAAGC	150
35	TGATTGTGCT	ATCTTAATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATCTCCAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTATT	AGCATTCAAC	250
	TTAGGTGTTA	AGCAATTAAT	TGTTGCTATC	AACAAGATGG	ACTCTGTAA	300
	GTGGGATGAA	AAGAGATTTG	AAGAAATTGT	CAAGGAAACC	CAAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATTTCT	400
40	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTACTAACT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTTAAG	GGTAAGACCT	500
	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGACAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTGT	TATTAAGCCA	GGTATGGTTG	650
45	TTGTTTTTCG	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCATGAAC	AATTAGAACA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTCAAGAAC	GTCTCTGTTA	AGGATATTAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGACCCACCA	CAAGGTTGTG	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCCTGG	TCAAATTTCT	GCAGGTTACT	CTCCAGTTTT	900
50	AGATTGTCAC	ACTGCCACCA	TTGCATGTAA	GTTTCGATGAA	TTAATCGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCATGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
	A					1101

55

2) INFORMATION FOR SEQ ID NO: 426

(i) SEQUENCE CHARACTERISTICS:

257

- (A) LENGTH: 1095 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*
(B) STRAIN: ATCC 90018

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426

	CAAATTGAAG	GCTGAAAGAG	AAAGAGGTAT	CACCATTGAT	ATCGCTTTGT	50
15	GGAAATTCGA	AACTCCAAAA	TACCATGTTA	CTGTTATTGA	TGCTCCAGGT	100
	CACAGAGATT	TCATCAAGAA	TATGATTACT	GGTACTTCTC	AAGCTGATTG	150
	TGCTATTTTG	ATTATTGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATCT	200
	CTAAGGATGG	TCAAACCAGA	GAACACGCTT	TGTTGGCTTA	CACCTTGGGT	250
	GTTAAGCAAT	TGATTGTTGC	CATCAACAAG	ATGGACTCAG	TCAAATGGGA	300
20	CAAGAACAGA	TACGAAGAAA	TTGTCAAGGA	AACTTCCAAC	TTCGTCAAGA	350
	AGGTTGGTTA	CAACCCTAAA	GCTGTCCCAT	TCGTCCCAAT	CTCTGGTTGG	400
	AACGGTGACA	ATATGATTGA	ACCATCAACC	AACTGTCCAT	GGTACAAGGG	450
	TTGGGAAAAG	GAAACTAAAG	CTGGTAAGGT	TACCGGTAAG	ACCTTGTTGG	500
	AAGCTATCGA	TGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	550
25	AGATTGCCAT	TGCAAGATGT	CTACAAGATT	GGTGGTATTG	GAAGTGTGCC	600
	AGTTGGTAGA	GTTGAAACCG	GTATCATCAA	GGCTGGTATG	GTTGTTACTT	650
	TTGCCCCAGC	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	700
	GAACAATTGA	CTGAAGGTGT	CCCAGGTGAC	AATGTTGGTT	TCAACGTCAA	750
	GAACGTTTCA	GTTAAGGAAA	TCAGAAGAGG	TAACGTTTGT	GGTGACTCCA	800
30	AGAACGATCC	ACCAAAGGGA	TGTGAYTCCT	TCAATGCTCA	AGTTATTGTC	850
	TTGAACCACC	CAGGTCAAAT	CTCTGCTGGT	TACTCACCAG	TCTTGGATTG	900
	TCACACTGCC	CACATTGCTT	GTAAATTCTG	CACTTTGATT	GAAAAGATTG	950
	ACAGAAGAAC	CGGTAAGAAA	TTGGAAGATG	AACCAAAATT	CATCAAGTCC	1000
	GGTGATGCTG	CYATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	1050
35	AGCTTTCACT	GACTACCCAC	CATTGGGAAG	ATTCGCTGTT	AGAGA	1095

2) INFORMATION FOR SEQ ID NO: 427

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*
(B) STRAIN: ATCC 96275

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427

55	CTCCGTCAAG	TGGTCTCAGT	CTCGTTTCTG	GGAGATCGTC	AAGGAGGTTT	50
	CCAAGTTCAT	CAAGAAGGTT	GGTTACAAGC	CCGATGAGGT	TCCTTTCGTC	100
	CCCATCTCTG	GCTGGAACGG	CGACAACATG	CTTGAGCCCT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGATGGA	CCAAGAAGAC	CAAGAAGGGT	GAGGTCAAGG	200
	GTAAGACTCT	TCTCGAGGCC	ATTGACGCCA	TCGAGCCCCC	CTCCCGTCCT	250
60	ACCGACAAGC	CCCTCCGCTT	GCCTCTTCAG	GATGTCTACA	AGATCGGCGG	300

	TATCGGTACG	GTACCTGTCG	GCCGTGTCGA	GACCGGTATC	ATCAAGCCCCG	350
	GCATGGTCGT	CACTTTCGCC	CCCGCTGGTG	TCACCACTGA	AGTGAAGTCC	400
	GTCGAGATGC	ACCACGAGCA	GATCCCCGAG	GGTCTCCCCG	GTGACAACGT	450
	CGGTTTCAAC	GTCAAGAACG	TTACCGTCAA	GGATATCCGC	CGTGGTAACG	500
5	TCTGCGGTGA	CTCCAAGAAC	GACCCCCCA	AGGGCTGCTC	TTCCTTCACT	550
	GCCCAGGTCA	TCGTTTTTCAA	CCACCCCGGT	CAGATCTCCA	ACGGTTACTC	600
	CCCCGTTTTG	GACTGCCACA	CCGCCCACAT	TGCCTGCCGC	TTCGACGAGA	650
	TCCAGTCCAA	GATGGACCGT	CGTACTGGTA	AGACCCTTGA	GGAGAACCCC	700
	AAGTTCATCA	AGGCTGGTGA	CTCCGCTATC	GTCAAGATGG	TTCCCTCCAA	750
10	GC					752

2) INFORMATION FOR SEQ ID NO: 428

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428

30	AGTTAAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATCGATAT	CGCTTTGTGG	50
	AAGTTCGAAA	CTCCAAAGTA	CCAAGTTACC	GTTATCGATG	CTCCAGGTCA	100
	CAGAGATTTC	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGACTGTG	150
	CTATCTTGAT	TATTGCTGGT	GGTGTCGGTG	AATTCGAAGC	CGGTATCTCC	200
	AAGGATGGTC	AAACCAGAGA	ACACGCTTTG	TTGGCTTTCA	CCTTGGGTGT	250
35	TAGACAATTG	ATTGTTGCTG	TTAACAAGAT	GGATTCCGTT	AAGTGGGATG	300
	AATCTCGTTT	CCAAGAAATT	GTCAAGGAAA	CCTCTAACTT	CATCAAGAAG	350
	GTCGGTTACA	ACCCAAAGAC	TGTTCCATTC	GTCCCAATCT	CTGGTTGGAA	400
	CGGTGACAAC	ATGATTGAAG	CCACCACCAA	TGCTTCATGG	TACAAGGGTT	450
	GGGAAAAGGA	AACCAAGTCC	GGTGTCGTCA	AGGGTAAGAC	CTTGTTGGAA	500
40	GCTATTGACG	CTATCGAACC	ACCATCCAGA	CCAAC TGACA	AGCCATTGAG	550
	ATTGCCATTG	CAAGATGTCT	ACAAGATTGG	TGGTATCGGA	ACTGTGCCAG	600
	TCGGTAGAGT	CGAAACCGGT	GTTATCAAGC	CAGGTATGAT	TGTTACCTTT	650
	GCCCCAGCCG	GTGTTACTAC	TGAAGTTAAG	TCCGTCGAAA	TGCACCACGA	700
	ACAATTGGAA	GAAGGTCTAC	CAGGTGACAA	CGTCGGTTTC	AACGTCAAGA	750
45	ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTCTGTGG	TGACTCCAAG	800
	AACGATCCAC	CAAAGGCTGC	TGCTTCTTTC	AACGCCACTG	TTATCGTCTT	850
	GAACCATCCA	GGTCAAATCT	CTGCTGGTTA	CTCTCCAGTT	TTGGATTGTC	900
	ACACTGCTCA	CATTGCTTGT	AAGTTCGACG	AATTGTTGGA	AAAGAACGAT	950
	AGAAGATCCG	GTAAGAAGTT	GGAAGACTCT	CCAAAGTTCT	TGAAGTCCGG	1000
50	TGATGCTGCT	TTGGTTAAGT	TCGTTCCATC	TAAGCCAATG	TGTGTTGAAG	1050
	CCTTCTCTGA	CTACCCACCT	CTAGGTAGAT	TCGCTGTCAG	AGA	1093

55 2) INFORMATION FOR SEQ ID NO: 429

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida tropicalis*

(B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429

10
 AAATTGAAGG CTGAAAGAGA AAGAGGTATC ACCATTGATA TCGCTTTGTG 50
 GAAATTTCGAA ACTCCAAAAT ACCACGTTAC CGTTATTGAT GCTCCAGGTC 100
 ACAGAGATTT CATCAAGAAC ATGATTACTG GTACTTCCCA AGCTGATTGT 150
 GCTATTTTGA TTATTGCTGG TGGTACTGGT GAATTCGAAG CTGGTATTTT 200
 15 TAAAGATGGT CAAACCAGAG AACACGCTTT GTTGGCTTAC ACCTTGGGTG 250
 TCAAACAATT GATTGTTGCT GTCAACAAGA TGGACTCTGT TAAATGGGAC 300
 AAAAACAGAT TTGAAGAAAT TATCAAGGAA ACTTCTAACT TCGTCAAGAA 350
 GGTTGGTTAC AACCCTAAGG CTGTTCCATT CGTTCCAATC TCTGGTTGGA 400
 ATGGTGACAA CATGATTGAA GCTTCTACCA ACTGTCCATG GTACAAGGGT 450
 20 TGGGAAAAAG AAACCAAGGC TGGTAAGGTT ACCGGTAAGA CTTTGTTGGA 500
 AGCCATTGAT GCTATTGAAC CACCTTCAAG ACCAACTGAC AAGCCATTGA 550
 GATTGCCATT GCAAGATGTT TACAAGATTG GTGGTATTGG TACTGTGCCA 600
 GTCGGTAGAG TTGAAACTGG TGTCATCAA GCGGTATGG TTGTTACTTT 650
 CGCCCCAGCT GGTGTTACCA CTGAAGTCAA ATCCGTCGAA ATGCACCACG 700
 25 AACAATTGGC TGAAGGTGTC CCAGGTGACA ATGTTGGTTT CAACGTTAAG 750
 AACGTTTCTG TTAAAGAAAT TAGAAGAGGT AACGTTTGTG GTGACTCCAA 800
 GAACGATCCA CCAAAGGGTT GTGACTCTTT CAACGCTCAA GTTATTGTCT 850
 TGAACCACCC AGGTCAAATC TCTGCTGGTT ACTCTCCAGT CTTGGATTGT 900
 CACACTGCTC ATATTGCTTG TAAATTCGAC ACCTTGGTTG AAAAGATTGA 950
 30 CAGAAGAACT GGTAAGAAAT TGGAAGAAA TCCAAAATTC GTCAAATCCG 1000
 GTGATGCTGC TATTGTCAAG ATGGTTCCAA CCAAACCAAT GTGTGTTGAA 1050
 GCTTTCCTG ACTACCCACC ATTAGGTAGA TTCGCTGTCA GAGA 1094

35

2) INFORMATION FOR SEQ ID NO: 430

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida utilis*

(B) STRAIN: Csp 388

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430

CAAGCTTAAA GCTGAGAGAG AGAGAGGTAT CACTATCGAC ATTGCTCTCT 50
 GGAAGTTCGA GACTCCAAAG TACCACGTTA CTGTCATTGA TGCCCCAGGT 100
 CACAGAGATT TCATCAAGAA CATGATTACT GGTACCTCCC AGGCTGACTG 150
 55 TGCTATTCTT ATCATTGCCG GTGGTGTGTTG TGAGTTCGAG GCTGGTATCT 200
 CTAAGGATGG TCAGACCAGA GAGCACGCTT TGCTCGCTTT CACCCTTGGT 250
 GTTAGACAGA TGATTGTTGC TATCAACAAG ATGGACTCTG TCAAGTGGGA 300
 CGAGAAGAGA TTCGAGGAGA TCGTTAAGGA GACCTCTAAC TTCATCAAGA 350
 AGGTTGGTTA CAACCCAAAG ACTGTTCCAT TTGTCCCAAT TTCYGGTTGG 400
 60 AACGGTGACA ACATGATTGA GGCCTCTACC AACTGTCCAT GGTACAAGGG 450

260

	TTGGGAGAAG	GAGACCAAGG	CTGGTGTGTTGT	CAAGGGTAAG	ACCTTGCTCG	500
	ATGCCATTGA	CGCCATTGAG	CCACCAACAA	GACCAACTGA	CAAGCCATTG	550
	AGATTGCCAC	TCCAGGATGT	CTACAAGATT	GGTGGTATCG	GAAGCTGTTCC	600
	AGTCGGTAGA	GTCGAGACCG	GTGTCATCAA	GCCAGGTATG	GTTGTTACCT	650
5	TTGCCCCATC	CGGTGTCACC	ACTGAGGTTA	AGTCCGTCGA	GATGCACCAC	700
	GAGCAGCTTG	CTGAGGGTAT	CCCAGGTGAC	AACGTTGGTT	TCAACGTTAA	750
	GAACGTCTCT	GTTAAGGAGA	TCAGAAGAGG	TAACGTTGCC	GGTGACTCCA	800
	AGAACGACCC	ACCACAGGGT	GCTGAGTCCT	TCAACGCTCA	GGTCATTGTC	850
	TTGAACCACC	CAGGTCAGAT	CTCTGCTGGT	TACTCTCCAG	TTTTGGACTG	900
10	TCACACCGCC	CACATTGCTT	GTAAGTTCTC	TGAGCTTTTG	GAGAAGATTG	950
	ACAGAAGATC	CGGTAAGTCC	CTTGAGGCCT	CTCCAAAGTT	CGTCAAGTCT	1000
	GGTGATGCCG	CTATCGTCAA	GATGGTTCCA	TCCAAGCCAT	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CACTCGGTAG	ATTCGCTGTC	AGAGA	1095

15

2) INFORMATION FOR SEQ ID NO: 431

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1085 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida viswanathii*

(B) STRAIN: ATCC 28269

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431

	GCTGAAAGAG	AAAGAGGTAT	CACCATCGAT	ATCGCTTTGT	GGAAATTCTGA	50
	AACTCCAAAR	TACCACGTTA	CCGTCATTGA	YGCTCCAGGT	CACAGAGATT	100
35	TCATCAAGAA	CATGATYACT	GGTACTTCTC	AAGCTGATTG	TGCTATYTTG	150
	ATTATCGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATYT	CTAAGGATGG	200
	TCAAACCAGA	GAACACGCTT	TGTTGGCCTA	CACCTTGGGT	GTCAAGCAAT	250
	TGATTGTTGC	TGTCAACAAG	ATGGACTCTG	TCAAATGGGA	CAAGAACAGA	300
	TTCGAAGAAA	TCATCAAGGA	AACCTCCAAC	TTCGTCAAGA	AGGTTGGTTA	350
40	CAACCCAAAG	ACTGTTCCAT	TCGTCCCAAT	CTCTGGTTGG	AACGGTGACA	400
	ACATGATTGA	AGCCTCCACC	AACTGCCCAT	GGTACAAGGG	TTGGGAAAAG	450
	GAAACCAAGG	CTGGTAAGGT	TACCGGTAAG	ACTTTGTTGG	AAGCCATTGA	500
	CGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	AGATTGCCAT	550
	TGCAAGATGT	CTACAAGATT	GGTGGTATCG	GAAGCTGTCC	AGTCGGTAGA	600
45	GTTGAAACTG	GTGTCATCAA	GGCCGGTATG	GTTGTCACCT	TYGCCCCAGC	650
	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	GAACAATTGG	700
	CTGAAGGTGT	CCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	GAACGTTTCC	750
	GTCAAGGAAA	TCAGAAGAGG	TAACGTCTGT	GGTGACTCCA	AGAACGACCC	800
	ACCAAAGGGT	TGTGASTCTT	TCAACGCTCA	AGTCATTGTC	TTGAACCACC	850
50	CAGGTCAAAT	CTCTGCTGGT	TACTCTCCAG	TCTTGATTG	TCACACTGCC	900
	CACATTGCTT	GTAAGTTTGA	CACCTTGGTT	GAAAAGATTG	ACAGAAGAAC	950
	CGGTAAGAAG	TTGGAAGAAA	ACCCAAAGTT	TGTCAAGTCC	GGTGACGCTG	1000
	CTATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	AGCYTTCCT	1050
	GACTACCCAC	CATTGGGTAG	ATTCGCTGTC	AGAGA		1085

55

2) INFORMATION FOR SEQ ID NO: 432

60 (i) SEQUENCE CHARACTERISTICS:

261

(A) LENGTH: 1072 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432

	AGGTATTACC	ATTGACATTG	CCTTGTGGAA	GTTTCGAGACC	CCCAAGTACC	50
15	AGGTCACCGT	CATTGACGCT	CCTGGCCACA	GAGATTTTCAT	TAAGAACATG	100
	ATCACTGGTA	CCTCCCAGGC	TGACTGTGCC	ATCTTGATCA	TTGCTGGTGG	150
	TGTTGGTGAG	TTCGAGGCTG	GTATCTCCAA	GGATGGCCAG	ACCAGAGAGC	200
	ACGCCTTGCT	TGCCTACACC	TTGGGTGTCA	AGCAATTGAT	TGTTGCTGTC	250
	AACAAGATGG	ACTCCGTCAA	GTGGGACAAG	AACAGATTCG	AGGAGATTGT	300
20	CAAGGAGACC	TCCAACCTTCG	TCAAGAAGGT	TGGCTACAAC	CCCAAGACTG	350
	TCCCCTTCGT	TCCCATCTCC	GGTTGGAACG	GTGACAACAT	GATTGAGGCC	400
	TCCACCAACT	GCCCTTGGTA	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	450
	TAAGGTCACT	GGTAAGACCT	TGTTGGAGGC	TATTGACGCC	ATTGAGCCCC	500
	CCACCAGACC	CACCGACAAG	CCCTTGAGAT	TGCCCTTGCA	GGATGTCTAC	550
25	AAGATTGGTG	GTATTGGAAC	GGTGCCCGTT	GGCAGAGTTG	AGACCGGCAT	600
	CATCAAGGCC	GGTATGGTTG	TCACCTTTGC	CCCCGCTGGT	GTCACTACTG	650
	AAGTGAAGTC	TGTCGAGATG	CACCACGAGC	AATTGGCTGA	GGGTGTCCCA	700
	GGTGACAATG	TTGGTTTCAA	CGTGAAGAAC	GTTTCCGTTA	AGGAGATCAG	750
	AAGAGGTAAC	GTTTGCGGTG	ACTCCAAGAA	CGACCCCCCC	AAGGCTGCTG	800
30	CTTCTTTCAA	CGCCCAGGTT	ATCGTCTTAA	ACCACCCCCG	TCAAATCTCT	850
	GCTGGTTACT	CTCCGGTTTT	GGATTGCCAC	ACTGCCCACA	TTGCTTGCAG	900
	ATTCGACCAG	TTGATTGAGA	AGATCGACAG	AAGAACCGGT	AAGAAGATGG	950
	AGGACGACCC	TAAGTTCATC	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	1000
	GTTCCCTTCCA	AGCCCATGTG	TGTTGAGGCC	TTCACTGACT	ACCCTCCCTT	1050
35	GGGTCGTTTC	GCTGTCAGAG	AC			1072

2) INFORMATION FOR SEQ ID NO: 433

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433

55	AGCACCAACT	GGTCCGAGCC	TCGTTTCAAC	GAAATCGTCA	AGGAAGTCTC	50
	CAACTTCATC	AAGAAGGTCG	GATACAACCC	CAAGGCTGTT	CCATTCGTCC	100
	CCATCTCTGG	TTTCGAAGGT	GACAACATGA	TTCAACCCTC	CACCAACGCT	150
	CCTTGGTACA	AGGGCTGGAA	CAAGGAGACC	GCCTCTGGCA	AGCACACTGG	200
	CAAGACCCTC	CTCGACGCCA	TTGATGCCAT	CGACCCCCCA	ACCCGCCCCA	250
60	CCGAGAAGCC	CCTCCGTCTC	CCACTTCAGG	ATGTGTACAA	GATCTCTGGT	300

	ATCGGAACAG	TCCCAGTCGG	CCGTGTCGAA	ACCGGTGTTA	TCAAGCCTGG	350
	TATGGTTGTG	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	400
	TCGAAATGCA	CCACCAGCAG	CTCACCCAGG	GTAACCCTGG	TGACAACGTT	450
	GGCTTCAACG	TCAAGAACGT	CTCTGTCAAG	GAAGTCCGCC	GCGGTAACGT	500
5	CGCTGGTGAC	TCCAAGAACG	ACCCACCAAA	GGGCTGCGAC	TCCTTCAACG	550
	CCCAGGTCAT	CGTCCTCAAC	CACCCTGGTC	AAGTCGGTGC	TGGTTATGCC	600
	CCAGTCCTTG	ACTGCCACAC	TGCCCACATT	GCTTGCAAGT	TCTCCGAGCT	650
	CCTCGAGAAG	ATCGACCGCC	GTACCGGTAA	ATCCGTTGAG	AACAACCCCA	700
	AGTTCATCAA	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCATCCAAG	750
10	C					751

2) INFORMATION FOR SEQ ID NO: 434

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Cryptococcus albidus*
 (B) STRAIN: ATCC 66030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434

30	AAGCTCAAGG	CCGAGCGAGA	GCGAGGTATC	ACCATCGACA	TCGCCTTGTC	50
	GAAGTTCGAG	ACCCCCAAGT	ACAATGTAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGAGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	GGCCGACTGT	150
	GCCATCCTCA	TCATCGCCTC	CGGTATCGGA	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGACGGT	CAGACCCGAG	AGCACGCCCT	TTTGGCCTTC	ACCCTCGGTG	250
35	TCCGACAGCT	CATCATTGCC	ATCAACAAGA	TGGACACCTG	CAAGGTTAGT	300
	TCGCAGGTCC	TGGTCTCTGT	ACGAATCTTG	CTGACCCCTT	TTACAGTGGT	350
	CCGAAGACCG	ATACAACGAA	ATCGTCAAGG	AGGCTTCCGG	TTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GACCGTTCCC	TTCGTCCCCA	TCTCCGGATG	450
	GCACGGAGAC	AACATGTTGG	AGGAGTCCAC	CAACATGCCC	TGGTACAAGG	500
40	GATGGCACAA	GGAGTCCAAG	GCCGGTGTTG	TCAAGGGAAA	GACCTTGCTC	550
	GAGGCCATCG	ACGCCATCGA	GCCCCCTACC	CGACCTTCCG	ACAAGCCCTT	600
	GCGATTGCCC	CTCCAGGATG	TCTACAAGAT	CGGTGGTATC	GGTACGGTGC	650
	CCGTCGGTCG	AGTCGAGACC	GGTGTCATCA	AGGCTGGTAT	GGTCGTCACC	700
	TTCGCCCTTG	CCAACGTCAC	CACCGAAGTC	AAGTCCGTCG	AAATGCACCA	750
45	CGAACAGCTC	GCTGAGGGTG	TTCCCGGTGA	CAACGTCGGT	TTCAACGTCA	800
	AGAACGTTTC	CGTCAAGGAC	ATCCGACGAG	GAAACGTCTG	CTCCGACTCG	850
	AAGAACGACC	CCGCTATGGA	GTCTGCTTCC	TTCAACGCTC	AGGTCATTGT	900
	CTTGAACCAC	CCGGGTCAGA	TCGGTGCCGG	CTACTCCCCC	GTTTTGGACT	950
	GCCACACCGC	TCACATTGCC	TGCAAGTTCG	CTGAGCTCGT	TGAGAAGATC	1000
50	GACCGACGAA	CCGGTAAGGT	CATGGAGGCC	GCCCCCAAGT	TCGTCAAGTC	1050
	CGGTGACGCC	GCCATCGTCA	AGTTGATCCC	GTCCAAGCCC	ATGTGTGTCG	1100
	AGTCCTACTC	CGAGTACCCC	CCCTTGGGTC	GATTCGCCGT	CCGAGA	1146

55

2) INFORMATION FOR SEQ ID NO: 435

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Exophiala jeanselmei*
(B) STRAIN: ATCC 64755

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435

	CAAGCTGAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCTTGT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CTGTCATCGA	CGCCCCTGGT	100
	CATCGTGACT	TTATCAAGAA	CATGATCACT	GGTACTTCCC	AGGCTGACTG	150
15	CGCCATTCTC	ATCATTGCCG	CCGGTACTGG	TGAATTTCGAA	GCCGGTATCT	200
	CCAAGGATGG	TCAGACTCGT	GAGCACGCTC	TGCTCGCCTA	CACCCTGGGT	250
	GTCAAGCAGC	TCATTGTGCG	CATCAACAAG	ATGGACACCA	CCAAGTGGTC	300
	CGAGGATCGT	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	350
	AGGTCGGCTA	CAACCCCAAG	TCCGTTCTT	TCGTCCCCAT	CTCCGGCTTC	400
20	AACGGTGACA	ACATGATCGA	TGTCTCCACC	AACTGCCCT	GGTACAAGGG	450
	CTGGGAGAAG	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTCG	500
	AGGCCATCGA	CGCCATCGAC	CCCCCCTC	GTCCCACCGA	CAAGCCTCTC	550
	CGTCTTCCTC	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	GAACGGTGCC	600
	CGTCGGTCGT	GTTGAGACTG	GTGTCATCAA	GGCCGGTATG	GTCGTTACCT	650
25	TCGCTCCTGC	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	700
	GAACAACCTCG	CCGAGGGTGT	TCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	750
	GAACGTCTCC	GTCAAGGAGG	TTCGTCTGGG	AAACGTCTGC	GGTGACTCCA	800
	AGAACGACCC	ACCCAAGGGT	GCTGATTCCT	TCAACGCCCA	GGTCATCGTC	850
	TTGAACCACC	CTGGTCAAGT	CGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	900
30	CCACACTGCC	CACATTGCTT	GCAAGTTCTC	TGAGCTTCTC	GAGAAGATTG	950
	ACCGCCGTAC	CGGTAAATCC	ATCGAAAACA	ACCCAAGTT	CATCAAGTCT	1000
	GGTGACGCTG	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCA	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CTCTTGGTCG	TTTCGCCGTC	CGTGA	1095

35

2) INFORMATION FOR SEQ ID NO: 436

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium oxysporum*
(B) STRAIN: WSA-212

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436

	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
	GAAGTTCGAG	ACTCCTCGCT	ACTATGTCAC	CGTCATTGGT	ATGTTGTCGC	100
55	TCATGCTTCA	TTCTACTTCT	CTTCGTACTA	ACACATCACT	CAGACGCTCC	150
	CGGTCAACCGT	GATTTCATCA	AGAACATGAT	CACTGGTACT	TCCCAGGCCG	200
	ATTGCGCCAT	TCTCATCATT	GCCGCCGGTA	CTGGTGAGTT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTTCTTG	CCTACACCCT	300
	TGGTGTCAAG	AACCTCATCG	TCGCCATCAA	CAAGATGGAC	ACCACCAAGT	350
60	GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	CTCTTTCATC	400

	AAGAAGGTCG	GCTACAACCC	CAAGGCTGTC	GCTTTCGTCC	CCATCTCCGG	450
	TTTCAACGGT	GACAACATGC	TTACCCCCTC	CACCAACTGC	CCCTGGTACA	500
	AGGGTTGGGA	GCGTGAGATC	AAGTCCGGCA	AGCTCACTGG	CAAGACCCTC	550
	CTCGAGGCCA	TTGACTCCAT	CGAGCCCCCC	AAGCGTCCCG	TTGACAAGCC	600
5	CCTTCGTCTT	CCCCTTCAGG	ATGTCTACAA	GATCGGTGGT	ATTGGAACGG	650
	TTCCCGTCGG	CCGTATCGAG	ACTGGTGTCA	TCAAGCCCGG	TATGGTCGTT	700
	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACGAGCAA	CTCACTGAGG	GCCAGCCCGG	TGACAACGTT	GGTTTCAACG	800
	TGAAGAACGT	CTCCGTCAAG	GACATCCGAC	GTGGTAACGT	CGCTGGTGAC	850
10	TCCAAGAACG	ACCCCCCTAT	GGGTGCCGCT	TCTTTCACCG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGTC	AGGTCGGTGC	TGGTTACGCT	CCCGTCCTCG	950
	ATTGTCACAC	TGCCCACATT	GCCTGCAAGT	TCGCCGAGAT	CCAGGAGAAG	1000
	ATCGACCGCC	GAACCGGTAA	GGCTACTGAG	GCCGCCCCCA	AGTTCATCAA	1050
	GTCTGGTGAC	TCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCCATGTGTG	1100
15	TTGAGGCTTT	CAC				1113

2) INFORMATION FOR SEQ ID NO: 437

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Geotrichum* spp.
 (B) STRAIN: LEV-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437

35	GGTCCGAGGA	CAGATTCAAC	GAGATTGTCA	AGGAGACTTC	CAACTTCATC	50
	AAGAAGGTTG	GTTAYAACCC	CAAGACTGTT	GCTTTCGTCC	CCATCTCTGG	100
	TTGGAACGGT	GACAACATGA	TTGAGCCCTC	CACCAACTGC	CCCTGGTACA	150
	AGGGATGGCA	GAAGGAGACC	AAGGCTGGTG	TCACTAAGGG	TAAGACCCTC	200
	CTTGAGGCCA	TCGATGCCAT	TGAGCCCCCT	GTCAGACCTT	CCGACAAGCC	250
40	CCTCCGTCTT	CCCCTCCAGG	ATGTCTACAA	GATCGGTGGT	ATCGGAACTG	300
	TGCCCCGTGG	CCGTGTGCGA	ACCGGTGTCA	TCAAGGCCCG	TATGGTCGTC	350
	ACCTTCGCCC	CCGCTGGTGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	400
	CCACGAGCTC	CTCACTGAGG	GTCTCCCCCG	TGACAACGTT	GGTTTCAACG	450
	TCAAGAACGT	CTCCGTTAAG	GATATCAGAC	GTGGTAACGT	CTGCGGTGAC	500
45	TCCAAGAACG	ATCCCCCCTA	GGCTTGCGCT	TCTTTCACCG	CCCAGGTCAT	550
	TATCTTCAAC	CACCCTGGTC	AGATCTCTGC	TGGATACTCT	CCCGTCCTTG	600
	ATTGCCACAC	CGCCCATATT	GCTTGCAAGT	TCGACACTTT	GATCGAGAAG	650
	ATTGACCGTC	GTACTGGTAA	GAAGACTGAG	GACTCCCCCA	AGTTCGTCAA	700
50	GGCCGGTGAT	GCTGCTATCG	TCAAGA			726

2) INFORMATION FOR SEQ ID NO: 438

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 5 (B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438

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10 CACCACCAAG TGGTCCGAGT CCCGTTTCAA CGAAATCATC AAGGAGGTTT      50
   CCAACTTCAT CAAGAAGGTC GGATATAACC CCAAGGCTGT TCCCTTCGTG      100
   CCAATCTCTG GTTTCGAGGG TGACAACATG ATTGAACCCT CCCCCAAGT      150
   CACATGGTAC AAGGGCTGGA ACAAGGAGAC TGCCTCTGGC AAGTCTTCTG      200
   GTAAAACCCCT TCTCGATGCC ATTGACGCCA TTGAACCCCC AACCCGTCCT      250
   ACCGATAAGC CCCTCCGTCT TCCCCTCCAG GATGTGTACA AAATCTCTGG      300
15 TATTGGCACT GTTCCCCTCG GACGTGTTGA GACTGGTGTC ATCAAGCCCG      350
   GTATGGTCGT GACTTTCGCT CCCTCCAACG TCACCACTGA AGTCAAGTCC      400
   GTCGAAATGC ACCACCAACA ACTCCAGGCT GGTTACCCTG GCGACAACGT      450
   CGGCTTCAAC GTCAAGAACG TTTCAAGTCAA GGAAGTCCGC CGTGGCAACG      500
   TTGCTGGCGA CTCCAAAAAT GATCCCCCTA AGGGCTGCGA ATCCTTCAAT      550
20 GCCCAGGTCA TCGTCCTTAA CCACCCCGGC CAGGTTGGCG CTGGTTATGC      600
   CCCAGTCCTC GACTGCCACA CTGCCCACAT TGCTTGCAAG TTCTCTGAGC      650
   TTATTGAGAA GATCGACCGC CGTACCGGAA AGTCTGTTGA GAACAACCCC      700
   AAGTTCATCA AGTCTGGTGA TGCTGCTATC GTCAAGATGG TTCCCTCCAA      750
   GCCC
25

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2) INFORMATION FOR SEQ ID NO: 439

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Issatchenkia orientalis*
 40 (B) STRAIN: ATCC 6258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439

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45 TGGGATGAAA ACAGATTTGA AGAAATTGTC AAGGAAACCC AAAACTTCAT      50
   CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTCGTT CCAATCTCTG      100
   GTTGGAATGG TGACAACATG ATTGAAGCAT CCACCAACTG TCCATGGTAC      150
   AAGGGTTGGA CTAAGGAAAC CAAGGCAGGT GTTGTTAAGG GTAAGACCTT      200
   ATTAGAAGCA ATCGATGCTA TTGAACCACC TGTCAGACCA ACCGAAAAGC      250
   CATTAAGATT ACCATTACAA GATGTTTACA AGATTGGTGG TATTGGTACT      300
50 GTGCCAGTCG GTAGAGTCGA AACCGGTGTC ATTAAGCCAG GTATGGTTGT      350
   CACTTTTGCT CCAGCAGGTG TCACCACCGA AGTCAARTCC GTTGAAATGC      400
   ACCATGAACA ATTAGAACAA GGTGTTCCAG GTGATAACGT TGGTTTCAAC      450
   GTTAAGAACG TCTCTGTCAA GGATATCAAG AGAGGTAACG TTTGTGGTGA      500
   CTCCAAGAAC GACCCACCAA TGGGTGCAGC TTCYTTCAAT GCTCAAGTCA      550
55 TTGTCTTGAA CCACCTGGT CAAATTTCCG CTGGTTACTC TCCAGTCTTG      600
   GATTGTCACA CTGCCCACAT TGCATGTAAG TTCGACGAAT TAATCGAAAA      650
   GATTGACAGA AGAACTGGTA AGTCTGTTGA AGACCATCCA AAGTCYGTCA      700
   AGTCTGGTGA TGCAGCTATC GTCAAGATGG TCCCAACCAA GCC          743

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60

2) INFORMATION FOR SEQ ID NO: 440

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1091 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440

	CAAGCTCAAG	GCTGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCTCTGT	50
	GGAAGTTCGA	GACCCCTAAG	TACCACGTTA	CCGTCATTGA	CGCTCCTGGT	100
20	CACCGTGACT	TCATCAAGAA	CATGATTACG	GGTACCTCGC	AGGCTGACTG	150
	CGCTATCCTC	ATCATTGCCG	GTGGTACCGG	TGAGTTCGAG	GCTGGTATCT	200
	CGAAGGACGG	TCAGACCCGT	GAGCACGCTC	TGCTCGCTTT	CACCCTGGGT	250
	GTGCGTCAGC	TCATTGTGGC	CGTCAACAAG	ATGGACACCA	CCAAGTACTC	300
	GGAGGACCGC	TTCAACGAGA	TTGTCCGCGA	AGTGTCGAAC	TTCATCAAGA	350
25	AGGTCGGTTT	CAACCCCAAG	ACTGTTGCCT	TCGTCCCCAT	CTCGGGCTGG	400
	CACGGTGACA	ACATGATCGA	GGCCACCACC	AACATGCCTT	GGTACAAGGG	450
	CTGGGAGAAG	GAGACCAAGT	CGGGCAAGGT	CACTGGTAAG	ACTCTGCTGG	500
	ACGCCATCGA	CGCCATCGAG	CCCCCGACCC	GCCCCACTGA	CAAGCCCCTG	550
	CGTCTCCCTC	TGCAGGATGT	GTACAAGATC	GGTGGTATCG	GTACTGTCCC	600
30	TGTCGGTCGT	GTTGAGACCG	GTGTGATCAA	GCCCGGTATG	GTTGTGACCT	650
	TCGCTCCCTC	GAACGTCACC	ACTGAAGTTA	AGTCGGTTGA	GATGCACCAC	700
	GAGTCGCTCC	CTGAGGGTCT	CCCCGGTGAC	AACGTTGGTT	TCAACGTGAA	750
	GAACGTCTCG	GTTAAGGACA	TTCGCCGTGG	TAACGTTGCC	TCGGACTCGA	800
	AGAACGACCC	CGCTCAGGAG	GCTGCTTCGT	TCAACGCGCA	GGTCATTGTC	850
35	ATGAACCACC	CTGGTCAGAT	CAGCAACGGT	TACTCGCCCCG	TGCTTGACTG	900
	CCCACTGCG	CACATTGCCT	GCCGCTTCAA	CAACATCCTC	CAGAAGATCG	950
	ACCGTCGCTC	GGGTAAGGTG	CTTGAGGAGA	ACCCCAAGTT	CATCAAGTCG	1000
	GGTGACGCTG	CCATGGTGGA	GATGATCCCC	ACCAAGCCCA	TGTGTGTGGA	1050
40	GTCGTTCAAC	GAGTACCCCC	CTCTGGGTCG	TTTCGCTGTG	C	1091

2) INFORMATION FOR SEQ ID NO: 441

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 749 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Malassezia pachydermatis*
 (B) STRAIN: ATCC 42756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441

	ACCACCAAGT	ACTCGGAGGA	CCGCTTCAAC	GAGATTATTC	GCGAGACTTC	50
60	GAACCTTCATC	AAGAAGGTCG	GTTACAACCC	GAAGACTGTT	GCCTTCGTCC	100

	CGATCTCGGG	CTGGCACGGT	GACAACATGA	TTGAGGCGAC	CACCAACATG	150
	CCGTGGTACA	AGGGCTGGGA	GAAGGAGACC	AAGTCGGGCA	AGGCCACTGG	200
	TAAGACCCTT	CTGGACGCTA	TTGACGCCAT	TGAGCCGCCG	ACGCGCCCGA	250
	CCGACAAGCC	TCTCCGTCTT	CCTCTCCAGG	ATGTGTACAA	GATCGGTGGT	300
5	ATCGGTACYG	TCCCGGTTCG	CCGTGTTGAG	ACCGGTGTTA	TCAAGCCCGG	350
	TATGGTTGTG	ACCTTCGCTC	CGTCGAACGT	CACSACTGAA	GTTAAGTCGG	400
	TCGAGATGCA	CCACGAGCAG	ATCCCTGAGG	GTCCTCCGGG	TGACAACGTT	450
	GGTTTCAACG	TGAAGAACGT	GTCGGTCAAG	GACATTTCGCC	GTGGTAACGT	500
	CGCCTCGGAC	TCGAAGAACG	ACCCGGCTCA	GGAGGCTGCC	TCGTTCAATG	550
10	CTCAGGTCAT	TGTGATGAAC	CACCCTGGTC	AGATCAGCAA	CGGTTACTCG	600
	CCRGTGCTCG	ACTGCCACAC	TGCTCACATT	GCCTGCCGCT	TCAACAACAT	650
	CCTCCAGAAG	ATCGACCGTC	GTTCCGGTAA	GGTTCTYGAA	GAGAACCCCA	700
	AGTTCATCAA	GTCGGGTGAC	GCTGCCATGG	TTGAGATGAT	CCCGACCAA	749

15

2) INFORMATION FOR SEQ ID NO: 442

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1150 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442

	ACTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	CATGTCACCG	TCATTGGTAC	GTTCGACATG	100
35	TTCGACCTTT	TGCCTAGTGT	CCCCTTCTAA	CCACAGTTTA	TAGACGCCCC	150
	TGGCCATCGT	GATTTTCGTCA	AGAACATGAT	CACTGGTACT	TCCCAGGCTG	200
	ATTGCGCTAT	CCTCATCATT	GCTTCCGGCA	CTGGTGAATT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTTT	CCTTCACCCT	300
	CGGTGTTAGG	CAGCTCATTG	TCGCCCTCAA	CAAGATGGAC	ACTGTCAACT	350
40	TCGCTGAGGC	CCGTTACAAC	GAGATTGTCA	AGGAAGTCTC	CAACTTCATC	400
	AAGAAGGTCG	GCTACAACCC	CAAGGCCGTT	CCTTTCGTCC	CCATCTCCGG	450
	TTTCGAGGGT	GACAACATGA	TCGAGGCCTC	CACCCGCATT	CCTTGGTACA	500
	AGGGCTGGAA	CAAGGAGACC	GCCAGTGGCA	AGAGCACCGG	CAAGACCCTY	550
	CTCGAGGCCA	TTGATGCCAT	CGAACCCCCG	GTCCGTCCCA	CCGACAAGCC	600
45	CCTYCGTCTC	CCTCTTCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	650
	TTCCTGTCGG	TCGTGTTGAG	ACTGGTGTCA	TCAAGCCTGG	TATGGTCGTT	700
	ACTTTCGCCC	CCGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACCAGCAG	CTCCAGGCCG	GTAACCCCCG	TGACAACGTC	GGCTTCAACG	800
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCTCCGAC	850
50	TCCAAGAACG	ACCCCGCCAA	GGGCTGCGAC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTTAAC	CACCCCGGTC	AGGTCGGTGC	TGGATACGCT	CCCGTCCTCG	950
	ATTGCCACAC	TGCCCACATT	GCTTGCAAGT	TCTCTGAGCT	TCTTGAGAAG	1000
	ATCGATCGCC	GTACCGGTAA	ATCCGTTGAG	GACCACCCCA	AGTTCATCAA	1050
	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100
55	TTGAGGCTTT	CACTGACTAC	CCTCCCCTTG	GTCGTTTCGC	CGTCCGTGAC	1150

60

2) INFORMATION FOR SEQ ID NO: 443

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Metschnikowia pulcherrima*
 (B) STRAIN: DSM 70336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443

15	GGACAAGTTG	AAGGCTGAGA	GAGAGAGAGG	TATCACCATC	GACATTGCCT	50
	TGTGGAAGTT	CGAGACTCCT	AAGTACCACG	TCACCGTYAT	TGACGCCCCA	100
	GGTCACAGAG	ATTTCATCAA	GAACATGATC	ACTGGTACTT	CCCAGGCTGA	150
	CTGTGCTATC	TTGATTATCG	CYGGTGGTGT	TGGTGAGTTC	GAGGCTGGTA	200
	TCTCCAAGGA	TGGCCAGACC	AGAGAGCACG	CTTTGTTGGC	YTACACCTTG	250
20	GGTGTTAGAC	ARTTGATTGT	TGCCGTCAAC	AAGATGGACT	CTGTCAAGTG	300
	GGACAAGAAC	AGATTTGAGG	AGATCATCAA	GGAGACCTCT	AACTTCGTCA	350
	AGAAGGTTGG	TTACAACCCT	AAGACYGTGC	CATTCGTGCC	AATYTCTGGT	400
	TGGAACGGTG	ACAACATGAT	TGAGGCYTCC	ACTAACTGCC	CATGGTACAA	450
	GGGTTGGGAG	AAGGAGACCA	AGGCCGGTAA	GTCTWCCGGT	AAGACCTTGT	500
25	TGGAGGCCAT	TGACGCCATT	GAGCCACCAA	CCAGACCTAC	CGACAAGGCC	550
	TTGAGATTGC	CTTTGCAGGA	TGTCTACAAG	ATCGGTGGTA	TCGGAACGGT	600
	GCCAGTCGGC	CGTGTCGAGA	CCGGTGTCAT	TAAGGCCGGT	ATGGTTGTYA	650
	CCTTYGCCCC	AGCTGGTGTC	ACCACTGAGG	TCAAGTCCGT	CGAGATGCAC	700
	CACGAGCAGT	TGGTCGAGGG	TCTTCCAGGT	GACAAYGTTG	GTTTCAACGT	750
30	CAAGAACGTC	TCCGTTAAGG	AGATCAGAAG	AGGTAACGTC	TGTGGTGAAT	800
	CCAAGCAGGA	CCCACCAAAG	GGTGCCGCTT	CTTTCACCGC	YCAGGTTATT	850
	GTGTTGAACC	ACCCTGGTCA	GATCTCCTCT	GGTTACTCTC	CAGTGTGGA	900
	CTGYCACACC	GCCCACATTG	CCTGTAARTT	CGACACCTTG	TTGGAGAAGA	950
	TTGACAGAAG	AACTGGTAAG	TCCTTGAGAG	CYGAGCCTAA	GTTTCGTCAAG	1000
35	TCYGGTGACG	CCGCCATTGT	CAAGATGGTG	CCAACCAAGC	CAATGTGTGT	1050
	TGAGGCTTTC	ACCGACTACC	CACCTTTGGG	TAGATTTCGCC	GTCAGAGAC	1099

2) INFORMATION FOR SEQ ID NO: 444

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444

55	CAAGCTCAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCCCTCT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CCGTCATTGG	TACGTCGACT	100
	CGCGCGAGAC	TGGTCGCAAT	TTCCACGTCG	CTAACGTGCT	TGAACAGACG	150
	CTCCCGGCCA	CCGTGACTTC	ATCAAGAACA	TGATCACTGG	TACCTCCCAG	200
60	GCTGACTGCG	CTATCCTCAT	TATCGCTGCC	GGCACTGGTG	AGTTCGAGGC	250

	TGGTATCTCC	AAGGATGGCC	AGACCCGTGA	GCACGCTCTG	CTCGCCTACA	300
	CCCTCGGTGT	TAAGCAGCTC	ATCGTCGCTA	TCAACAAGAT	GGACACCACC	350
	AAGTGGTCTG	AGGCCCGTTT	CCAGGAGATC	ATCAAGGAGA	CCTCCAACCT	400
	CATCAAGAAG	GTCGGCTACA	ACCCCAAGAC	CGTCGCTTTC	GTCCCCATCT	450
5	CTGGTTTCCA	CGGCGACAAC	ATGCTTTCCC	CCTCCACCAA	CTGCCCCCTGG	500
	TACAAGGGCT	GGGAGAAGGA	GACCAAGGCT	GGCAAGTCCA	CCGGCAAGAC	550
	CCTCCTTGAG	GCCATCGACT	CCATCGAGCC	CCCCAAGCGC	CCCAGCGACA	600
	AGCCCCCTCCG	CCTTCCCCTT	CAGGATGTGT	ACAAGATCGG	CGGTATCGGC	650
	ACAGTCCCTG	TCGGCCGTAT	CGAGACTGGT	GTCATCAAGC	CCGGCATGGT	700
10	CGTGACCTTC	GCTCCTTCCA	ACGTCACCAC	CGAAGTCAAG	TCCGTTGAGA	750
	TGCACCACGA	GCAGCTCTCC	GAGGGTGTCC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCAAGA	ACGTCTCCGT	CAAGGAGATC	CGTCGTGGCA	ACGTCGCCCG	850
	TGACTCCAAG	AACGACCCCC	CTCTGGGTGC	CGCTTCTTTC	GATGCCCAGG	900
	TCATCGTCCT	CAACCACCCC	GGCCAGGTCG	GTGCTGGCTA	CGCCCCCGTC	950
15	CTCGACTGCC	ACACCGCCCA	CATTGCCTGC	AAGTTCGCCG	AGATCAAGGA	1000
	GAAGATCGAC	CGCCGTACCG	GCAAGTCTGT	CGAGTCCGCC	CCCAAGTTCA	1050
	TCAAGTCTGG	CGACTCTGCC	ATCGTCAAGA	TGATTCCCTC	CAAGCCCATG	1100
	TGCGTTGAGG	CTTTCACCGA	CTACCCTCCT	CTGGGCCGCT	TCGCCGTCCG	1150
	TGA					1153
20						

2) INFORMATION FOR SEQ ID NO: 445

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 35 (B) STRAIN: ATCC 32071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445

	TACCACTAAG	TGGTCCGAGA	CCCGATTCAA	TGAAATTATC	AAGGAAGTCA	50
40	CCAATTTTCAT	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	100
	CCCATTCTG	GTTTCGAGGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
	GCAAGACCCT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250
	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
45	TATTGGCACT	GTTCTGTGCG	GACGTGTTGA	GACTGGAGTC	ATCAAGCCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCCG	GTGACAACGT	450
	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
50	GCCCAGGTCA	TCGTCCTCAA	CCACCCTGGT	CAGGTGCGG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCACAT	TGCCTGCAAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACCGGAA	AGTCTGTTGA	GAACAACCCC	700
	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
55	GCCCATGTGC	GTC				763

2) INFORMATION FOR SEQ ID NO: 446

60 (i) SEQUENCE CHARACTERISTICS:

270

(A) LENGTH: 1346 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*
 (B) STRAIN: ATCC 64101

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446

	AAGCTCAAGG	CTGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
15	GAAGTTCCAG	ACTGCCAAGT	ACGAGGTTAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGTGATTT	CATCAAGAAC	ATGATCACTG	GTACCTCCCA	GGCCGATTGC	150
	GCTATTCTCA	TCATTGCCTC	TGGTACTGGT	GAATTCGAGG	CTGGTATCTC	200
	CAAGGATGGC	CAGACTCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTCGGTG	250
	TCCGTCAGCT	CATTGTTGCC	CTCAACAAGA	TGGACACTTG	CAAGTGGTCT	300
20	CAGGGTGAGT	ACTCGTACCT	GCGTTTGGCC	TTGAATATCT	TACTAATGCA	350
	CCATAGATCG	TTACAACGAA	ATTGTCAAGG	AGACTTCCAA	CTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GAACGTTTCT	TTCGTTCCCTA	TCTCCGGTTT	450
	CAACGGTGAC	AACATGCTTG	AGCCCTCCCC	CAACTGCCCC	TGGTACAAGG	500
	GTTGGGAGAA	GGAGACCAAG	GCCGGTAAGG	TCACTGGTAA	GACCCTCCTC	550
25	GAGGCCATCG	ACGCCATTGA	GCCCCCTACC	CGTCCCGCCA	ACAAGGTTAG	600
	TCCCTCCTCG	ACTACTCAAA	CCCTCCTCAT	AAGTTCAGAT	TACTGACTCG	650
	TTACACAGCCC	CTCCGTCTTC	CCCTCCAGRA	TGTCTACAAG	ATCGGTGGTA	700
	TTGGAACGGT	TCCCGTCGGT	CGTGTTGAGA	CTGGTACCAT	CGTTCCTGGT	750
	ATGGTTGTCA	CCTTGTAAGT	CACTCTCCTC	GCTTATCCTA	CCTGAAATCA	800
30	TCATGTGCTA	ACTTGACACT	CAGCGCTCCC	GCCAACGTCA	CCACTGAAGT	850
	CAAGAGTGTT	GAAATGCACC	ACCAGCAGCT	CACTGCCGGT	CAGCCCGGTG	900
	ACAACGTTGG	TTTCAACGTG	AAGAACGTCT	CCGTCAAGGA	AATCCGTCGT	950
	GGTAACGTTG	CTGGTGACAG	CAAGAACGAC	CCCCCTGCCG	GTGCTGCCTC	1000
	CTTCAACGCC	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	1050
35	GTTACGCCCC	AGTCCTCGAT	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	1100
	GCTGAGCTCC	TCGAGAAGAT	TGACCGTCGT	ACCGGAAAGT	CTGTTGAGGA	1150
	CCACCCCAAG	TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	1200
	CTTCCAAGCC	CATGTGTGTT	GAGGCTTTCA	CCGAGTACCC	TCCCTCTCGGT	1250
	CGTTTCGCCG	TTCGCGAGTA	AGTTTTATCT	CCGTTGTCTA	TTTTCCATCC	1300
40	TTCCCTTCTC	CTCCGTCTTC	CATATATACT	TTTTCAGTTA	TATGTG	1346

2) INFORMATION FOR SEQ ID NO: 447

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 18205

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447

60	AAGTTAAAAG	CTGAACGTGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
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	GAAATTTCGAA	ACTCCAAAAT	ACCATGTTAC	CGTTATTGAT	GCTCCAGGTC	100
	ACAGAGATTT	CATCAAAAAT	ATGATTACTG	GTACTTCCCA	AGCTGATTGT	150
	GCTATYTTAA	TTATTGCCGG	TGGTATTGGT	GAATTCGAAG	CTGGTATCTC	200
	AAAAGATGGT	CAAACCAGAG	AACACGCTTT	NTTAGCTTAC	ACCTTAGGGT	250
5	TTAAACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAAATGGGAT	300
	GAATCTCGTT	TCGAAGAAAT	TGTCAAGGAA	ACYTCAAAC	TTATCAAGAA	350
	AGTTGGTTAC	AACCCAAAAA	CTGTTCCATT	CGTTCCAATC	TCAGGTTGGA	400
	ATGGTGATAA	CATGATTGAA	CCATCAWCTA	ACTGTCCATG	GTACAAAGGT	450
	TGGAAAAAAG	AAACCAAAGC	TGGTGAAGCT	AAAGGTAAAA	CTTTATTAGA	500
10	AGCCATTGAT	GCTATTGACC	CACCATCAAG	ACCAACTGAT	AAACCATTAC	550
	GTTTACCATT	ACAAGATGTT	TACAARATTG	GTGGTATTGG	TACTGTGCCA	600
	GTCGGTAGAG	TTGAAACCGG	TGTTATCAAA	CCAGGTATGG	TTGTTACCTT	650
	TGCCCCAGCT	GGTGTTACCA	CTGAAGTCAA	ATCTGTTGAA	ATGCATCATG	700
	AACAATTGAC	TGAAGGTTTA	CCAGGTGACA	ATGTTGGTTT	CAACGTTAAG	750
15	AATGTTTCTG	TTAAAGAAAT	CCGTCGTGGT	AACGTCTGTG	GTGACTCTAA	800
	AAACGATCCA	CCAAAAGCTG	CTGAATCATT	CAATGCTCAA	GTTATTGTCT	850
	TAAACCATCC	AGGTCAAATC	TCTGCTGGTT	ACTCTCCAGT	TTTAGATTGT	900
	CACACTGCTC	ACATTGCTTG	TAAATTTGAC	ACTTTAATTG	AAAAAATTGA	950
	CAGACGTACT	GGTAAGAAAT	TAGAAGAAGC	TCCAAAATTC	ATCAAATCAG	1000
20	GTGATGCTGC	TATTGTTAAA	TTTGTTCCAT	CAAACCATTC	ATCAGTTGAA	1050
	GCTTTCACCTG	ACTACCCACC	ATTAGGTCGT	TTCGCTGTCA	GAGA	1094

25 2) INFORMATION FOR SEQ ID NO: 448

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448

40	CTTAGATAAG	TTAAAAGCTG	AACGTGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTTCGAACT	CCAAAATACC	ATGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAAAATATG	ATTACTGGTA	CTTCCCAAGC	150
	TGATTGTGCT	ATMTTAATTA	TTGCCGGTGG	TATTGGTGAA	TTCGAAGCTG	200
45	GTATCTCAAA	AGATGGTCAA	ACCAGAGAAC	ACGCTTTRTT	AGCTTACACC	250
	TTAGGTGTTA	AACAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCCGTTAA	300
	ATGGGATGAA	TCTCGTTTCG	AAGAAATTGT	CAAGGAAACY	TCAAACCTTA	350
	TCAAGAAAGT	TGGTACAACC	CAAAAACCTG	TCCATTTCGT	CCAATCTCAG	400
	GTTGGAATGG	TGATAACATG	ATTGAACCAT	CAACTAACTG	TCCATGGTAC	450
50	AAAGGTTGGA	AAAAAGAAAC	CAAAGCTGGT	GAAGCTAAAG	GTAAAACCTT	500
	ATTAGAAGCC	ATTGATGCTA	TTGATCCACC	ATCAAGACCA	ACTGATAAAC	550
	CATTACGTTT	ACCATTACAA	GATGTTTACA	ARATTGGTGG	TATTGGTACT	600
	GTGCCAGTCG	GTAGAGTTGA	AACCGGTGTT	ATCAAACCAG	GTATGGTTGT	650
	TACCTTTGCC	CCAGCTGGTG	TTACCACTGA	AGTCAAATCT	GTTGAAATGC	700
55	ATCATGAACA	ATTGACTGAA	GGTTTACCAG	GTGACAATGT	TGGTTTCAAC	750
	GTTAAGAATG	TTTCTGTAA	AGAAATCCGT	CGTGGTAACG	TCTGTGGTGA	800
	CTCTAAAAAC	GATCCACCAA	AAGCTGCTGA	ATCATTCAAT	GCTCAAGTTA	850
	TTGTCTTAAA	CCATCCAGGT	CAAATCTCTG	CTGGTTACTC	TCCAGTTTAA	900
	GATTGTCACA	CTGCTCACAT	TGCTTGTAAG	TTTGACACTT	TAATTGAAAA	950
60	AATTGACAGA	CGTACTGGTA	AGAAATTAGA	AGAAGCTCCA	AAATTCATCA	1000

AATCAGGTGA	TGCTGCTATT	GTTAAATTTG	TTCCATCAAA	ACCATTATCA	1050
GTTGAAGCTT	TCACTGACTA	CCCACCATTA	GGTCGTTTCG	CTGTCAGAGA	1100

5

2) INFORMATION FOR SEQ ID NO: 449

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1201 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
(B) STRAIN: ATCC 44331

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449

CAAGCTCAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	50
GGAAGTTCGA	GACCCCAAG	TACCAGGTCA	CCGTCATTGG	TATGTCTTTG	100
TGCTTTTTGT	GCTTTTTGTG	CCTGTGCCTC	GCACAATTCC	AGCCCTCGAT	150
25 AATTATGAAC	CTCGTACTAA	TATGTCGTTC	TCCCACTACC	CACAGACGCC	200
CCCGGCCATC	GTGATTTTCAT	CAAGAACATG	ATTACTGGTA	CCTCCCAGGC	250
TGATTGCGCC	ATTCTCATCA	TTGCCTCCGG	TACTGGTGAG	TTGAGGCTG	300
GCATCTCCAA	GGATGGCCAG	ACCGTGAGC	ACGCTCTTCT	CGCCTTCACC	350
CTCGGTGTCA	AGAACCTCAT	TGTTGCCATC	AACAAGATGG	ACACCAACAA	400
30 CTGGTCCGAG	GACCGATACA	AGGAGATCAT	CAAGGAGACC	TCCAACCTCA	450
TCAAGAAGGT	CGGCTACAAC	CCCAAGGCCG	TTCCTTTCGT	CCCCATCTCC	500
GGTTTCCACG	GAGACAACAT	GCTTACCCCC	TCCACCAACT	GCCCCTGGTA	550
CAAGGGTTGG	GTCCGTGAGG	TCAAGGGTAA	CACCCTTACC	GGCAAGACCC	600
TTCTCGAGGC	CATCGACTYC	ATCGAGCCCC	CCAAGCGTCC	CACCGAGAAG	650
35 CCCCTCCGTC	TTCCCCTTCA	GGACGTCTAC	AAGATCGGTG	GTATTGGCAC	700
TGTGCCCGTC	GGCCGTATCG	AGACCGGTAT	CCTCAAGCCC	GGTATGGTCG	750
TCACCTTCGC	TCCCTCCAAC	GTCACCACTG	AAGTCAAGTC	CGTCGAGATG	800
CACCACGAGC	AGCTTACCGA	GGGTGTCCCC	GGTGACAACG	TTGGTTTCAA	850
CGTGAAGAAC	GTCTCCGTCA	AGGATATCCG	CCGTGGCAAC	GTCTGCGGTG	900
40 ACTCCAAGAA	CGACCCCCCC	GCTGCTGCCG	CCTCTTTCCA	GGCCCAGGTC	950
ATTGTCCTCA	ACCACCCCGG	CCAGATCGGT	GCTGGTTACG	CTCCCGTTCT	1000
TGACTGCCAC	ACTGCCACAA	TTGCTTGCAA	GTTGCGCCGAG	CTCCTTGAGA	1050
AGATCGACCG	CCGTACCGGT	AAGTCGGTCG	AGAACAACCC	CAAGTTCGTC	1100
AAGTCTGGTG	ATGCCGCCAT	CGTCAAGATG	GTTCCCTCCA	AGCCCATGTG	1150
45 TGTTGAGTCC	TTCACCGAGT	ACCCCCCTCT	CGGTCGTTTC	GCCGTCCGTG	1200
A					1201

50

2) INFORMATION FOR SEQ ID NO: 450

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1095 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhizopus oryzae*
 (B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450

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5  CAAGCTTAAG GCTGAACGTG AACGTGGTAT CACCATCGAT ATTGCTCTCT      50
   GGAAGTTCGA AACCCCCAAG TACCAAATTA CCGTTATTGA TGCTCCCGGT      100
   CACCGTGATT TCATCAAGAA CATGATTACC GGTACTTCTC AAGCCGATTG      150
   TGCTATTCTT ATCATTGCTG GTGGTACTGG TGAATTTCGAA GCTGGTATCT      200
10  CCAAGGATGG TCAAACCCGT GAACACGCCC TTTTGGCTTT CACTCTCGGT      250
   GTCCGTCAAT TGATTGTTGC TGTCAACAAG ATGGATACCA CCAAGTGGTC      300
   CGAAGCTCGT TTCAACGAAA TYGTCAAGGA AGTTTCTTCC TTCATCAAGA      350
   AGATTGGTTA CAACCCCCAAG TCTGTTCCCT TCGTCCCCAT CTCTGGTTGG      400
   CACGGTGACA ACATGTTGGA AGAATCTACC AACATGCCCT GGTACAAGGG      450
15  ATGGAACAAG GAAACCAAGG CTGGTGCCAA GTCTGGTAAG ACCCTCTTGG      500
   ATGCCATTGA CAACATTGAC CCTCCTACCC GTCCTGTTGA CAAGCCTCTC      550
   CGTCTTCCTC TTCAAGATGT TTACAAGATT GGTGGTATCG GTACTGTCCC      600
   CGTCGGTCGT GTCGAAACTG GTGTCATCAA GGCTGGTATG GTTGTACACT      650
   TCGCTCCTGC TGCTGTCACC ACTGAAGTTA AGTCCGTCGA AATGCACCAC      700
20  GAAACCCTCA CTGAAGGTCT CCCCAGGTGAC AACGTCGGTT TCAACGTCAA      750
   GAACGTCTCC GTCAAGGATA TCCGTCGTGG TAACGTCTGT TCTGACTCCA      800
   AGAACGACCC CGCCAAGGAA GCCGGTTCCT TCACCGCTCA AGTCATTATC      850
   TTGAACCACC CTGGTCAAAT TGGTGCTGGT TACGCTCCYG TTTTGGATTG      900
   TCACACTGCT CACATTGCCT GTAAGTTCGC TGAATTGATC GAAAAGATTG      950
25  ACAGACGTTT CGGTAAGTCC TTGGAAGCTA CTCCAAGTT CGTCAAGTCT      1000
   GGTGACTCTG CCATCGTCAA GATGATCCCC TCCAAGCCCA TGTGTGTTGA      1050
   AGCTTACACT GACTACCCTC CTCTCGGTCTG TTTCGCTGTT CGTGA          1095

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30

2) INFORMATION FOR SEQ ID NO: 451

(i) SEQUENCE CHARACTERISTICS:

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35  (A) LENGTH: 1092 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*
 (B) STRAIN: ATCC 10658

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451

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   GCTGAAGGCC GAGCGAGAGC GTGGTATCAC CATCGATATC GCTCTATGGA      50
   AGTTCGAGAC CCCCAAGTAC AACGTCACCG TCATTGACGC TCCAGGACAT      100
   CGTGATTTC AAGAGAGTGA GTTAACCATA ACATCAAACA GTGTTGCAAA      150
50  CATCAGCTAA TGCATGTTAT GCGTCCAGAC ATGATTACTG GTACTTCCCA      200
   GGCCGATTGC GCTATTCTCA TCATCGCCAC CGGTGTTGGT GAGTTCGAGG      250
   CTGGTATCTC CAAGGATGGC CAGACCCGAG AGCACGCCCT TCTCGCCTTC      300
   ACCCTCGGTG TCAGACAGCT CATCGTTGCC TTGAACAAGA TGGACTCGGT      350
   CAAGGTAGGC TAACTTCACA ACGTCGGCTT CCCATCATTC ATTCACTTAC      400
55  CTGTCTTGTC TTCCACCCTC CAGTTCTCCG AGTCCCGATA CGATGAAATC      450
   GTCAAGGAGA CATCCGGTTT CATCAAGAAG GTCGGATTCTG ACCCCAAGGG      500
   TGTTCCCTTC GTCCCCTCT CAGGATGGCA CGGAGACAAC ATGATCGAGG      550
   AGTCCACCAA CATGCCTTGG TACAAGGGAT GGAAGAAGAC CACCAAGACC      600
   GGCGAGTACA AGGGAAAGAC CCTGCTCGAG GCCATCGACT CCATCGAGCC      650
60  CCCACCCCGT CCTACCGACA AGCCTCTCCG ACTTCCCCTC CAGGATGTCT      700

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	ACAAGATTGG	TGGTATCGGA	ACAGTGCCAG	TCGGACGAGT	CGAGACTGGT	750
	ACCATCAAGG	CTGGTATGGT	CGTCACCTTC	GCTCCTTCAG	CTGTCACCAC	800
	CGAAGTCAAG	TCTGTTGAGA	TGCACCACGA	GCAGCTCGAG	GCTGGTCTTC	850
	CAGGTGACAA	CGTCGGATTG	AACATCAAGA	ACGTTTTCAGT	CAAGGATATC	900
5	CGAAGAGGAA	ACGTCTGCGG	TGACTCCAAG	AACGATCCCC	CCAAGGAGGC	950
	TGCTTCCTTC	ACCGCCCAGG	TCATTGTCCT	CAACCACCCC	GGTCAAATCG	1000
	GTAACGGATA	CTCTCCAGTT	CTCGATTGCC	ACACTGGTGA	GTCATTCTTC	1050
	CATATTAGTT	TGAACTCTTT	TGAACAATAC	TAACGTGAAT	CATTATACTT	1100
	TTCAGCCCAC	ATTGCATGCA	AGTTCGACAC	CCTCCTAGAG	AAGATTGACC	1150
10	GACGATCCGG	AAAGTCCATC	GAAGATACCC	CCAAGTTCGT	CAAGTCTGGT	1200
	GACGCCGCCA	TCGTCAAGAT	GGTCCCCACC	AAGCCAATGT	GCGTTGAGGC	1250
	TTTCACCGAC	TACCCACCTC	TTGGACGATT	CGCCGTCCGT	GA	1292

15

2) INFORMATION FOR SEQ ID NO: 452

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1289 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Sporobolomyces salmonicolor</i>
(B)	STRAIN: ATCC 32311

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452

	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCTCTCTG	50
	GAAGTTCGAG	ACCCCCAAGG	TGCGTTCTCA	CCCCGGCTGA	GGAGCACGCA	100
	CGCGAGGGCT	CACGCTGCGC	CTCTTACAGT	ACATGATCAC	CGTCATCGAC	150
35	GCCCCGGGTC	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	200
	GGCCGACTGC	GCCATCCTCA	TCATCGCCGC	CGGTACCGGT	GAGTTCGAGG	250
	CTGGTATCTC	GAAGGACGGC	CAGACCCGCG	AGCACGCCCT	CCTCGCCTTC	300
	ACCCTCGGTG	TCCGTCAGCT	CATCGTCGCC	ATCAACAAGA	TGGACACGAC	350
	CAAGTACTCG	GAGGCCCGTT	TCGAGGAGAT	CATCAAGGAG	ACCTCCAACT	400
40	TCATCAAGAA	GGTCGGCTTC	AACCCCCAAGA	ACGTCCCCTT	CGTCCCCATC	450
	TCGGGATGGC	ACGGTGACAA	CATGATTGAG	GAGACCGCCA	ACATGCCCTG	500
	GTACAAGGGA	TGGAAGAAGG	AGACCAAGGC	CGGTGAGGTC	AAGGGCAAGA	550
	CCCTCCTCGA	CGCCATCGAC	GCGATCGAGC	CCCCTTCGCG	CCCTACCGAC	600
	AAGCCCCTCC	GTCTTCCCCT	CCAGGTTCGT	TTCCCTGCTC	GCGGTTTACG	650
45	CTGCTACTTC	GAGCTGACCC	GCGAGCTCTG	CCCGAACAGG	ATGTCTACAA	700
	GATCGGTGGT	ATCGGCACAG	TCCCCGTCGG	CCGTGTCGAG	ACCGGCACGA	750
	TCAAGGCCGG	TATGGTCGTC	GTCTTCGCCC	CGGCCAACGT	CACCACTGAG	800
	GTCAAGTCGG	TCGAGATGCA	CCACGAGCAG	CTCGAGGCTG	GTCTCCCGGG	850
	AGACAACGTC	GGCTTCAAGT	GCGTCTCATC	ATGTTTTTGC	TTCGCTCGGC	900
50	CATTTTTTCA	GTCCTGACCC	CGTTTTTGCC	CTCGACAGCG	TCAAGAACGT	950
	TTCCGTTAAG	GACATCCGTC	GCGGTAACGT	CTGCGGTGAC	TCGAAGAACG	1000
	ACCCCCCAA	GGAGGCCGCT	TCCTTCAAGG	CCCAGGTCAT	CGTCATGAAC	1050
	CACCCCGGTC	AGATCGGCAA	CGGTTACGCT	CCCGTTCTCG	ACTGCCACAC	1100
	CGCCACATT	GCCTGCAAGT	TCGACACCCT	CCTCGAGAAG	ATCGACCGTC	1150
55	GCTCGGGCAA	GTCGATTGAG	GACCTCCCCA	AGTTCGTCAA	GTCGGGTGAC	1200
	GCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCGATGTGTG	TCGAGTCGTT	1250
	CGCCGAGTAC	CCCCCTCTCG	GACGTTTCGC	CGTCCGTGA		1289

60

2) INFORMATION FOR SEQ ID NO: 453

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: WSA-148

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453

GTGAGCGCGG TATCACCATC GATATTGCTC TGTGGAAGTT CGAGACCCCC 50
 AAGTACTACG TCACCGTCAT TGACGCCCCC GGTCATCGCG ATTTTCATCAA 100
 GAACATGATC ACTGGTACCT CGCAGGCCGA CTGCGCCATT CTCATCATTG 150
 20 CCGCTGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACT 200
 CGTGAGCACG CTCTGCTCGC CTACACCCTG GGTGTGCGGC AGCTGATCGT 250
 CGCCATCAAC AAGATGGACA CGGCCAAGTG GGCTGAGGCT CGTTACCAGG 300
 AGATCATCAA GGAGACCTCC AACTTCATCA AGAAGGTCGG CTACAACCCC 350
 AAGACTGTTG CCTTCGTCCC CATCTCGGGC TTCCACGGCG ACAACATGCT 400
 25 TACTCCCTCG ACCAACTGCC CCTGGTACAA GGGCTGGGAG AAGGAGGGCA 450
 AGAGCGGCAA GGTTACCGGT AAGACTCTGC TGGACGCCAT TGACGCCGTC 500
 GAGCCCCCA AGCGCCCCAC GGACAAGCCC CTGCGTCTGC CCCTCCAGGA 550
 TGTCTACAAG ATCGGCGGTA TCGGCACTGT CCCTGTCGGC CGTATCGAGA 600
 CTGGTGTCTT GAAGCCCGGC ATGGTCGTCA CCTTTGCCCC GTCCAACGTC 650
 30 ACCACTGAAG TCAAGTCCGT CGAGATGCAC CACGAGCAGC TTGTTGAGGG 700
 TGTTCCCGGC GACAACGTCG GCTTCAACGT CAAGAACGTC TCCGTCAAGG 750
 AGATCCGTCG TGGCAACGTT GCCGGTGAAT CCAAGAACGA CCCCCCTCG 800
 GGCGCCGCCA CCTTCAACGC CCAGGTCATT GTCCTGAACC ACCCCGGCCA 850
 GGTCGGCAAC GGCTACGCCC CGGTTCTGGA CTGCCACACC GCCCACATTG 900
 35 CCTGCAAGTT CACCGAGATC CTTGAGAAGA TCGACCGCCG TACCGGCAAG 950
 TCGGTTGAGA ACAACCCCAA GTTCATCAAG TCGGGTGACG CCGCCATTGT 1000
 CAAGCTGACG CCCTCGAAGC CCATGTGCGT TGAGGCCTTC ACTGACTACC 1050
 CCCCTCTGGG CCGTTTCGCC 1070

40

2) INFORMATION FOR SEQ ID NO: 454

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1092 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
 (B) STRAIN: ATCC 52550

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454

CTTAAGTCTG AGCGTGAGAG AGGTATCACC ATCGATATTG CTCTCTGGAA 50
 ATTCGAGACT CCTAAGTACA ACGTTACCGT CATTGATGCT CCAGGTCACA 100
 60 GAGATTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC CGATCTTGCC 150

	ATCCTTATCA	TTGCTGGTGG	TGTCGGTGAG	TTCGAGGCTG	GTATCTCCAA	200
	GGACGGTCAG	ACCAGAGAGC	ACGCTCTTCT	TTCTTTCACC	CTTGGTGTCA	250
	GAAACATGAT	TGTTGCTGTC	AACAAGATGG	ACTCCGTCAA	GTGGTCTGAG	300
	GATCGTTTCA	ACGAAATTGT	CAAGGAGACC	TCCAACCTCG	TCAAGAAGGT	350
5	TGGTTACAAC	CCTAAGAATA	TTGCTTTCGT	TCCTATCTCC	GGTTGGAACG	400
	GTGACAATAT	GATTGAGCCA	TCCACCAACT	GCCCATGGTA	CAAGGGTTGG	450
	GAGCGTGAGA	CCAAGAACGG	TACTGCCAAG	GGTAAGACCA	TCTTGGAGGC	500
	CATTGACTCT	ATGGAGCCAC	CTTCCAGACC	AGTTGACAAG	CCTCTCCGTC	550
	TTCTCTTTCA	GGACGTTTAC	AAGATTGGTG	GTATTGGTAC	GGTGCCAGTT	600
10	GGTCGTGTTG	AGACTGGTGT	TATCAAGCCA	GGTATGGTTG	TTACCTTTGC	650
	CCCAGCTGGT	GTCACCACTG	AAGTCAAGTC	TGTCGAGATG	CACCACGAAC	700
	AGATCCCAGA	AGGTACCCCA	GGTGACAACG	TTGGTTTCAA	CGTCAAGAAC	750
	GTCTCCGTCA	AGGAAATCAG	ACGTGGTAAC	GTTACTGGTG	ACTCCAAGAA	800
	CGACCCACCA	AAGGGCTGCG	ACTCTTTCAA	CGCTCAGGTC	ATCATCTTCA	850
15	ACCACCCTGG	TCAGATCTCT	GCTGGTTACG	CTCCAGTTTT	GGACTGCCAC	900
	ACTGCTCACA	TTGCTTGCAA	GTTTGAGGAG	CTCATTGAGA	AGATTGACAG	950
	ACGTTCCGGT	AAGAAGGTCG	AAGACTCTCC	TAAGTTCGTC	AAGGCCGGTG	1000
	ATGCCGCCAT	TGTCAAGATG	GTTCCATCCA	AGCCAATGTG	TGTTGAAACC	1050
	TTCACTGAGT	ACCCACCTCT	TGGTCGTTTC	GCCGTCCGTG	AC	1092
20						

2) INFORMATION FOR SEQ ID NO: 455

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455

	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	GGAAGTTCGA	50
40	GACCCCCAAG	TACAATGTCA	CCGTCATTGG	TATGTTTTCT	CTTTACCTTT	100
	CCCCTCCATC	GTCTTGCTGT	GCCATAACTA	ACGAGAGTAG	ACGCCCCCGG	150
	TCACCGTGAC	TTCATCAAGA	ACATGATCAC	TGGTACCTCC	CAGGCCGACT	200
	GTGCTATTCT	CATCATTGCT	GCCGGTACTG	GTGAGTTCGA	GGCTGGTATC	250
	TCCAAGGATG	GCCAGACCCG	TGAGCACGCT	CTGCTCGCCT	TCACCCTTGG	300
45	TGTCAAGCAG	CTCATCGTTG	CCATCAACAA	GATGGACACC	ACCAACTGGT	350
	CCGAGGACCG	TTTCAAGGAA	ATCATCAAGG	AAGTCACCAA	CTTCATCAAG	400
	AAGGTTGGCT	ACGACCCCAA	GGGTGTTCCA	TTCGTTCCAA	TCTCTGGTTT	450
	CAACGGTGAC	AACATGATTG	AGGCCTCCAC	CAACTGCCCA	TGGTACAAGG	500
	GATGGAACAA	GGAGACTAAG	GCCGGTGGTG	CCAAGACTGG	CAAGACCCTC	550
50	CTCGAGGCCA	TCGATGCCAT	CGACATGCCA	ACCCGTCCTA	CCGACAAGCC	600
	CCTCCGTCTC	CCACTCCAGG	ATGTCTACAA	GATCTCTGGT	ATCGGAACTG	650
	TACCAGTCGG	TCGTGTTGAG	ACCGGTATCA	TCAAGCCCGG	TATGGTCGTC	700
	ACCTTCGCCC	CTGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAAATGCA	750
	CCACCAGCAG	CTTCAGCAGG	GTGTCCCCGG	TGACAACGTC	GGCTTCAACG	800
55	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGTAACGT	TGCCGGTGAC	850
	TCCAAGAACG	ACCCACCATC	CGGCTGTGCC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGCC	AGATCGGTGC	TGGTTACGCC	CCAGTCCTCG	950
	ACTGCCACAC	TGCTCACATT	GCTTGCAAGT	TCGCTGAGCT	CCTCGAGAAG	1000
	ATTGACCGCC	GTACCGGTAA	ATCCGTCGAA	GCCAACCCCA	AGTTCGTCAA	1050
60	GTCTGGTGAT	GCCGCTATCG	CCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100

TTGAGGCTTT CACTGACTAC CCCCCACTTG GTCGTTTCGC CGTCCGTGA' 1149

5 2) INFORMATION FOR SEQ ID NO: 456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
(B) STRAIN: ATCC 62965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456

20 TCTTGACAAG CTTAAAGCTG AACGTGAACG TGGTATCACC ATTGATATCG 50
CTCTCTGGAA GTTCGAAACT CCTAAGTACT ACGTTACTGT TATTGATGCT 100
CCAGGTCACC GTGATTTCAT CAAGAACATG ATTACTGGTA CTTCCCAAGC 150
CGACTGCGCC ATTCTTATCA TTGCTGCCGG TGTCCGGTGAA TTCGAAGCTG 200
25 GTATCTCCAA GGAAGGTCAA ACCAGAGAAC ACGCTCTTCT CGCTTTCACC 250
CTTGGTGTCA GACAACTTAT CATTGCCATC AACAAAGATGG ACTCTGTCAA 300
GTGGGACCAA AAGAGATACG AAGAAATCGT CAAGGAGGCT TCCAACCTCG 350
TCAAGAAGGT TGGTTACAAC CCCAAGTCTG TTCCATTCTG TCCTATCTCT 400
GGTTGGAACG GTGACAACAT GTTGGAACCT ACCACCAACG CCCCATGGTA 450
30 CAAGGGATGG ACCAAGGAAA CCAAGGCTGG TGCCACTAAG GGTATGACTC 500
TTATTGAAGC CATTGACGCC ATTGAACCAC CAGTAAGACC ATCCGACAAG 550
CCACTCCGTC TCCCACTCCA AGATGTTTAC AAGATTGGTG GTATCGGAAC 600
TGTGCCAGTC GGCCGTGTCG AAACCGGTAT CATCAAGGCC GGTATGGTCG 650
TCACCTTTGC TCCACCAATG GTCACAACTG AAGTTAAGTC CGTTGAAATG 700
35 CACCACGAAC AACTTGCTCA AGGTAACCCA GGTGACAACG TTGGTTTCAA 750
CGTCAAGAAC GTTTCGGTTA AGGAAATCAG ACGTGGTAAC GTCTGTGGTG 800
ACTCCAAGAA CGATCCACCA AAGGGCTGCG AATCTTTCAA CGCTCAAGTT 850
ATCGTCTTGA ACCACCCTGG TCAAATCTCT GCTGGTACT CTCCAGTTCT 900
CGATTGCCAC ACTGCCACCA TTGCCTGCAG ATTCGACGAA CTCCTTGAAA 950
40 AGATCGACCG TCGTTCCGGT AAGAAGATTG AAGACTCTCC AAAGTTTGTC 1000
AAGTCTGGTG ATGCCGCTAT CGTCAAGATG ATCCCAACCA AGCCAATGTG 1050
CGTTGAAACC TTCACTGAAT ACCCACCCT TGGTCGTTTC GCCGTCCGTG 1100
A 1101

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2) INFORMATION FOR SEQ ID NO: 457

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1085 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
60 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457

	GTTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	TATGTCACCG	TCATCGACGC	CCCGGGTCAT	100
5	CGTGACTTTA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CCGACTGCGC	150
	CATCTTGATC	ATTGCCGCCG	GTACCGGTGA	ATTCTGAAGCC	GGTATCTCCA	200
	AGGATGGTCA	GACCCGTGAG	CACGCTCTGC	TCGCCTACAC	CTTGGGTGTC	250
	AAGCAGCTCA	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCCGA	300
	GGAGCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAACCTC	ATCAAGAAGG	350
10	TCGGCTACAA	CCCCAAGGCC	GTTCCCTTTCG	TCCCCATCTC	CGGCTTCAAC	400
	GGTGACAACA	TGATTGAGGT	CTCCACCAAC	TGCCCCGTGGT	ACAAGGGATG	450
	GGAGAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTCGAGG	500
	CCATTGACGC	CATCGACCCA	CCCACCCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCTCTCC	AGGATGTCTA	CAAGATCTCT	GGTATCGGAA	CGGTTCTCTG	600
15	CGGTCGTGTC	GAGACCGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTCG	650
	CTCCGGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAAAT	GCACCACGAG	700
	CAGCTCGCCG	AGGGTCTGCC	AGGTGACAAC	GTTGGCTTCA	ACGTCAAGAA	750
	CGTCTCCGTC	AAGGAGGTTC	GTCGTGGTAA	CGTTGCCGGT	GACTCCAAGA	800
	ACGACCCGCC	CAAGGGTGCC	GAGTCCTTCA	ACGCCCAGGT	CATTGTCCTC	850
20	AACCACCCTG	GTCAGATCGG	TGCCGGCTAC	GCTCCAGTCT	TGGATTGCCA	900
	CACTGCCCAC	ATTGCTTGCA	AGTTCGCCGA	GTTGCTCGAG	AAGATCGACC	950
	GTCGTACCGG	AAAGTCCATC	GAGAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
	GATGCTGCCA	TCGTCAAGAT	GATTCCCAGC	AAGCCCATGT	GTGTCGAGGC	1050
25	TTTCACCGAC	TATCCTCCTC	TGGGTCGTTT	CGCTG		1085

2) INFORMATION FOR SEQ ID NO: 458

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*

40 (B) STRAIN: DAL-95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458

	TGTCTTCATC	CGGAATTGAT	TGTGAGTCGT	TCCACATGCT	CACCTAGTTT	50
45	TCGCTCGATC	TTTTCACTAA	CGCAAACCAT	GTAGAACAAC	ATTGCCAAGG	100
	CCCACGGTGG	TTACTCCGTC	TTCACTGGTG	TTGGTGAGCG	TACTCGTGAG	150
	GGTAACGATC	TGTACCACGA	AATGCAGGAG	ACTGGTGTC	TTCAGCTCGA	200
	GGGTGAATCC	AAGGTCGCAC	TGGTGTTCCG	ACAGATGAAC	GAGCCCCCCG	250
	GTGCCCCGTG	CCGTGTGCGC	CTTACCGGTC	TGACCATTCG	CGAGTACTTC	300
50	CGTGACGAGG	AGGGTCAGGA	CGTGCTGCTC	TTCATTGACA	ACATTTTCCG	350
	TTTCACCCAG	GCCGGTTCTG	AGGTGTCTGC	CCTTCTCGGT	CGTATCCCCT	400
	CTGCCGTCGG	TTACCAGCCC	ACCCTGGCCG	TCGACATGGG	TGGTATGCAG	450
	GAGCGTATCA	CCACCACCAA	GAAGGGTTCT	ATTACCTCCG	TC	492

55

2) INFORMATION FOR SEQ ID NO: 459

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 1154 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastoschizomyces capitatus*
 (B) STRAIN: ATCC 10663

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459

	GTCCGTGGTC	AAGAAGTTAT	TGACACTGGT	GCCCCAATTA	CCATTCCTGT	50
	TGGTCGTGGT	ACTCTTGGTA	GAATTATCAA	CGTCATTGGT	GAACCAATTG	100
15	ACGAACGTGG	TCCTATCAAG	GCTTCTAAGT	ATGCTCCTAT	CCATACTGAA	150
	CCACCAACCT	TTGCTGAACA	ATCTACTTCT	GCTGAAGTTC	TTGAAACTGG	200
	TATCAAGGTT	GTCGATCTTC	TTGCTCCTTA	CGCCCGTGGT	GGTAAGATTG	250
	GTCTTTTCGG	TGGTGCTGGT	GTCGGTAAGA	CTGTCTTCAT	TCAAGAACTT	300
	ATTAACAACA	TTGCCAAGGC	TCACGGTGGT	TTCTCTGTCT	TCACTGGTGT	350
20	CGGTGAAAGA	ACCCGTGAAG	GTAACGATCT	TTACCGTGAA	ATGAAGGAAA	400
	CTGGTGTCAT	CAACCTCGAA	GGTGACTCCA	AGGTCGCTCT	CGTTTTTCGGT	450
	CAAATGAACG	AACCTCCAGG	TGCCCCGTGCC	CGTGTCGCTT	TGACTGGTCT	500
	TACCATTGCC	GAATACTTCC	GTGATGAAGA	AGGACAAGAT	GTCTTGCTTT	550
	TCGTTGACAA	CATTTTCAGA	TTCACCCAAG	CCGGTTCTGA	AGTCTCTGCT	600
25	CTTTTGGGTC	GTATTCCATC	TGCCGTCGGT	TACCAACCTA	CCCTTGCTAC	650
	CGATATGGGT	GCCCTCCAAG	AACGTATTAC	CACCACCCAA	AAGGGTTCCG	700
	TCACATCTGT	CCAAGCCGTC	TATGTCCCAG	CAGACGATTT	GACTGATCCT	750
	GCCCCAGCCA	CCACTTTCGC	TCACTTGGAC	GCCACCACTG	TCTTGCTCTCG	800
	TTCCATTTCC	GAATTGGGTA	TCTACCCAGC	TGTCGATCCT	CTCGATTCCA	850
30	AGTCTCGTCT	TTTGGATCCT	GAAGTTATTG	GACACGAACA	CTACGAAGTT	900
	GCCACTCAAG	TTCAACAAAC	CCTCCAAGCT	TACAAGTCTC	TCCAAGATAT	950
	CATTGCCATT	TTGGGTATGG	ATGAATTGTC	TGAAGCTGAT	AAGCTTACTG	1000
	TCGAACGTGC	CCGTAAGATC	CAAAGATTCC	TTTCCCAACC	ATTCGCTGTT	1050
	GCCGAAGTTT	TCACTGGTAT	CGAAGGTCGT	CTCGTTCCAT	TGAAGGAAAC	1100
35	CGTCAGATCT	TTCAAGGAAA	TCCTTGAAGG	TAAGTACGAT	CACCTTCCAG	1150
	AAGC					1154

40 2) INFORMATION FOR SEQ ID NO: 460

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1295 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460

55

	CCAATTTCGAC	GAAGGAAACT	TGCCAGCTAT	TTTGAATGCT	TTGACTTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCTCAACA	TTTGGGTGAA	100
	AACACCGTCA	GAGCTATTGC	TATGGATGGT	ACTGAAGGTT	TAGTCAGAGG	150
	TACCGAAGTC	AACGATACCG	GTGCCCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
60	GTACTIONTAGG	TAGAATCATC	AATGTTGTTG	GTGAACCAAT	TGATGACAGA	250

	GGTCCAATTG	AATGTAAGGA	AAAGAAACCA	ATTCACGCTG	AACCACCATC	300
	ATTCGTTGAA	CAATCCACTG	CTGCCGARAT	TTTGGAACC	GGTATCAAGG	350
	TTGTCGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAARAT	TGGTTTATTC	400
	GGTGGTGCTG	GTGTCGGTAA	GACCGTCTTT	ATCCAAGAAT	TGATTAACAA	450
5	CATTGCCAAA	GCCCATGGTG	GTTTCTCTGT	CTTTACCGGT	GTGCGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAAGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTCTTCG	GTCAAATGAA	600
	CGAACCACCA	GGTGCTAGAG	CTAGAGTTGC	TTTGAAGTGG	TTGACCATTC	650
	CTGAATACTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTCAATTGAT	700
10	AACATTTTCA	GATTCACCCA	AGCTGGTTCC	GAAGTGTCTG	CTTTGTTAGG	750
	TCGTATTCCA	TCTGCTGTCG	GTTATCAACC	AACCTTAGCC	ACTGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAAGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTCCC	AGCTGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACTACATTC	GCCCATTTGG	ATGCCACTAC	TGTCTTGCTC	AGAGGTATTT	950
15	CTGAATTGGG	TATCTACCCA	GCTGTCGATC	CATTGGATTC	CAAATCCAGA	1000
	TTATTGGACG	CTTCTGTTGT	TGGTCAAGAA	CATTACGATG	TCGCTACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAATC	CTTACAAGAT	ATCATTGCTA	1100
	TTTTGGGTAT	GGATGAATTG	TCTGAAGCTG	ATAAATTGAC	TGTCGAAAGA	1150
	GCCCGTAAGA	TCCAAAGATT	CTTGTCTCAA	CCATTCGCTG	TTGCTGAAGT	1200
20	TTTCACTGGT	ATCCCAGGTA	GATTAGTCAG	ATTGCAAGAC	ACTGTCAAAT	1250
	CATTCAAGGA	TGTTTTGGAA	GGTAAATACG	ATAACTTGCC	AGAAA	1295

25 2) INFORMATION FOR SEQ ID NO: 461

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461

40	TAAGTTGCCA	GCTATTTTGA	ATGCTTTGAC	TTTGAAGAAC	GGTGACCAAG	50
	ATTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	CGTCAGAGCT	100
	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	AGAGGTACTG	AAGTCAACGA	150
	TACCGGTGCC	CCAATCTCCG	TTCCAGTCGG	TAGAGGTACC	TTAGGTAGAA	200
45	TCATCAATGT	TGTTGGTGAA	CCAATTGATG	ACAGAGGTCC	AATTGAATGT	250
	AAGGAAAAGA	AACCAATTCA	TGCAGAACCA	CCATCCTTCG	TTGAGCAATC	300
	CACTGCTGCC	GAAATTTTGG	AAACCGGTAT	CAAGGTTGTC	GACTTATTGG	350
	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTCCGGTG	TGCTGGTGTC	400
	GGTAAGACCG	TCTTTATCCA	AGAATTGATT	AACAACATTG	CTAAAGCCCA	450
50	TGGTGGTTTC	TCCGTCTTTA	CCGGTGTCGG	TGAAAGAACC	AGAGAAGGTA	500
	ACGATTTGTA	CCGTGAAATG	AAAGAAACCG	GTGTCATCAA	CTTAGAAGGT	550
	GACTCCAAGG	TCGCTTTGGT	CTTTGGACAA	ATGAACGAAC	CACCAGGTGC	600
	TAGAGCTAGA	GTTGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCAGAG	650
	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTCA	TCGATAACAT	TTTCAGATTC	700
55	ACCCAAGCTG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTCGTA	TTCCATCTGC	750
	CGTCGGTTAT	CAACCAACCT	TAGCTACTGA	TATGGGTCTT	TTGCAAGAAC	800
	GTATTACCAC	CACCAAGAAA	GGTTCCGTCA	CCTCTGTCCA	AGCTGTCTAT	850
	GTCCCAGCTG	ATGATTTGAC	CGATCCTGCT	CCAGCCACCA	CATTCGCCCA	900
	TTTGATGCC	ACTACTGTCT	TGTCTAGAGG	TATTTCTGAA	TTGGGTATTT	950
60	ACCCAGCTGT	CGATCCATTG	GATTCCAAAT	CCAGATTATT	GGACGCTGCC	1000

	GTTGTTGGTC	AAGAACATTA	TGATGTCGCT	ACTGGTGTTCT	AAACAACTTT	1050
	GCAAGCTTAC	AAATCCTTAC	AAGATATCAT	TGCTATTTTG	GGTATGGATG	1100
	AATTGTCTGA	AGCTGATAAA	TTGACTGTCG	AAAGAGCCCG	TAAGATTCAA	1150
	AGATTCTTGT	CTCAACCATT	CGCCGTTGCT	GAAGTTTTCA	CTGGTATTCC	1200
5	AGGTAGATTA	GTCAGATTGC	AAGACACTGT	CAAATCATTCT	AAGGATGTTT	1250
	TGGAAGGTAA	ATACGATCAC	TTGCCAG			1277

10 2) INFORMATION FOR SEQ ID NO: 462

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida famata*
 (B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462

25	GTA	ACTT	GCC	AGCT	ATTTT	G	AAC	GCTT	TGA	CCT	TGA	AAG	AA	CGG	TGA	AA	AA	50
	GAC	TTAG	TTT	TAGA	AGTT	G	CCA	ACAT	TTG	GGT	GAA	AA	AC	CCG	TCAG	AG	C	100
	TAT	TGCT	ATG	GAT	GGT	ACT	AAG	GTTT	AGT	TAG	AGGT	ACT	CC	CAG	TTAC	CG		150
	ATT	CTGG	TGC	TCCA	ATTT	CT	GTCC	CAGT	CG	GTA	GAGG	TAC	TT	TAG	GTA	GA		200
30	ATC	TTGA	ACG	TTAT	TGGT	G	ACCA	ATTG	AT	GAAC	AAGG	TC	CA	GAT	TGAT	GC		250
	CAAG	GAA	ACC	AGAC	CAAT	TC	ACCA	AGAC	CC	ACC	AGCA	TT	CT	GTT	GAT	CA	AT	300
	CCAC	CAAG	GC	TGA	AGTT	TTG	GAA	ACTG	GTA	TCA	AGGT	TG	CG	ATTT	TAT	TA		350
	GCCC	CTT	ACG	CTAG	AGGT	TG	TAAG	ATTG	GT	TTAT	TCGG	TG	GTG	CCG	GT	T	400	
	CGGT	AAG	ACC	GTCT	TTAT	CC	AAGA	ATTG	AT	TAAC	AAC	ATT	GCC	AAG	G	CC	450	
35	ATG	GTGG	TTT	CTCT	GTTT	TC	ACT	GGT	GTC	GTG	AAAG	AA	CAG	AGA	AAG	G	500	
	AAC	GATTT	TAT	ATAG	AGAA	AT	GAAG	GAA	ACT	GGT	GTC	ATTA	ACT	TGG	AAG	G	550	
	TGAC	TCCA	AG	GTC	GCCT	TG	TTTT	CGGT	CA	AAT	GAA	CGAA	CCAC	CAGG	TG		600	
	CTAG	AGCT	AG	AGTT	GCTT	TA	ACCG	GTTT	AA	CCAT	TGCC	GA	ATA	CTTC	AG		650	
	GAC	GAAG	AAG	GTCA	AGAT	GT	GTT	ATTG	TTC	GTC	GATA	ACA	TTTT	TAG	ATT		700	
40	CAC	CCAAG	CC	GGTT	CCGA	AG	TGT	CTG	CTT	GTT	AGGT	CGT	ATT	CCAT	CG	G	750	
	CTGT	CGGT	TA	TCA	ACCA	ACC	TTAG	CCAC	TG	ATAT	GGGT	CT	TTT	ACA	AG	AA	800	
	AGA	ATTAC	CA	CCAC	CACCA	AA	GGGT	TCCG	TT	ACT	TCTG	TCC	AAG	CTGT	CT	A	850	
	CGT	CCCAG	CC	GAT	GATTT	AA	CCG	ATC	CTG	TCC	AGCT	ACC	ACT	TTTC	G	CC	900	
	ACT	TGG	ATG	TAC	CACT	GTG	TTGT	CTC	GTG	GTAT	CTCT	GA	ATT	GGG	TAT	T	950	
45	TAC	CCAG	CTG	TCG	ATCC	ATT	GGAT	TCC	AAA	TCC	AGAT	TGT	TAG	ATG	CT	GA	1000	
	TAT	CGTT	GGT	AAAG	AAC	ACT	ACGA	AGTT	G	CACT	GGT	GTC	CAAC	AAAC	CT		1050	
	TACA	AGCT	TA	CAA	ATCT	TTA	CAAG	ATAT	CA	TTG	CTAT	TTT	AGG	TATG	GAT		1100	
	GAAT	TGT	CTG	AAG	CCG	ATA	ATT	GACT	GTC	GAA	AGAG	CCA	GAA	AGAT	CCA		1150	
	AAG	ATTCT	TG	TCT	CAAC	CAT	TCG	CCGT	TG	CGA	AGTT	TTT	ACC	GGT	AT	CC	1200	
50	CAG	GTA	GATT	AGTT	AGAT	TG	CAAG	ACAC	TG	TTAA	ATCT	TTT	CAAG	GAAG	TC		1250	
	TTAG	AAG	GTA	AAT	ATG	ATCA	CTT	ACC	AG								1278	

55 2) INFORMATION FOR SEQ ID NO: 463

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida glabrata*

(B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463

10 TCTGGTCAGA GCGAGAAGG TCGTCGACAC AGGTGCCCCA ATCTCCGTCC 50
 CTGTCGGCAG AGAGACCCTG GGCAGAATCA TCAACGTTAT CGGTGAACCT 100
 ATCGACGAGC GTGGCCCAAT CAACTCAAAG TTGAGAAAGC CTATCCACGC 150
 CGACCCTCCT TCCTTCGCAG AACAGTCCAC CGCCGCCGAA GTCCTGGAAA 200
 15 CAGGTATCAA GGTCGTCGAC TTGCTGGCCC CTTACGCCAG AGGTGGTAAG 250
 ATCGGTCTGT TCGGTGGTGC CGGTGTCGGT AAGACCGTGT TCATCCAAGA 300
 ACTGATCAAC AACATCGCAA AGGCTCACGG TGGTTTCTCC GTGTTACACAG 350
 GTGTCGGTGA AAGAACCAGA GAAGGTAACG ATTTGTACAG AGAAATGAAG 400
 GAAACCGGTG TCATCAACTT GGAAGGTGAC TCTAAGGTCG CCTTGGTCTT 450
 20 CGGCCAAATG AACGAACCAC CAGGAGCCAG AGCCAGAGTC GCCTTGACCG 500
 GTTTGACCAT CGCAGAATAC TTCAGAGATG AAGAAGGTCA AGATGTCCTG 550
 CTGTTTCGTCG ACAACATTTT CAGATTCACC CAAGCCGGTT CAGAAGTCTC 600
 CGCTTTGCTA GGTCGTATCC CATCCGCCGT CGGTTATCAA CCAACCTTGG 650
 CCACCGATAT GGGTCTGTTG CAAGAAAGAA TTACCACCAC AAAGAAGGGT 700
 25 TCCGTCACCT CCGTCCAAGC CGTCTACGTG CCTGCAGATG ATTTAACAGA 750
 TCCTGCCCCT GCCACTACTT TCGCGCACTT GGACGCCACC ACCGTCTTGT 800
 CCAGAAGTAT CTCAGAATTG GGTATCTACC CAGCTGTGCA CCCATTGGAC 850
 TCCAAGTCTA GATTGCTAGA CGCTGCCGTT GTCGGTGAAG AGCATTACAA 900
 CGTCGCCACA AAGGTCCAAG AAACCTTACA AACTTACAAG TCTCTGCAAG 950
 30 ATATCATCGC CATTTTGGGT ATGGATGAAT TGTCCGAACA AGATAAGCTA 1000
 ACTGTCGAAA GAGCAAGAAA GATCCAAAGA TTCTTGTTCC AACCATTTCG 1050
 TGTCGCTGAA GTTTTCACCG GTATCGAAGG TAAGCTGGTC AGATTGAAGG 1100
 ACACCATCTC CTCTTTCAAG GCTGTCTTGG AAGGTAAGTA CGATGATCTT 1150
 CCAG 1154

35

2) INFORMATION FOR SEQ ID NO: 464

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida guilliermondii*

50 (B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464

CCACTACGAG GACGGTAACC TTCCTGCTAT TTTCAACGCC TTGACTCTTA 50
 55 AGAACGGTGA CCAAAACTTG GTTTTGAAG TTGCCCAGCA TTTGGGTGAA 100
 AACACCGTCA GAACCATTGC TATGGATGGT ACTGAAGGTT TGGTTAGAGG 150
 TGCCAGCGTC ACTGACACTG GTGCTCCTAT CTCTGTGCCT GTTGGTCGTG 200
 GTACTTTGGG TCGTATCATC AACGTTATTG GTGAGCCAAT TGACGAGCGT 250
 GGACCAATCG AGTCCAAGCA AAAGAAGCCC ATTCACGCTG AACCACCATC 300
 60 GTTCGTCGAA CAATCCACTT CTGCCGAGGT TTTGGAAACC GGTATCAAGG 350

	TTGTCGACTT	GTTGGCTCCA	TACGCCAGAG	GTGGTAAGAT	TGGATTGTTG	400
	GGTGGTGCCG	GTGTCGGTAA	GACTGTGTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCTCACGGTG	GTTTCTCCGT	GTTCACCGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTC	550
5	ATCAACTTGG	AAGGTGAATC	CAAGGTGGCC	TTGGTGTTCG	GTCAAATGAA	600
	CGAACCTCCA	GGAGCTAGAG	CCAGAGTTGC	CCTTACCGGT	TTGACCATCG	650
	CTGAATACTT	CAGAGATGAG	GAGGGTCAAG	ATGTGTTGTT	GTTTCGTCGAC	700
	AACATTTTCA	GATTCACCTCA	AGCTGGTTCT	GAAGTGTCCG	CTTTGTTGGG	750
	TCGTATTCCCT	TCGGCTGTCG	GTTACCAACC	TACTTTGGCC	ACCGATATGG	800
10	GTTTGTGCA	AGAGCGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTGCC	AGCCGATGAT	TTGACCGATC	CTGCTCCTGC	900
	TACTACTTTT	GCTCACTTGG	ATGCTACCAC	TGTGTTGTCT	AGAGGTATCT	950
	CCGAGTTGGG	TATTTACCCA	GCTGTCGATC	CTTTGGATTG	CAAGTCGAGA	1000
	TTGTTGGATG	CCTCTGTTGT	CGGTGAGGAG	CACTACTCGG	TTGCTTCTAA	1050
15	CGTTCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
	TTTTGGGTAT	GGACGAATTG	TCGGAAGCTG	ACAAGTTGAC	CGTCGAGAGA	1150
	GCCCGTAAGA	TCGAGAGATT	CTTGTCTCAA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCAGTGGTA	AGTTGGTCAG	ATTGGAGGAC	ACTATCAGAT	1250
	CTTTCAAGGA	AGTCTTGGAA	GGTAAGTACG	ATCACTTGCC	AGA	1293
20						

2) INFORMATION FOR SEQ ID NO: 465

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
 35 (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465

	CACTTTGACG	ATGGTAACTT	GCCAGCCATT	TTCAACGCCT	TGAAGTTGAA	50
40	GAACGGTGAC	CAGGACTTGG	TCTTGAGAGT	CGCCCAGCAC	TTGGGTGAGA	100
	ACACCGTCAG	AACCATTGCC	ATGGACGGTA	CCGATGGTTT	GGTCAGAGGC	150
	GAGGCTGTCA	CTGACACTGG	TGCTCCAATC	TCCGTGCCTG	TTGGTCGTGA	200
	GACTTTGGGT	CGTATCATCA	ACGTTATTGG	TGAGCCAATT	GACGAGAGAG	250
	GACCAATCAA	GTCCAAGAAG	AGAAACCCAA	TCCACACTGA	CCCACCAACC	300
45	TTCGTTGAGC	AGTCTACTTC	TGCTGAGGTT	TTGGAGACTG	GTATTAAGGT	350
	TGTCGACTTG	TTGGCCCCTT	ACGCCAGAGG	TGGTAAGATT	GGTTTGTTCG	400
	GTGGTGCCGG	TGTCGGTAAG	ACCGTCTTTA	TCCAAGAGTT	GATTAACAAC	450
	ATTGCCAAGG	CCCACGGTGG	TTTCTCTGTC	TTTACCGGTG	TCGGTGAGAG	500
	AACCAGAGAA	GGTAACGATT	TGTACCGTGA	AATGCAGGAG	ACCGGTGTCA	550
50	TCAACTTCGA	GGGTGACTCC	AAGGTCGCCT	TGGTCTTCGG	TCAGATGAAC	600
	GAGCCACCAG	GAGCTAGAGC	TAGAGTTGCT	TTGACCGGTT	TGACCATTCG	650
	CGAATACTTC	AGAGATGAAG	AAGGTCAGGA	TGTGTTGTTG	TTCGTTGACA	700
	ACATTTTCAG	ATTCACCTCAG	GCTGGTTCCG	AGGTGTCCGC	CTTGTTGGGT	750
	CGTATTCCAT	CTGCTGTCCG	TTACCAGCCA	ACCTTGGCCA	CCGATATGGG	800
55	TACCTTGCAA	GAAAGAATTA	CCACCACCAA	GAAGGGTTCC	GTCACCTCTG	850
	TCCAGGCCGT	TTACGTGCCA	GCTGATGATT	TGACCGATCC	TGCCCCAGCT	900
	ACCACTTTTCG	CTCACTTGGA	TGCTACCACT	GTGTTGTCTA	GAGGTATTTC	950
	CGAGTTGGGT	ATCTACCCAG	CTGTCGACCC	ATTGGACTCC	AAGTCTAGAT	1000
	TGTTGGATGC	CTCTGTTGTC	GGTAAGGAGC	ACTACGATGT	TGCTACCAAC	1050
60	GTCCAGCAGA	CCTTGCAGGC	CTACAAGTCC	TTGCAGGATA	TCATTGCCAT	1100

TTTGGGTATG	GATGAATTGT	CCGAAGCCGA	CAAGTTGACT	GTCGAGAGAG	1150
CTAGAAAGAT	TCAGAGATTC	TTGTCCCAGC	CATTCGCCGT	CGCCGAGGTT	1200
TTCAGTGGTA	TCGAGGGTAA	GTTGGTCAGA	TTGGAGGAGA	CCGTCAAGTC	1250
TTTCAAGGAG	GTCTTGGATG	GTAAGTACGA	CCACTTGCCA	GAG	1293

5

2) INFORMATION FOR SEQ ID NO: 466

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*
- (B) STRAIN: ATCC 16783

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466

AACGGTGGAT	CTAAGTTAGT	CTTAGAAGTT	GCTCAACATT	TGGGTGAAAA	50
CACTGTCAGA	ACCATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTAGAGGTC	100
AACCAGTTAA	TGATACTGGT	GCTCCAATCT	CTGTCCCAGT	CGGTAGAGGT	150
ACTTTAGGTA	GAATCTTAAA	CGTTATTGGT	GATCCAGTCG	ATGAAAGAGG	200
TCCAATTGAT	TGTAAGGAAA	GAAAACCAAT	TCATCAAGAT	CCTCCTGCTT	250
TCGTTGAACA	ATCTACTGAA	GCTGAAGTTT	TAGAAACCGG	TATTAAGGTT	300
GTTGATTTAT	TAGCTCCTTA	CGCTAGAGGT	GGTAAGATTG	GTTTATTTCG	350
TGGTGCTGGT	GTCGGTAAAA	CCGTTTTCAT	TCAAGAATTA	ATTAACAATG	400
TTGCAAAGGC	TCATGGTGGT	TTCTCAGTTT	TCACTGGTGT	CGGTGAAAGA	450
ACCAGAGAAG	GTAATGATTT	ATACAGAGAA	ATGAAGGAAA	CTGGTGTTAT	500
TAACTTAGAA	GGTGAATCTA	AGGTCGCCTT	AGTTTTTCGGT	CAAATGAATG	550
AACCACCAGG	AGCAAGAGCA	AGAGTTGCTT	TAACCGGTTT	AACTATTGCT	600
GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCATTGATAA	650
CATTTTCAGA	TTTACTCAAG	CAGGTTCTGA	AGTTTCTGCA	TTGTTAGGTA	700
GAATTCCATC	CGCTGTCGGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	750
CTTTTACAAG	AAAGAATTAC	AACTACTAAG	AAAGGTTCCG	TTACTTCTGT	800
CCAAGCAGTT	TATGTCCCAG	CAGATGATTT	AACTGATCCT	GCTCCAGCAA	850
CTACTTTCGC	CCACTTAGAT	GCAACTACTG	TCTTATCTAG	AGGTATTTCC	900
GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCTAGATT	950
ATTAGATGTT	GCTGTTGTTG	GTCAAGAACA	TTATGATGTT	GCAACTCAAG	1000
TTCAAGAAAC	TTTACAAGCA	TACAAATCTT	TACAAGATAT	TATTGCTATT	1050
TTAGGTATGG	ATGAATTATC	TGAACAAGAT	AAATTAACCG	TTGAAAGAGC	1100
AAGAAAGATT	C				1111

50 2) INFORMATION FOR SEQ ID NO: 467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Candida kefyr*
 (B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467

5
 TCGAACAAGG TCAATTGCCA GAAATTTTGA ACGCTTTGGA GATTGAWACT 50
 CCTCAAGGTA AGTTGGTTTT GGAAGTTGCC CAACATTTGG GTGAAAACAC 100
 CGTCAGAACC ATTGCTATGG ACGGTACCGA AGGTTTGGTC CGTGGTGAGA 150
 AGGTTTTTGA CACTGGTGCT CCAATTTCCG TCCCAGTCGG TAGAGAAACT 200
 10 TTGGGTAGAA TCATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGCCC 250
 AATCAAGTCC AAGATGAGAA AGCCAATTCA CGCTGACCCT CCATCCTTTG 300
 TTGAACAATC CACTGCTGCT GAAGTTTTGG AAACCGGTAT CAAGGTTGTC 350
 GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTCGGTGG 400
 TGCCGGTGTC GGTAAGACCG TTTTCATCCA AGAGTTGATT AACAAATTG 450
 15 CCAAGGCCCA TGGTGGTTTC TCCGTCTTCA CCGGTGTCGG TGAAAGAACC 500
 AGAGAAGGTA ACGATTTGTA CCGTGAAATG AAGGAAACCG GTGTCATCAA 550
 CTGGGAAGGT GACTCCAAGG TCGCCTTGGT CTTCGGTCAA ATGAACGAAC 600
 CACCTGGAGC TAGAGCCAGA GTTGCCCTTGA CCGGTTTGAC TATCGCTGAA 650
 TACTTCAGAG ATGAAGAAGG TCAAGATGTG TTGTTGTTTA TCGACAACAT 700
 20 TTTCAGATTC ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA 750
 TTCCATCCGC TGTCGGTTAC CAACCTACTT TGGCCACCGA TATGGGTTTG 800
 TTGCAAGAAA GAATTACCAC TACCAAGAAG GGTTCCGTTA CCTCCGTCCA 850
 AGCTGTCTAC GTCCCTGCTG ATGATTTGAC TGATCCTGCT CCAGCTACYA 900
 CTTTCGCCCA TTTGGACGCC ACCACCGTGT TGTCAGAGG TATCTCCGAA 950
 25 TTGGGTATCT ACCCAGCTGT CGATCCATTG GATTCCAAGT CTAGATTGTT 1000
 GGACGCTGCC GTTGTCGGTC AAGAACATTA CGACGTCGCT ACTCAAGTTC 1050
 AACAACTTT GCAAGCTTAC AAGTCTTTGC AAGATATCAT TGCCATTTTG 1100
 GGTATGGATG AATTGTCTGA ACAAGACAAG TTGACTGTCG AAAGAGCCAG 1150
 AAAGATCCAA AGATTCTTGT CTCAACCATT CGCCGTCGCC GAAGTTTTCA 1200
 30 CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACACCAT CGCTTCCTTC 1250
 AAGGCTGTTT TGGAAGGTAA GTACGATCAC TTG 1283

35 2) INFORMATION FOR SEQ ID NO: 468

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1287 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*
 (B) STRAIN: ATCC 34135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468

50
 CTTCGAACAA GGCCAATTAC CACAAATTTT AAACGCTTTA GTTATGGATA 50
 ATGGTGGTAA CAAGTTAGTT TTAGAAGTTG CTCAACATTT AGGTGAAAAC 100
 ACTGTCAGAA CCATTGCTAT GGATGGTACT GAAGGTTTAG TTAGAGGTCA 150
 AACCGTTAAC GATACCGGTG CTCCAATCTC TGTCCTCAGT GGTAGAGGTA 200
 55 CCTTAGGTAG AATCTTGAAC GTCATTGGTG ATCCAGTCGA TGAAAGAGGT 250
 CCAGTTGACT GTAAGGAAAG AAAGCCAATT CACGCTGATC CTCCAGCTTT 300
 CGTTGAACAA TCCACTGAAG CTGAAGTTTT GGAACTGGT ATTAAGGTTG 350
 TCGATTTATT AGCACCTTAC GCAAGAGGTG GTAAGATTGG TTTATTCCGT 400
 GGTGCTGGTG TTGGTAAGAC CGTTTTTATC CAAGAATTGA TCAACAATGT 450
 60 YGCAAAGGCT CATGGTGGTT TCTCCGTTTT CACTGGTGTT GGTGAAAGAA 500

	CCAGAGAAGG	TAACGATTTA	TACAGAGAAA	TGAAGGAAAC	TGGTGTATT	550
	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	GTTTTCGGTC	AAATGAACGA	600
	ACCACCAGGA	GCTAGAGCAA	GAGTTGCTTT	AACTGGTTTG	ACCATTGCAG	650
	AATATTTCAG	AGATGAAGAA	GGTCAAGATG	TCTTGTTATT	CATTGATAAC	700
5	ATTTTCAGAT	TCACCCAAGC	AGGTTCTGAA	GTCTCTGCAT	TATTAGGTAG	750
	AATTCCATCT	GCTGTCGGTT	ATCAACCAAC	TTTAGCAACC	GATATGGGTC	800
	TTTTACAAGA	AAGAATTACC	ACCACCAAGA	AGGGTTCCGT	TACTTCTGTC	850
	CAAGCTGTTT	ATGTCCCAGC	CGATGATTTA	ACCGATCCTG	CTCCAGCTAC	900
	TACTTTCGCC	CACTTGGATG	CAACCACTGT	CTTGTCYAGA	GGTATTTCCG	950
10	AATTAGGTAT	CTACCCAGCT	GTCGATCCAT	TAGATTCTAA	GTCTAGATTA	1000
	TTAGATGTTG	CAGTTGTTGG	TCAAGAACAT	TATGAAGTTG	CAACTCAAGT	1050
	CCAAGAACT	TTACAAGCTT	ACAAGTCTTT	ACAAGATATT	ATTGCTATTT	1100
	TGGGTATGGA	TGAATTATCT	GAACAAGATA	AGTTAACYGT	TGAAAGAGCA	1150
	AGAAAGATCC	AAAGATTCTT	ATCTCAACCA	TTCTCTGTTG	CAGAAGTTTT	1200
15	CACTGGTATT	CCAGGTAAGT	TAGTCAGATT	AGAAGAAACC	ATCAAGTCTT	1250
	TCAGGGATGT	TCTTGCAGGT	AAGTACGATC	ACTTACC		1287

20 2) INFORMATION FOR SEQ ID NO: 469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*
 (B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469

35	TCGAACAAGG	TCAATTACCA	CCAATTCTTA	ACGCTTTGGT	CATGGAAAAC	50
	GATGGTCAAA	AGTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	100
	CGTCAGAACC	ATTGCTATGG	ACGGTACCGA	AGGTTTAGTT	AGAGGTCAAC	150
	CTGTTAACGA	CACTGGTGCT	CCAATCTCTG	TCCAGTTGG	TAGAGGTACT	200
40	CTTGGTAGAA	TCTTGAACGT	CACTGGTGAC	CCAGTYGATG	AAAGAGGTCC	250
	TGTCGAMTGT	AAGGAGAGAA	GACCAATTCA	CCAAGACCCA	CCTGCTTTTCG	300
	TTGACCAATC	CACTGAAGCT	GAAGTTTTGG	AAACCGGTAT	TAAGGTTGTC	350
	GATTTATTAG	CACCTTACGC	TAGAGGTGGT	AAGATTGGTT	TGTTCCGGTGG	400
	TGCTGGTGTC	GGTAAGACCG	TTTTCATCCA	AGAATTGATT	AACAATGTTG	450
45	CTAAGGCCCA	CGGTGGTTTC	TCCGTTTTCA	CTGGTGTCCG	TGAAAGAACC	500
	AGAGAAGGTA	ACGATTTATA	CAGAGAAATG	AAGGAAACCG	GTGTTATTAA	550
	CCTTGAAGGT	GAATCTAAGG	TCGCCCTCGT	TTTCGGTCAA	ATGAACGAAC	600
	CACCAGGAGC	AAGAGCTAGA	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAA	650
	TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGCTTTTCA	TTGACAACAT	700
50	TTTCAGATTC	ACCCAAGCAG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTAGAA	750
	TTCCWTCTGC	CGTTGGTTAC	CAACCAACCT	TAGCAACCGA	TATGGGTTTG	800
	TTACAAGAAA	GAATTACCAC	CACCAAGAAG	GGTTCCGTCA	CCTCCGTCCA	850
	AGCTGTTTAC	GTCCCAGCTG	ATGATTTRAC	TGACCCTGCA	CCAGCAACCA	900
	CTTTCGCCCA	CTTGGATGCT	ACCACCGTCT	TGTCTAGAGG	TATTTCCGAA	950
55	TTAGGTATTT	ACCCAGCTGT	CGATCCATTA	GATTCTAAGT	CTAGATTATT	1000
	GGATGTCGCT	GTTGTCGGTC	AAGAACATTA	TACCGTTGCA	ACYCAAGTCC	1050
	AAGAACTTT	ACAAGCTTAC	AAGTCCTTAC	AAGATATCAT	TGCTATTTTG	1100
	GGTATGGACG	AATTATCTGA	ACAAGATAAG	CTTACTGTTG	AAAGAGCAAG	1150
	AAAGATCCAA	AGATTCTTTT	CCCAACCTTT	CTCCGTCGCA	GAAGTTTTCA	1200
60	CTGGTATCCC	AGGTAAGCTT	GTCAGATTAG	AAGAAACCAT	TATTTCTTTC	1250

5 2) INFORMATION FOR SEQ ID NO: 470

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1140 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
(B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470

20 AGGTGCCTCT GTCACTGACA CTGGTTCTCC AATCTCTGTC CCTGTTGGTC 50
GTGAAACCTT GGGTAGAATT ATCAACGTTG TTGGTGAGCC AATTGACGAG 100
AGAGGCCCAA TCAACTCCAA GAAGAGAAAC CCAATTCACA CTGAGCCACC 150
ATCGTTTGTT GAACAATCCA CTTCTGCTGA AGTTTTGGAG ACTGGTATCA 200
25 AGGTTGTCGA CTTGTTGGCC CCTTACGCCA GAGGTGGTAA GATTGGTTTG 250
TTCGGTGGTG CCGGTGTCGG TAAGACCGTT TTCATCCAAG AGTTGATTAA 300
CAACATTGCC AAGGCCACG GTGGTTTCTC TGTTTTCACT GGTGTCGGTG 350
AAAGAACCAG AGAAGGTAAC GATTTGTACC GTGAAATGCA AGAGACCGGT 400
GTCATCAACT TCGAGGGTGA CTCCAAGGTC GCCTTGGTCT TCGGTCAAAT 450
30 GAACGAACCA CCAGGAGCCA GAGCTAGAGT TGCTTTGACC GGTTTGACTA 500
TTGCCGAGTA CTTCAGAGAC GAAGAGGGCC AAGATGTCTT GTTGTTTCGTT 550
GACAACATTT TCAGATTCAC CCAGGCCGGT TCTGAAGTGT CTGCTTTGTT 600
GGGTCGTATT CCATCCGCTG TCGGTTACCA ACCAACCTTG GCCACCGATA 650
TGGGTGCTTT GCAAGAGAGA ATTACCACCA CCAAGAAGGG TTCCGTCACC 700
35 TCTGTCCAAG CCGTTTATGT TCCAGCTGAT GACTTGACTG ACCCTGCTCC 750
AGCCACCACC TTCGCCACT TGGACGCCAC CACTGTGTTG TCCAGAGGTA 800
TCTCTGAATT GGGTATCTAC CCAGCTGTCG ACCCATGGA CTCCAAGTCT 850
AGATTGTTGG ACGCTTCTAT TGTTGGTAAG GAGCACTACG AAGTTGCTTC 900
TAACGTTCAA CAACTTTGC AAGCTTACAA GTCTTTGCAA GATATCATTG 950
40 CCATTTTGGG TATGGATGAA TTGTCTGAGG CTGACAAGTT GACCGTTGAG 1000
AGAGCCAGAA AGATCCAAAG ATTCTTGTCT CAACCATTCG CTGTTGCCGA 1050
GGTTTTCACT GGTATCCCAG GTAGATTGGT CAGATTGGAG GACACTGTCA 1100
GATCCTTCAA GGAAGTTTTG GACGGTAAGT ACGACCACTT 1140

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2) INFORMATION FOR SEQ ID NO: 471

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1296 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
(B) STRAIN: ATCC 22977

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471

	TCAATTCGAA	CAAGGTCAAT	TACCACCAAT	TTTAAACGCT	TTAGTCATGG	50
	ACAACGGTGG	AACTAAGTTA	GTTTTAGAAG	TTGCTCAACA	TTTAGGTGAA	100
5	AACACCGTCA	GAACCATTCG	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TCAACCAGTT	AATGATACTG	GTGCTCCAAT	CTCTGTCCCA	GTCGGTAGAG	200
	GTA CTTTAGG	TAGAATCTTA	AACGTTATTG	GTGATCCAGT	CGATGAAAGA	250
	GGTCCAATCG	ATTGTAAGGA	AAGAAAACCA	ATTCATCAAG	ATCCTCCTGC	300
	TTTCGTTGAA	CAATCAACTG	AAGCTGAAGT	TTTAGAAACT	GGTATTAAAG	350
10	TTGTCGATTT	ATTAGCTCCT	TACGCTAGAG	GTGGTAAGAT	TGGTTTATTC	400
	GGTGGTGCAG	GTGTTGGTAA	AACCGTTTTT	ATTCAAGAAT	TAATTAACAA	450
	TGTTGCAAAA	GCTCATGGTG	GTTTCTCCGT	TTTCACTGGT	GTCGGTGAAA	500
	GAAC TAGAGA	AGGTAACGAT	TTATACAGAG	AAATGAAGGA	AACTGGTGTT	550
	ATTAATTTAG	AAGGTGATTC	TAAGGTCGCA	TTAGTTTTTCG	GTCAAATGAA	600
15	CGAACCACCT	GGAGCAAGAG	CAAGAGTTGC	TTTAACTGGT	TTAACTATTG	650
	CTGAATATTT	CAGAGATGAA	GAAGGTCAAG	ATGTCCTTGTT	ATTCATTGAT	700
	AACATTTTCA	GATTTACTCA	AGCAGGTTCT	GAAGTTTCCG	CTTTGTTAGG	750
	TAGAATTCCA	TCCGCTGTCG	GTTATCAACC	AACTTTAGCA	ACTGATATGG	800
	GTCTTTTACA	AGAAAGAATT	ACTACTACTA	AGAAAGGTTC	TGTTACTTCC	850
20	GTTCAAGCAG	TTTATGTCCC	AGCAGATGAT	TTAACTGATC	CTGCTCCAGC	900
	AACTACTTTC	GCCCACTTAG	ATGCAACTAC	TGTCTTATCT	AGAGGTATTT	950
	CCGAATTAGG	TATTTACCCA	GCTGTCGATC	CATTAGATTC	TAAATCTAGA	1000
	TTATTAGATG	TTGCAGTTGT	TGGTCAAGAA	CATTATGATG	TTGCAACTCA	1050
	AGTTCAAGAA	ACTTTACAAG	CTTACAAATC	TTTACAAGAT	ATTATTGCTA	1100
25	TTTTAGGTAT	GGATGAATTA	TCTGAACAAG	ATAAATTAAC	CGTTGAAAGA	1150
	GCTAGAAAAA	TTCAAAGATT	CTTATCTCAA	CCTTTCTCTG	TCGCAGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	AGCTTGTTAG	ATTAGAAGAA	ACTATTTCTT	1250
	CATTCAGAGA	TGTCTTAGCA	GGTAAGTACG	ATCACTTACC	AGAAAA	1296

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2) INFORMATION FOR SEQ ID NO: 472

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 90018

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472

	AACTTCGAA	GAAGGAAACT	TGCCAGCTAT	TTTGAACGCT	TTGACCTTGA	50
	AAAACGGTAA	ACAAGACTTG	GTCTTGGAAG	TTGCCCAACA	TTTGGGTGAA	100
50	AACACCGTCA	GAGCAATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TACTTCTGTC	ACTGACACTG	GTGCCCAAT	TTCTGTCCCA	GTTGGTAGAG	200
	GTA CTTTGGG	TAGAATCATC	AATGTTACTG	GTGACCCAAT	TGATGAAAGA	250
	GGTCCAATTG	AATGTAAGAA	GAGAAACCCA	ATCCACGCTG	AACCACCTTC	300
	ATTCATTGAA	CAATCCACTG	CTGCTGAAGT	TTTGGAACCC	GGTATTAAAG	350
55	TTGTCGACTT	GTTGGCTCCA	TACGCTAGAG	GTGGTAAGAT	TGGTTTGTTC	400
	GGTGGTGCCG	GTGTCGGTAA	AACCGTGTTT	ATCCAAGAAT	TGATCAACAA	450
	CATTGCCAAG	GCACATGGTG	GTTTCTCGGT	TTTCACTGGT	GTTGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTT	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTTTTTCG	GTCAAATGAA	600
60	CGAACCACCT	GGAGCTAGAG	CTAGAGTTGC	TTGACTGGT	TTGACCATTG	650

	CTGAATACTT	TAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCTGGTTCA	GAAGTGTCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCCGCTGTCG	GTTATCAACC	AACCTTGGCC	ACCGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACTACCA	AAAAGGGTTC	AGTTACTTCA	850
5	GTCCAAGCCG	TTTACGTGCC	AGCTGATGAT	TTAACCGATC	CTGCTCCAGC	900
	TACCACTTTC	GCTCACTTGG	ATGCCACCAC	TGTGTTGTCT	AGAGGTATTT	950
	CGGAGTTGGG	TATTTACCCA	GCTGTCGATC	CATTGGATTC	CAAATCCAGA	1000
	TTGTTGGATG	CTGCCGTTGT	TGGTCAAGAA	CATTACGACG	TTGCCACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAGTC	CTTGCAAGAT	ATCATTGCTA	1100
10	TCTTGGGTAT	GGATGAATTG	TCCGAACAAG	ATAAATTGAC	TGTCGAAAGA	1150
	GCTCGTAAGA	TTCAAAGATT	CTTGTCTCAA	CCATTTGCTG	TCGCTGAAGT	1200
	TTTCACTGGT	ATTCCAGGTA	AATTGGTTAG	ATTGTCTGAA	ACTGTCAAGT	1250
	CATTCAAGGA	AGTCTTGGA	GGTAAGTACG	ATAACTTGCC	AGAAAAT	1297

15

2) INFORMATION FOR SEQ ID NO: 473

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1285 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida rugosa*

(B) STRAIN: ATCC 96275

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473

	CCAGTTTGGC	AACGACCTCC	CTGCCATTTT	GAACGCCCTC	ACTCTTCAGC	50
	GTGAAGACGG	TAACAAGCTT	GTTCTTGAGG	TTGCCCAGCA	TCTCGGTGAG	100
35	AACACCGTCC	GTACCATTCG	TATGGACGGT	ACCGAGGGTT	TGGTGCGTGG	150
	CACTGGTGTC	CACGACACCG	GACACCCCAT	CATGACTCCC	GTCGGTGACG	200
	GTACCCTGGG	ACGTATTCTT	AACGTCACCG	GTGACCCTGT	AGACGAGCGT	250
	GGTCCCGTCA	AGACTGACAA	GTTCCGCCCC	ATCCACGCCG	AGGCCCTGCT	300
	CTTCGATGAG	CAGGCTACCA	GTGCCGAGGT	TCTTGAGACC	GGTATCAAGG	350
40	TTGTCGACTT	GCTCGCTCCT	TACGCCAAGG	GTGGTAAGAT	TGGTTTGTTC	400
	GGTGGTGCCG	GTGTCGGCAA	GACCGTCTTC	ATCCAGGAGC	TGATTAACAA	450
	CATCGCCAAG	GCCCACGGTG	GTTACTCCGT	GTTCACTGGT	GTCGGTGAGC	500
	GTACTCGTGA	GGGTAACGAT	TTGTACAAGG	AAATGATCGA	GTCCGGTGTC	550
	ATCAACCTCG	ATGGTGAGTC	CAAGGTCGCC	TTGGTGTTCC	GTCAGATGAA	600
45	CGAGCCCCCT	GGAGCCCGTG	CCCGTGTCGC	CCTTACCGGT	CTTACCATCG	650
	CTGAGTATTT	CCGTGATGAG	GAGGGTAAGG	ATGTCTTGTT	GTTGCTTGAC	700
	AACATTTTCC	GCTTCACTCA	GGCCGGTTCT	GAGGTGTCCG	CCTTGCTTGG	750
	TCGTATTCCT	TCCGCTGTCG	GTTACCAGCC	TACCCTGGCC	ACCGATATGG	800
	GTGCCCTTCA	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	CGTTACATCC	850
50	GTCCAGGCCG	TCTACGTCCC	TGCCGATGAT	TTGACTGATC	CCGCCCTGCT	900
	CACCACCTTC	GCCCATTTGG	ATGCCACCAC	TGTCTTGTCT	CGTGCCATCT	950
	CTGAGTTGGG	TATCTACCCC	GCTGTCGACC	CTCTCGACTC	CAAGTCCCGT	1000
	CTTCTTGACG	CCGCTGTCGT	TGGTCAGGAG	CACTACGATA	CTGCCACCTC	1050
	CGTTCAGCAG	ACTTTGCAGG	CTTACAAGTC	TTTGCAGGAT	ATCATTGCCA	1100
55	TTCTTGGTAT	GGATGAGTTG	TCCGAGTCTG	ACAAGCTCAC	CGTCGAGCGT	1150
	GCTCGTAAGA	TCCAGCGTTT	CCTCTCCCAG	CCTTTCGCTG	TTGCTGAGGT	1200
	CTTCACTGGT	ATTCAGGGCC	GTCTTGTTCC	TCTCAAGGAC	ACTGTCCGCT	1250
	CCTTCAAGGA	GATTCTCGAA	GGTAAGTACG	ATGCT		1285

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2) INFORMATION FOR SEQ ID NO: 474

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474

	TTGAACAAGG	TCAATTGCCA	GCTATTTTGA	ACGCTTTTGA	AATCGACACT	50
	CCAGAAGGAA	AGTTGGTTTT	GGAAGTCGCT	CAACATTTGG	GTGAAAACAC	100
20	TGTCAGAACC	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	CGTGGTGAAA	150
	ACGTTTCTGA	CACTGGTGCT	CCAATTTCCG	TCCCAGTTGG	TAGAGAAACC	200
	TTGGGTAGAA	TTATCAACGT	TATTGGTGAG	CCAATTGACG	AAAGAGGTCC	250
	AATCAACTCC	AAGATGAGAA	AGCCAATTCA	TGCTGATCCT	CCATTATTCG	300
	TTGAACAATC	CACTGCTGCT	GAAGTTTTGG	AAACTGGTAT	CAAGGTTGTC	350
25	GACTTGTTGG	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTCCGGTGG	400
	TGCCGGTGTC	GGTAAGACCG	TTTTCATCCA	AGAATTGATT	AACAACATTG	450
	CCAAGGCTCA	TGGTGGTTTC	TCTGTCTTCA	CTGGTGTCGG	TGAAAGAACC	500
	AGAGAAGGTA	ACGATTTGTA	CCGTGAAATG	AAGGAAACTG	GTGTTATCAA	550
	CTTGGAAGGT	GATTCTAAGG	TCGCGTTGGT	TTTCGGTCAA	ATGAACGAAC	600
30	CTCCTGGAGC	TAGAGCTAGA	GTCGCCTTGA	CTGGTTTGAC	CATCGCTGAA	650
	TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTTA	TCGACAACAT	700
	TTTCAGATTC	ACACAAGCCG	GTTCCGAAGT	GTCCGCTTTG	TTGGGTCGTA	750
	TTCCATCCGC	TGTCGGTTAT	CAACCAACTT	TGGCCACCGA	TATGGGTTTG	800
	TTGCAAGAAA	GAATTACTAC	CACCAAGAAG	GGTTCCGTCA	CTTCTGTCCA	850
35	AGCCGTTTAC	GTGCCAGCTG	ATGATTTGAC	TGATCCTGCT	CCAGCTACCA	900
	CTTTCGCGCA	TTTGGATGCC	ACCACTGTGT	TGTCCAGAGG	TATCTCTGAA	950
	TTGGGTATCT	ACCCAGCTGT	CGATCCTTTG	GATTCCAAAT	CTAGATTGTT	1000
	GGATGCTGCC	GTCGTTGGTC	AAGAACATTA	CGATGTCGCT	ACTCAAGTTC	1050
	AACAAACTTT	GCAAGCTTAC	AAGTCTTTGC	AAGATATCAT	TGCCATTTTG	1100
40	GGTATGGATG	AATTGTCCGA	ACAAGATAAG	TTGACCGTCG	AAAGAGCTAG	1150
	AAAGATTCAA	AGATTCTTGT	CTCAACCTTT	CGCTGTGCGT	GAAGTCTTCA	1200
	CTGGTATCCC	AGGTAGATTG	GTCAGATTAA	AGGACACCAT	CTCTTCTTTC	1250
	AAGGCTGTCT	TGGACGGTAA	GTACGATCAC	TTG		1283

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2) INFORMATION FOR SEQ ID NO: 475

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1290 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 13803

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475

	CGACGAAGGT	AACTTGCCAG	CTATTTTGAA	TGCTTTGACT	TTGAAGAACG	50
	GTGACCAAGA	CTTGGTTTTG	GAAGTTGCTC	AACATTTGGG	TGAAAACACC	100
5	GTCAGGGCTA	TTGCTATGGA	TGGTACCGAA	GGTTTAGTCA	GAGGTACTGC	150
	TGTCACTGAT	ACCGGTGCTC	CAATTTCTGT	CCCAGTTGGT	AGAGGTACCT	200
	TGGGTAGAAT	TATCAACGTT	GTTGGTGAAC	CAATTGATGA	CAGAGGTCCA	250
	ATTGAATGTA	AGGAAAGAAA	GCCAATTAC	GCTGAACCAC	CTTCATTTCGT	300
	TGAACAATCT	ACTGCTGCCG	AAATTTTGGA	AACCGGTATT	AAGGTTGTCTG	350
10	ATTTGTTGGC	TCCTTACGCT	AGAGGTGGTA	AGATTGGTTT	GTTTCGGTGGT	400
	GCTGGTGTCTG	GTAAAACCGT	CTTCATCCAA	GAATTGATTA	ACAACATTGC	450
	CAAAGCTCAT	GGTGGTTTCT	CTGTCTTTAC	CGGTGTCGGT	GAAAGAACCA	500
	GAGAAGGTAA	CGATTTGTAC	CGTGAAATGA	AAGAACTGG	TGTCATCAAC	550
	TTGGAAGGTG	ACTCCAAGGT	CGCCTTGGTC	TTCGGTCAAA	TGAACGAACC	600
15	ACCTGGTGCT	AGAGCTAGAG	TTGCTTTGAC	TGGTTTGACC	ATTGCTGAAT	650
	ACTTCAGAGA	TGAAGAAGGT	CAAGATGTCT	TGTTGTTCAT	TGACAACATT	700
	TTCAGATTCA	CCCAAGCTGG	TTCCGAAGTG	TCTGCTTTGT	TGGGTCGTAT	750
	TCCATCTGCT	GTCGGTTATC	AACCAACCTT	GGCCACTGAT	ATGGGTCTTT	800
	TGCAAGAACG	TATTACCACC	ACCAAGAAAG	GTTCTGTTAC	TTCTGTCCAA	850
20	GCTGTTTATG	TCCCAGCCGA	TGATTTAACC	GATCCAGCTC	CAGCTACCAC	900
	CTTCGCTCAC	TTGGATGCCA	CTACTGTCTT	GTCTAGAGGT	ATTTCTGAAT	950
	TGGGTATTTA	CCCAGCTGTC	GATCCATTGG	ATTCTAAATC	CAGATTATTG	1000
	GATGCTACTG	TTGTTGGTCA	AGAACATTAT	GATGTTGCCA	CTGGTGTTCA	1050
	ACAAACTTTA	CAAGCTTACA	AGTCCTTGCA	AGATATCATT	GCTATTTTGG	1100
25	GTATGGATGA	ATTGTCCGAA	GCCGATAAAT	TGACTGTCTGA	AAGAGCTCGT	1150
	AAGATTCAAA	GATTCTTGTC	CCAACCATT	GCTGTTGCCG	AAGTTTTTCA	1200
	TGGTATCCCA	GGTAGATTGG	TTAGATTACA	AGATACTGTT	AAATCTTTCA	1250
	AAGATGTCTT	GGAAGGTAAA	TACGATCACT	TGCCAGAAAA		1290

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2) INFORMATION FOR SEQ ID NO: 476

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1267 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida utilis*
 (B) STRAIN: Csp 388

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476

	TTTGAACGCC	CTTGAGATCA	AGAACCACGA	GTCTGGAAGA	TTGGTCCTCG	50
	AGGTTGCCCA	GCACTTGGGT	GAGAACACTG	TCAGAACTAT	TGCCATGGAT	100
50	GGTACCGAAG	GTCTCGTCCG	TGGTGAGTCT	GTTGTTGACA	CCGGTTCTCC	150
	AATTACTGTC	CCAGTTGGTC	GTGAGACCTT	GGGTCGTATC	ATCAACGTTA	200
	TTGGTGAGCC	AATTGATGAG	CGTGGTCCAA	TCAACACCAA	GCACAGAAAC	250
	CCAATTCACG	CTGAGCCACC	ATCCTTCGCT	GAGCAGTCTA	CTGCTGCTGA	300
	GGTTTTGGAG	ACTGGTATCA	AGGTTGTCTG	CCTTCTCGCC	CCATACGCCA	350
55	GAGGTGGTAA	GATTGGTCTC	TTTGGTGGTG	CCGGTGTCTG	TAAGACCGTT	400
	TTCATCCAGG	AGTTGATTAA	CAACATTGCC	AAGGCCACG	GTGGTTTCTC	450
	TGTTTTACAC	GGTGTCGGTG	AGAGAACCAG	AGAGGGTAAC	GATTTGTACC	500
	GTGAGATGAA	GGAGACTGGT	GTCATCAATC	TCGAGGGTGA	GTCCAAGGTT	550
	GCTCTCGTCT	TCGGTCAGAT	GAACGAGCCA	CCAGGTGCCC	GTGCCCCTGT	600
60	CGCTTTGACC	GGTTTGACCA	TTGCTGAGTA	CTTCAGAGAT	GAGGAGGGTC	650

	AGGATGTCTT	GTTGTTTATT	GACAACATTT	TCAGATTCAC	CCAGGCCGGT	700
	TCCGAGGTGT	CTGCCTTGCT	TGGTCGTATT	CCATCCGCTG	TCGGTTACCA	750
	GCCAACTTTG	GCCACCGATA	TGGGTTTGTT	GCAGGAGAGA	ATTACCACCA	800
	CCCAGAAGGG	TTCCGTCACT	TCTGTCCAGG	CCGTTTACGT	CCCAGCTGAT	850
5	GATTTGACTG	ATCCTGCTCC	AGCCACCACT	TTCGCCCCACT	TGGACGCCAC	900
	CACTGTGTTG	TCCCGTGGTA	TCTCTGAGTT	GGGTATTTAC	CCAGCTGTCG	950
	ACCCATTGGA	CTCCAAGTCC	AGATTGTTGG	ACGCTGCCGT	TGTTGGTGAC	1000
	GAGCACTACA	ACACCGCCAC	CGATGTCCAG	CAGACCCTTC	AGGCTTACAA	1050
	GTCTCTCCAG	GATATCATTG	CTATTTTGGG	TATGGATGAG	TTGTCTGAGG	1100
10	CTGACAAGTT	GACTGTGCGAG	AGAGCCAGAA	AGATTCAGCG	TTTCCTTTCC	1150
	CAGCCATTCTG	CTGTGCTGA	GGTTTTCCACC	GGTATCCCAG	GTAGATTGGT	1200
	TAGACTTCAG	GACACCATCA	AGTCCTTCAG	AGAGGTTTTG	GACGGTAAGT	1250
	ACGACCACTT	GCCAGAG				1267

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2) INFORMATION FOR SEQ ID NO: 477

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1296 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*
 (B) STRAIN: ATCC 28269

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477

	CCAATTGAC	GAAGGTAGCT	TGCCAGCTAT	CTTGAACGCC	TTGACCTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCCCAACA	CTTGGGTGAA	100
35	AACACTGTCA	GAGCTATTGC	TATGGATGGT	ACCGAAGGTT	TGGTCAGAGG	150
	TACTGCTGTC	ACTGACACCG	GTGCTCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
	GTACCTTGGG	TAGAATCATC	AACGTTGTTG	GTGAACCAAT	TGACGACAGA	250
	GGTCCAATTG	AATGTAAGGA	AAGAAAGCCA	ATTCACGCTG	AACCACCTTC	300
	TTTCGTTGAA	CAATCCACTG	CTGCCGAAAT	TTTGGAACCC	GGTATCAAGG	350
40	TTGTCGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTC	400
	GGTGGTGCCG	GTGTCGGTAA	GACTGTCTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCCCATGGTG	GTTTCTCTGT	CTTCACTGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTGCGC	TTGGTTTTTCG	GTCAAATGAA	600
45	CGAACCACCT	GGTGCTAGAG	CTAGAGTTGC	TTTGACTGGT	TTGACCATTG	650
	CCGAATACTT	CAGAGACGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCCGGTTCC	GAAGTGCTCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCTGCCGTCG	GTTATCAACC	AACCTTGGCC	ACCGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
50	GTCCAAGCTG	TCTATGTCCC	AGCCGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACCACCTTC	GCTCACTTGG	ATGCCACTAC	TGTCTTGTCT	AGAGGTATTT	950
	CCGAATTGGG	TATCTACCCA	GCTGTGCGATC	CATTGGACTC	CAAGTCCAGA	1000
	TTGTTGGATG	CTGCTGTTGT	TGGTCAAGAA	CATTACGATG	TTGCCACTGG	1050
	TGTCCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
55	TTTTGGGTAT	GGATGAATTG	TCTGAATCCG	ATAAGTTGAC	TGTGAAAGA	1150
	GCTCGTAAGA	TCCAAAGATT	CTTGTCGCAA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	GATTAGTTAG	ATTGCTGGAA	ACCGTCCAAT	1250
	CTTTCAAAGA	CGTCTTGGCT	GGTAAATACG	ATCACTTGCC	AGAAAA	1296

60

2) INFORMATION FOR SEQ ID NO: 478

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1295 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478

	TCAATTCGAG	CAAGGCAACC	TCCCTGCCAT	CTTGAACGCT	CTCACCTTGA	50
	AGAATGGTGA	CAACGACTTG	GTTTTGGAAG	TTGCCCAGCA	CTTGGGTGAG	100
20	AACACCGTCA	GAGCCATTGC	CATGGATGGT	ACCGAGGGTT	TGGTTAGAGG	150
	TGCGTCCGTC	AAGGACACTG	GCGCCCCTAT	CTCGGTCCCC	GTTGGCCGCG	200
	GGACTTTGGG	TCGTATCATC	AACGTCACCG	GTGACCCCAT	TGACGAGAGA	250
	GGTCCCATCG	AGCTGACCCA	GAGAAACCCT	ATCCACGCCG	ACCCCCCTC	300
	GTTTCGTTGAG	CAGTCCACCA	ACGCTGAGGT	TTTGGAGACT	GGTATCAAGG	350
25	TTGTCGATTT	GTTGGCTCCC	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGTAA	GACCGTCTTC	ATTGAGGAGT	TGATCAACAA	450
	CATCGCCAAG	GCCCACGGTG	GGTTCTCGGT	CTTCACTGGT	GTCGGTGAGA	500
	GAAC TAGAGA	GGGTAACGAC	TTGTACCGTG	AGATGAAGGA	GACCGGTGTC	550
	ATCAACTTGG	AGGGTGACTC	CAAGGTGGCC	TTGGTGTTTCG	GTCAGATGAA	600
30	CGAGCCCCCT	GGAGCCAGAG	CCAGAGTCGC	CTTGACCGGG	TTGACCATTG	650
	CCGAATACTT	TAGAGACGAG	GAGGGTCAGG	ATGTGTTGTT	GTTTCGTCGAC	700
	AACATCTTCA	GATTCACCCA	AGCTGGTTCG	GAGGTGTCGG	CCTTGTTGGG	750
	TCGTATTCCC	TCTGCCGTCG	GTTACCAGCC	CACCTTGGCA	ACTGATATGG	800
	GATTGTTGCA	GGAGCGTATC	ACCACGACCA	AGAAGGGTTC	CGTCACCTCA	850
35	GTGCAGGCCG	TCTACGTCCC	CGCTGATGAC	TTGACTGACC	CTGCTCCCGC	900
	CACCACCTTT	GCCCACTTGG	ACGCCACCAC	CGTGTTGTCC	AGAGGTATCT	950
	CTGAGTTGGG	TATCTACCCC	GCCGTCGACC	CCTTGGA CTC	CAAATCGAGA	1000
	TTGTTGGACG	CTGCCGTGGT	CGGTCAGGAG	CACTACGATG	TTGCCTCGAA	1050
	CGTCCAGCAG	ACCTTGCAGG	CCTACAAGTC	CTTGCAGGAT	ATCATTGCCA	1100
40	TTTTTGGGTAT	GGATGAGTTG	TCCGAGGCTG	ACAAGTTGAC	CGTTGAGAGA	1150
	GCCAGAAAGA	TCCAGAGATT	CTTGTCGCAG	CCCTTCGCTG	TTGCCGAGGT	1200
	TTTCACTGGT	ATCAAGGGTA	GATTGGTCAG	ATTGGAGGAC	ACCGTCAGAT	1250
	CTTTCAAGGA	GGTTTTGGAG	GGTAAGTACG	ACCACTTGCC	CGAGA	1295

45

2) INFORMATION FOR SEQ ID NO: 479

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479

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5   TTCAGGAATT GATTGTAAGT TCTGTTATCA ACTAAAGCCG ACAGCGGTTG      50
    CTGATATGCT CTAGAACAAC ATTGCTAAGG CTCACGGTGG TTACTCCGTG      100
    TTCACTGGTG TCGGTGAGCG TACCCGTGAG GGTAACGATT TGTACCATGA      150
    AATGCAAGAG ACCCGTGTCA TTCAACTCGA CGGAGAGTCC AAGGTCGCTC      200
    TTGTCTTCGG TCAAATGAAC GAGCCCCCTG GTGCCCCGTGC CCGTGTTGCC      250
    CTTACCGGTT TGACCATTCG TGAATACTTC CGTGACGAGG AAGGCCAAGA      300
    CGGTAGGCTT CATGCTTCTA TCGCTAGGGG CGTGTGATAC AGGAGGCTAA      350
10  TCGCTTTTCT AGTGCTTCTC TTTATTGACA ACATTTTCCG TTTCACTCAA      400
    GCTGGTTCTG AAGTGTCTGC CTTGCTCGGT CGTATTCCTT CCGCTGTCGG      450
    TTACCAACCT ACTCTCGCCG TCGACATGGG TGTTATGCAG GAACGTATCA      500
    CCACCACCAC CAAGGGATCC ATTACTTCAG TGCA                        534

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15

2) INFORMATION FOR SEQ ID NO: 480

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20  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 494 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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25 (ii) MOLECULE TYPE: Genomic DNA

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    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Cryptococcus albidus
    (B) STRAIN: ATCC 66030

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480

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    CGTCTTGATT CAAGAATTGA TCAACAACAT CGCCAAGGCC CACGGTGGTT      50
    ACTCGGTCTT CACCGGTGTC GGTGAGCGAA CTCGAGAGGG TAACGATCTG      100
35  TACCACGAAG TGAGTTGCGC CGTCCGAGTG TTTCCCGGGG AATCGCAAGA      150
    CTGATGTTGT CCCTTCTTCT CAGATGAGGG AAACCGGTGT CATCAACCTC      200
    GAGGGTGACT CCAAGGTCGC CTTGGTCTTC GGTCAGATGA ACGAGCCCCC      250
    TGGAGCCCGA GCCCGAGTCG CCTTGACCGG TTTGACCATT GCCGAATACT      300
    TCCGAGACGA GGAGGGTCAG GATGTCTTGT TGTTCAATTGA CAACATTTTC      350
40  CGATTACACC AAGCCGGTTC CGAAGTGTCC GCCTTGTTGG GTCGTATCCC      400
    CTCCGCCGTC GGTTACCAGC CCACTCTGTC CACCGACATG GGTACCATGC      450
    AGGAGCGAAT TACCACCACC AAGAAGGGTT CCATCACTTC CGTC            494

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45

2) INFORMATION FOR SEQ ID NO: 481

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50  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 415 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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55 (ii) MOLECULE TYPE: Genomic DNA

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    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Fusarium oxysporum
    (B) STRAIN: WSA-212

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60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481

	TTCAGGAGCT	TATCAACAAC	ATCGCCAAGG	CCCACGGTGG	TTACTCCGTC	50
	TTCACTGGTG	TCGGTGAGCG	AACTCGTGAG	GGTAACGATC	TGTACCACGA	100
	AATGCAGGAG	ACTTCCGTCA	TTCAGCTTGA	TGGCGAGTCC	AAGGTCGCCC	150
5	TGGTCTTCGG	TCAGATGAAC	GAGCCCCCTG	GAGCTCGTGC	CCGTGTCGCC	200
	CTTACCGGTC	TTACTGTAGC	TGAATACTTC	AGAGATGAGG	AGGGTCAGGA	250
	CGTGCTGCTC	TTCATTGACA	ACATTTTCCG	ATTCACTCAG	GCCGGTTCCG	300
	AGGTGTCTGC	CCTTCTCGGT	CGTATCCCCT	CTGCCGTCCG	TTACCAGCCC	350
	ACCCTCGCCG	TCGACATGGG	TGGTATGCAA	GAGCGTATTA	CCACCACCAC	400
10	CAAGGGTTCC	ATTAC				415

2) INFORMATION FOR SEQ ID NO: 482

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Geotrichum* spp.
 (B) STRAIN: Lev-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482

30	AGGACAACCT	CCCCGCTATT	CTTAACGCTC	TTGAGCTTAA	GAGAGATAAC	50
	GGTGAGAAGC	TCGTTCTCGA	GGTTGCCCAG	CATCTGGGTG	AGAACACTGT	100
	CCGTACTATT	GCTATGGACG	GTA CTGAGGG	TCTCGTCCGT	GGTCAGCCCCG	150
	TTGTTGACAC	CGGTGCCCCC	ATTACCATT C	CCGTTGGTCG	TGGTACTCTT	200
	GGTAGAATTA	TCAACGTCAT	TGGTGAGCCC	ATCGATGAGC	GTGGACCCAT	250
35	TGAGGCTACC	AAGTACCTCC	CCATCCACAC	CGAGCCCCCC	ACCTTCGCTG	300
	AGCAGTCTAC	CTCCGCTGAG	GTTCTTGAGA	CTGGTATCAA	GGTTGTGCGAT	350
	CTCCTTGCCC	CCTACGCCCG	TGGTGCTAAG	ATTGGTCTCT	TCGGTGGTGC	400
	CGGTGTCGGT	AAGACCGTTT	TCATTCAGGA	GCTGATTAAC	AACATTGCCA	450
	AGGCCCATGG	TGGTTTCTCC	GTTTTCAACG	GTGTCGGTGA	GAGAACCCGT	500
40	GAGGGTAACG	ATTTGTACCG	TGAGATGAAG	GAGACCGGTG	TCATCAACCT	550
	CGAGGGTGAG	TCTAAGGTCG	CTCTCGTTTT	CGGTCAGATG	AACGAGCCCC	600
	CTGGAGCCCC	TGCCCGTGTT	GCTCTTACTG	GTCTTACCAT	TGCTGAGTAC	650
	TTCCGTGATG	AGGAGGGTCA	GGATGTGTTG	CTCTTCGTTG	ACAACATTTT	700
	CCGTTTCACT	CAGGCCGGTT	CCGAGGTGTC	TGCCCTTTTG	GGTCGTATTC	750
45	CCTCCGCTGT	CGGTTACCAG	CCCACCCTTG	CCACTGATAT	GGGTGCCCTG	800
	CAAGAGCGTA	TTACCACCAC	CCAGAAGGGT	TCCGTCACTT	CCGTCCAGGC	850
	CGTCTACGTC	CCTGCCGATG	ATTTGACCGA	TCCTGCCCCCT	GCTACCACCT	900
	TCGCCCATT T	GGATGCCACC	ACCGTCTTGT	CGCGTTCCAT	TTCTGAGTTG	950
	GGTATCTACC	CCGCTGTCGA	TCCCCTTGAT	TCCAAGTCTC	GTCTTTTGGA	1000
50	TATCACCGTC	GTTGGCCAGG	AGCACTACGA	TGTTGCTACC	CAGGTCCAGC	1050
	AGACCCTCCA	GTCCTACAAG	TCTCTTCAGG	ATATCATTGC	CATTTTGGGT	1100
	ATGGATGAGT	TGTCTGAGGC	TGATAAGCTT	ACTGTCGAGC	GTGCCCCGTAA	1150
	GATCCAGAGA	TTCCTTTCCC	AGCCCTTCAC	TGTCGCTGAG	GTTTTCACTG	1200
	GTATCGAGGG	CCGTCTCGTT	CCTTTGAAGG	AACTGTTCG	CTCTTTCAAG	1250
55	GAGATCCTTG	AGGGCAAGTA	CGACCACCTC	C		1281

2) INFORMATION FOR SEQ ID NO: 483

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G185A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483

15	ATTCAAGAAT	TGATCGTACG	TTCCTCCGCC	CCACACACGA	TCAATGGAGA	50
	AAGAAACAAA	TTTTTTGGGA	GTGGTCATTT	TTTCTAATAA	TTCGAATAGA	100
	ACAACATTGC	CAAAGCCCAC	GGTGGTTACT	CCGTGTTCAC	TGGTGTCGGC	150
	GAGCGGACCC	GTGAAGGAAA	TGACTTGTAC	CACGAAATGC	AGGAAACCCG	200
	TGTTATCCAG	CTCGATGGAG	AGTCCAAGGT	CGCCCTCGTT	TTCGGTCAGA	250
20	TGAACGAGCC	TCCCGGAGCC	CGTGCCCGTG	TTGCCCTCAC	TGGTCTGACC	300
	GTTGCCGAGT	ACTTCCGTGA	CGAGGAAGGC	CAAGACGGTA	TGTATAAGTA	350
	TACACCGTAG	CAAATCAACA	CAGAGCTTCA	CTCACGCTCG	GATTTAGTGC	400
	TTCTCTTCAT	CGACAACATT	TTCCGCTTCA	CTCAGGCCGG	TTCCGAAGTG	450
	TCTGCCCTGC	TCGGCCGTAT	TCCCTCCGCC	GTCGGTTACC	AACCCACCCT	500
25	CGCCGTGGAC	ATGGGTGGTA	TGCAGGAACG	TATCACC ACT	ACCACCAAGG	550
	GCTCCATCAC	CTCTGTGCAR	GCCGTCTACG	TCCCCG		586

2) INFORMATION FOR SEQ ID NO: 484

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484

45	GCGTGGCCAG	AAGGTCATTG	ACACTGGTGC	TCCCATCACC	ATCCCCGTCG	50
	GTGGTGCCAC	ACTGGGTCGT	ATTCTGAACG	TCACGGGTGA	CCCTATTGAC	100
	GAGCGTGGCC	CCGTTAAGAC	TGACGTTTTC	CGCCCCATTC	ACCGTGACCC	150
	CCCTGCCTTT	GTCGAGCAGT	CGACTGATGC	CGAGATTCTC	GAGACTGGTA	200
50	TCAAAGTCGT	TGACCTGATT	GCCCCTTACG	CCC GTGGTGG	TAAGATTGGT	250
	CTGTTTCGGTG	GTGCCGGTGT	CGGTAAGACC	GTGCTTATCC	AGGAGCTCAT	300
	CAACAACATC	GCCAAGGCC	ACGGTGGTTT	CTCCGTGTTC	ACTGGTGTCG	350
	GTGAGCGTAC	TCGTGAGGGT	AACGATTTGT	ACCACGAGAT	GATTGAAACC	400
	GGTGTCATTA	ACCTCGAGGG	TGACTCGAAG	GTGGCTCTGG	TGTTCGGTCA	450
55	GATGAACGAG	CCCCCGGGTG	CCCGTGCGCG	TGTCGCTCTT	ACTGGTCTGA	500
	CTGTGGCCGA	GTACTTCCGT	GACGACGAGG	GCCAGGATGT	GCTGCTGTTC	550
	ATTGACAACA	TTTTCCGTTT	CACCCAGGCC	GGTTCGGAGA	CTTCGGCTCT	600
	GCTGGGTCGT	ATCCCTTCGT	CGGTCGGTTA	CCAGCCCACT	TTGTCGACCG	650
	ATATGGGTGC	CATGCAGGAG	CGTATCACCA	CCACCAAGAA	GGGTTCGATT	700
60	ACGTCGGTGC	AGGCCGTCTA	CGTGCCCGCC	GATGATGTCA	CTGACCCTGC	750

	CCCTGCCACT	ACCTTCGCCC	ACCTTGACGC	TACCACTGTG	CTTGACCGTT	800
	CGATCGCTGA	GCTGGGTATC	TACCCCGCTG	TTGACCCGTT	GAACTCGAAC	850
	TCGCGTATGC	TTGACCCCGC	TATTGTGGGT	CAGGAGCACT	ACGACGTGGC	900
	CTCTGGCGTG	CAGAAGCTGC	TCCAGGACTA	CAAGTCGCTT	CAAGATATCA	950
5	TTGCCATTCT	GGGTATGGAT	GAGCTTTCTG	AGGAGGACAA	GCTCACTGTC	1000
	GAGCGTGCCC	GTAAGATGCA	GCGTTTCATG	TCGCAGCCTT	TCGCTGTCGC	1050
	CCAGGTCTTT	ACTGGTATCG	AAGGTCGTCT	TGTTGCCCTG	AAGGACACGA	1100
	TCAAGGCCTG	CAAGGAGATC	CTGTCGGGCA	AGCACGACAA	CCTCC	1145

10

2) INFORMATION FOR SEQ ID NO: 485

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1261 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia pachydermatis*
 (B) STRAIN: ATCC 42756

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485

	TCCCGCCATC	TTCAACGCCC	TGGAGGTCCA	GGACATGAAG	AACGGTGGCC	50
	GCCTTGTTCT	GGAGGTTGCC	CAGCACCTTG	GTGAGAACAC	TGTTTCGTTGC	100
30	ATTGCTATGG	ACGGTACCGA	GGGTCTTGTC	CGTGGTCAGA	AGGTCCTTGA	150
	CACTGGTGCC	CCGATCACTA	TCCCTGTCCG	TAACGGTACC	TTGGGCCGYA	200
	TCCTGAACGT	CACTGGTGAG	CCTGTGGATG	AGCGTGGTCC	GGTTAAGACT	250
	GACGTCTACC	GTCCAATCCA	CCGTGAGCCC	CCGGCGTTCC	TTGAGCAGTC	300
	GACTGATGCT	GAGATTCTTG	AGACTGGTAT	CAAGGTGGTC	GACCTGCTCG	350
35	CCCCATACGC	TCGTGGTGGT	AAGATTGGTC	TWTTCCGTGG	TGCYGGTGTY	400
	GGTAAGACCG	TGCTGATTCA	GGAGCTTATC	AACAACATTG	CCAAGGCCCA	450
	CGGTGGTTTC	TCGGTGTTCA	CTGGTGTCGG	TGAGCGTACT	CGTGAGGGTA	500
	ACGATCTGTA	CCATGAAATG	ATTGAGACTG	GTGTCATCAA	CGTTGACGGT	550
	GACTCGAAGG	TCGCTCTCGT	GTTCCGGTCAG	ATGAACGAGC	CCCCGGGTGC	600
40	CCGTGCCCCG	GTCGCCCTGA	CYGGTCTGAC	CATCGCCGAG	TACTTCCGTG	650
	ACGACGAGGG	TCAGGATGTG	CTGCTCTTCA	TTGACAACAT	TTTCCGTTTC	700
	ACTCAGGCTG	GTTCGGAGAC	TTCGGCTCTG	CTGGGTCGTA	TCCCGTCGGC	750
	TGTCGGTTAC	CAGCCKACCC	TTGCCACGGA	TATGGGTGCC	ATGCAGGARC	800
	GTATYACCAC	CACCAAGAAG	GGTTCGATTA	CCTCGGTGCA	GGCYGTTTAC	850
45	GTTCCGGCCG	ACGATGTGAC	TGACCCTGCC	CCGGCCACGA	CCTTCGCCCA	900
	CTTGACGCC	ACCACGGTGT	TGGACCGTTC	GATTGCGYAG	CTGGGTATCT	950
	ACCCGGCCGT	CGACCCGCTG	AACTCGAAGT	CGCGTATGCT	TGACCCGTCA	1000
	ATTGTCGGTG	TGGAGCACTA	CAACGTTGCT	TCGGGTGTCC	AGAAGCTTCT	1050
	YCAGGACTAC	AAGTCGCTCC	AAGATATCAT	TGCCATTCTG	GGTATGGATG	1100
50	AGTTGTCCGA	GGAGGACAAG	CTCACTGTCC	AGCGTGCCCG	TAAGATGCAG	1150
	CGTTTCCTGT	CGCAGCCTTT	CGCTGTGGCC	CAGGTCTTCA	CTGGTATCGA	1200
	GGGTCGTCTT	GTGTCGCTCA	AGGACACCAT	CAACGCCTGC	AAGGAGATTC	1250
	TGTCCGGTAA	G				1261

55

2) INFORMATION FOR SEQ ID NO: 486

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1282 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Metschnikowia pulcherrima*

(B) STRAIN: DSM 70336

10

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 486

	AGGAGGGCAA	CTTGCCAGCT	ATCTTCAACG	CTTTGACGTT	GAAGAACGGC	50
	GACCAGAAGT	TGGTCTTGGA	GGTGGCCCAG	CACTTGGGTG	AGAACACCGT	100
15	CAGAACCATT	GCCATGGACG	GTACCGAGGG	TTTGGTCAGA	GGCGCCTCTG	150
	TCACCGACAC	YGGTGCCCCT	ATCTCCGTGC	CTGTCGGCCG	TGAGACCTTG	200
	GGTCGTATTA	TCAATGTTGT	TGGTGAGCCA	ATCGACGAGA	GAGGCCCAAT	250
	CAACACCAAG	AAGAGAAACC	CTATTCACAC	CGACCCACCT	TCGTTTGTCC	300
	AGCAATCCAC	TTCCGCCGAG	GTCTTGAGAG	CTGGTATCAA	GGTTGTCGAC	350
20	TTGTTGGCCC	CTTACGCCAG	AGGTGGTAAG	ATTGGTTTGT	TCGGTGGTGC	400
	CGGTGTCGGT	AAGACCGTGT	TCATCCAGGA	GTTGATTAAAC	AACATTGCCA	450
	AGGCCACCGG	TGGTTTCTCC	GTTTTACCCG	GTGTCGGTGA	GAGAACCAGA	500
	GAGGGTAACG	ATTTGTACCG	TGAAATGCAG	GAGACTGGTG	TCATCAACTT	550
	CGAGGGTGAC	TCCAAGGTCG	CCTTGTTTTT	CGGTCAGATG	AACGAGCCTC	600
25	CAGGAGCTAG	AGCYAGAGTT	GCCTTGACCG	GTTTGACCAT	CGCCGAGTAC	650
	TTCAGAGACG	AGGAGGGTCA	GGATGTGTTG	TTGTTTCGTCG	ACAACATTTT	700
	CAGATTCACC	CAAGCCGGTT	CTGAGGTGTC	TGCCTTGTTG	GGTCGTATTC	750
	CATCCGCTGT	CGGATACCAG	CCAACCTTGG	CCACCGATAT	GGGTGCCTTG	800
	CAGGAGAGAA	TTACCACCAC	CAAGAAGGGT	TCCGTCACCT	CCGTCCAGGC	850
30	CGTCTACGTG	CCAGCCGATG	ACTTGACTGA	CCCTGCGCCA	GCCACCACTT	900
	TCGCCCCTT	GGACGCCACC	ACTGTGTTGT	CCAGAGGTAT	CTCTGAGTTG	950
	GGTATCTACC	CCGCTGTCGA	CCCCTTGAC	TCCAACCTCA	GATTGTTGGA	1000
	CGCCACCGTT	GTTGGCCAGG	AGCACTACGA	CGTCGCCACC	AACGTCCAGC	1050
	AAACTTTACA	AGCTTACAAG	TCCTTGCAGG	ATATCATTCG	CATTTTGGGT	1100
35	ATGGATGAGT	TGTCCGAGAC	CCGACAAGTT	GACCCGTCGA	GAGAGCCAGA	1150
	AAGATCCAGA	AGTTCTTGTC	CCAGCCATTT	GCCGTCGCCG	AGGTTTTCAC	1200
	CGGTATTGAG	GGTAGATTGG	TTAGATTGGA	GGACACCGTT	AGATCCTTTA	1250
	AGGAGGTTTT	GGAAGGTAAG	TACGACCACT	TG		1282

40

2) INFORMATION FOR SEQ ID NO: 487

(i)SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 482 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*

(B) STRAIN: WSA-214

55

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 487

	TGTCTTTATC	CAGGAGTTGA	TTGTACGTCT	TTACCTTTCT	GCCTGACTGT	50
	TTACGACAAC	TAACGAAAGC	GTAGAACAAC	ATTGCCAAGG	CTCACGGTGG	100
60	TTACTCTGTC	TTCATGGTGT	TCGGTGAACG	TACTCGTGAG	GGTAACGATT	150

	TGTACCACGA	AATGCAGGAA	ACTGGTGTCA	TTCAGCTCGA	GGGTGAATCC	200
	AAGGTCGCCC	TCGTGTTCGG	TCAGATGAAC	GAGCCCCCCG	GTGCCCCGTGC	250
	CCGTGTCGCT	CTTACTGGTT	TGACCATTGC	CGAGTACTTC	CGTGACGAGG	300
	AAGGTCAGGA	CGTGCTTCTC	TTCATTGACA	ACATTTTCCG	TTTCACTCAG	350
5	GCCGGTTCTG	AGGTGTCTGC	CCTTCTGGGT	CGTATCCCCT	CTGCCGTCGG	400
	TTACCAGCCC	ACCCTTGCCG	TCGACATGGG	TATCATGCAG	GAGCGTATTA	450
	CCACCACCAC	CAAGGGTTCC	ATCACCTCCG	TC		482

10

2) INFORMATION FOR SEQ ID NO: 488

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488

	TCGAACAAGG	TAACCTACCA	GCTATCTTGA	ATGCTTTAGA	AATCAAAACC	50
	CCAAGTGGTA	CTCCATTAGT	TTTAGAAGTT	GCTCAACATT	TAGGTGAAAA	100
	CACTGTCAGA	ACTATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTCGTGGTG	150
30	AACAAGTTAC	TGATACTGGT	TCTCCAATCA	CTGTCCCAGT	TGGTCGTGAA	200
	ACTTTAGGTC	GTATTATCAA	CGTTGTTGGT	GAACCAATTG	ATGAACGTGG	250
	TCCAATTAAC	ACCAAACAAA	GAAACCCAAT	TCACGCTGAA	CCACCTTCAT	300
	TCAGTGAACA	ATCAACTGCT	GCTGAAGTTT	TAGAAACTGG	TATCAAAGTT	350
	GTYGATTTAT	TAGCTCCATA	CGCTAGAGGT	GGTAAAATTG	GTTTATTTCGG	400
35	TGGTGCCGGT	GTCGGTAAAA	CTGTCTTTAT	CCAAGAATTG	ATTAACAACA	450
	TTGCTAAAGC	TCATGGTGGT	TTCTCAGTTT	TCACCGGTGT	TGGTGAAAGA	500
	ACCAGAGAAG	GTAACGATTT	ATACCGTGAA	ATGAAAGAAA	CTGGTGTTAT	550
	TAACCTGGAA	GGTGATTCTA	AGGTCGCTTT	AGTTTTTCGGT	CAAATGAATG	600
	AACCACCAGG	TGCTAGAGCT	CGTGTTGCTT	TAACCTGGTTT	GACCATTGCT	650
40	GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCGTTGATAA	700
	CATTTTCAGA	TTCACCCAAG	CCGGTTCAGA	AGTTTCTGCC	TTATTAGGTC	750
	GTATTCCATC	TGCTGTCGGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	800
	TTGTTACAAG	AACGTATTAC	CACCACACAA	AAAGGTTTCAG	TTACTTCTGT	850
	CCAAGCTGTT	TATGTCCCAG	CTGATGATTT	AACAGATCCT	GCTCCAGCTA	900
45	CCACTTTCGC	CCATTGATG	GCTACTACTG	TCTTGCTCTG	TGGTATTTCA	950
	GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCAAGATT	1000
	ATTAGATGCT	TCAGTTGTTG	GTCAAGAACA	TTATGATGTT	GCTACCAACG	1050
	TTCAACAAAC	TTTACAAGCT	TACAAATCTT	TACAAGATAT	TATTGCTATT	1100
	TTAGGTATGG	ATGAATTGTC	TGAACAAGAT	AAATTGACTG	TCGAAAGAGC	1150
50	AAGAAAAATC	CAAAGATTCT	TATCTCAACC	ATTTGCTGTT	GCCGAAGTTT	1200
	TCACTGGTAT	YCCAGGTAGA	TTGGTTAGAT	TAAAAGACAC	TATCAAATCA	1250
	TTCAAAGATG	TTTTGGAAGG	TAAATATGAT	CACTTACCAG		1290

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2) INFORMATION FOR SEQ ID NO: 489

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 bases
 (B) TYPE: Nucleic acid

60

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(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 2149

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489

	CCAATTTCGAA	CAAGGTAAC	TACCAGCTAT	CTTGAATGCT	TTAGAAATCA	50
	AAACCCCAAG	TGGTACTCCA	TTAGTTT TAG	AAGTTGCTCA	ACATTTAGGT	100
	GAAACACTG	TCAGAACTAT	TGCTATGGAT	GGTACTGAAG	GTTTAGTCCG	150
15	TGGTGAACAA	GTTACTGATA	CTGGTTCTCC	AATCACTGTC	CCAGTTGGTC	200
	GTGAAACTTT	AGGTCGTATT	ATCAACGTTG	TTGGTGAACC	AATTGATGAA	250
	CGTGGTCCAA	TTAACACCAA	ACAAAGAAAC	CCAATTCACG	CTGAACCACC	300
	TTCATT CAGT	GAACAATCAA	CTGCTGCTGA	AGTTTTAGAA	ACTGGAATCA	350
	AAGTTGTTGA	TTTATTAGCT	CCATACGCTA	GAGGTGGTAA	AATTGGTTTA	400
20	TTCGGTGGTG	CCGGTGTCGG	TAAAACTGTC	TTTATCCAAG	AATTGATTAA	450
	CAACATTGCT	AAAGCTCATG	GTGGTTTCTC	AGTTTTCACC	GGTGTTGGTG	500
	AAAGAACCAG	AGAAGGTAAC	GATTTATACC	GTGAAATGAA	AGAAACTGGT	550
	GTTATTAACT	TGGAAGGTGA	TTCTAAGGTC	GCTTTAGTTT	TCGGTCAAAT	600
	GAATGAACCA	CCAGGTGCTA	GAGCTCGTGT	TGCTTTAACT	GGTTTGACCA	650
25	TTGCTGAATA	CTTCAGAGAT	GAAGAAGGTC	AAGATGTCTT	GTTATTCGTT	700
	GATAACATTT	TCAGATTCAC	CCAAGCCGGT	TCAGAAGTTT	CTGCCTTATT	750
	AGGTCGTATT	CCATCTGCTG	TCGGTTATCA	ACCAACTTTA	GCAACTGATA	800
	TGGGTTTGTT	ACAAGAACGT	ATTACCACCA	CACAAAAGG	TTCAGTTACT	850
	TCTGTCCAAG	CTGTTTATGT	CCCAGCTGAT	GATTTAACAG	ATCCTGCTCC	900
30	AGCTACCACT	TTCGCCCAT	TGGATGCTAC	TACTGTCTTG	TCTCGTGGTA	950
	TTTCAGAATT	AGGTATTTAC	CCAGCTGTCG	ATCCATTAGA	TTCTAAATCA	1000
	AGATTATTAG	ATGCTTCAGT	TGTTGGTCAA	GAACATTATG	ATGTTGCTAC	1050
	CAACGTTCAA	CAAAC TTTAC	AAGCTTACAA	ATCTTTACAA	GATATTATTG	1100
	CTATTTTAGG	TATGGATGAA	TTGTCTGAAC	AAGATAAATT	GACTGTCGAA	1150
35	AGAGCAAGAA	AAATCCAAAG	ATTCTTATCT	CAACCATTTG	CTGTTGCCGA	1200
	AGTTTTCACT	GGTATCCCAG	GTAGATTGGT	TAGATTAAAA	GACACTATCA	1250
	AATCATTCAA	AGATGTTTTG	GAAGGTAAAT	ATGATCACTT	A	1291

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2) INFORMATION FOR SEQ ID NO: 490

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*
(B) STRAIN: ATCC 10658

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490

	CGTATTGATT	CGTGAGTGGC	CGTTCCCTTA	CAGCAAGCTT	ATAAAGGAGC	50
	GAAAAAGATC	TGACATTCGG	CTTATGTGCT	ATACAGAGGA	ACTCATCAAC	100
	AACGTCGCCA	AGGCTCATGG	TGGTTACTCT	GTCTTCACCG	GTGTCGGAGA	150
60	GCGAACACGT	GAAGGTAACG	ATCTCTACCA	CGAAATGATT	GAAACCGGTG	200

	TCATTTCAGCT	CAAGAACGAC	AAGTCCAAGG	CCGCTCTGGT	CTTCGGACAG	250
	ATGAACGAGC	CCCCCGGAGC	TCGTGCCCCG	GTCGCTCTGA	CCGGTCTCAC	300
	CATCGCCGAG	TACTTCCGTG	ACGTCGAAGG	ACAGGATGTG	CTACTCTTCA	350
	TCGACAAACAT	TTTCCGATTC	ACCCAGGCCG	GTTTCAGAGG	ATCTGCCCTG	400
5	CTCGGACGTA	TCCCATCTGC	TGTCGGATAC	CAGCCCACAC	TCTCAACCGA	450
	TATGGGTGGT	ATGCAAGAGC	GAATCACAAC	CACCAAGAAG	GGTTCGATTA	500
	CCTCCGTC					508

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2) INFORMATION FOR SEQ ID NO: 491

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| | (A) | LENGTH: 686 bases |
| 15 | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- | | | |
|--|-----|---|
| | (A) | ORGANISM: <i>Rhodotorula mucilaginosa</i> |
| | (B) | STRAIN: ATCC 66034 |

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491

	TGTCCTCATT	CAGGAGCTCA	TCAACAACAT	CGCCAAGGCC	CACGGTGGTT	50
	ACTCGGTCTT	CACCGGTGTC	GGCGAGCGTA	CCCGTGAGGG	TAACGGTGAG	100
	TCTCCCCCTT	CAAACCTTTG	GCCGGCTAGT	TGGCGCAGCG	CAAACCTGACG	150
30	CGCGCGCCCT	GTCCAGACTT	GTACCACGAG	ATGATCGAGA	CTGGTGTCAT	200
	CCAGCTCGAG	AACGACAACT	CGAAGTGCGC	TCTCGTGTTT	GGCCAGATGA	250
	ACGAGCCCCC	TGGTGCCCCG	GCCCGTGTCG	CTCTCACTGG	GTTTCGTCCTT	300
	TCTCTCTCTC	GAGCGTCCTG	GCTTGATACG	GAACGCTGAC	ACGTCACGCA	350
	GTCTCACTAT	TGCTGAGTAC	TTCCGTGACG	AGGAGGGCCA	GGACGTGCTC	400
35	CTCTTCATCG	ACAACATCTT	CCGTTTCACC	CAGGGTGAGC	CGCCTCCGCG	450
	GGCATTCTCC	CGTTTCTTTC	GCGCTGACGT	CTGTCCCGTA	TAGCCGGTTC	500
	GGAGGTGTCT	GCCCTTCTCG	GACGTATCCC	GTCCGCTGTC	GGATACCAGC	550
	CGACTCTCTC	GACCGACATG	GGTCAGATGC	AGGAGCGTAT	CACGTAAGTT	600
	TGGCCGCAGC	TCCGTCCGCG	GCGCCCTTTG	TGTCTGACCG	TGTTCCACCG	650
40	CTCAGCACCA	CCAAGAAGGG	CTCGATCACC	TGTGTC		686

45 2) INFORMATION FOR SEQ ID NO: 492

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| | (A) | LENGTH: 625 bases |
| | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Double |
| 50 | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- | | | |
|----|-----|--|
| 55 | (A) | ORGANISM: <i>Sporobolomyces salmonicolor</i> |
| | (B) | STRAIN: ATCC 32311 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492

60	TGTCTTGATT	CAGGAGCTCA	TCAACAACGT	CGCCAAGGCG	CACGGTGGTT	50
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	ACTCCGTTTT	CACCGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGGTGAG	100
	CACACTTTTCG	CCGACCTGGC	CATTCCGGAA	CGTGCGGACT	GACGAGGACC	150
	ACCTCGAACA	GATCTCTACC	ACGAGATGAT	CGAGACCGGT	GTCATTTCAGC	200
	TCGACAACGA	CAAGTCGAAG	ACTGCTCTCG	TCTTCGGCCA	GATGAACGAG	250
5	CCCCCTGGCG	CCCGTGCCCC	TGTCGCTCTT	ACTGGTCTCA	CCATCGCGGA	300
	GTACTTCCGT	GACGACGAGG	GCCAGGACGT	GCTTCTCTTC	ATCGACAACA	350
	TCTTCCGTTT	CACCCAGGGT	ACGTTCGATC	CCGCCCCGTCC	AACACGAATG	400
	TCGTGGTGAC	TGACAACCTG	TTGCGCGTGC	AGCCGGTTCG	GAGGTGTCTG	450
	CCCTTCTCGG	TCGTATCCCC	TCCGCTGTCT	GATACCAGCC	CACTCTCTCG	500
10	ACCGACATGG	GTGGCATGCA	GGAGCGTATC	ACGTACGCC	TCTTCTGCTT	550
	TCTCTCGTTT	CGCTCTGCAT	CGCTCACGCA	TGTTCGCCCC	ACAGCACCAC	600
	CAAGAAGGGT	TCGATCACCT	GTGTC			625

15

2) INFORMATION FOR SEQ ID NO: 493

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1211 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
- (B) STRAIN: WSA-148

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493

	TCTCGTCCGT	GGTGCTAAGG	CCACTGACAC	TGGTTCCCCC	ATTACCATCC	50
	CCGTCGGCCC	CGGTACCCTC	GGTCGCATCA	TGAACGTCAC	CGGTGACCCG	100
35	ATCGACGAGC	GCGGTCCCAT	CAAGACCGAC	AAGTTCCGTC	CCATCCACGC	150
	TGAGGCTCCC	GAGTTCGTTG	ACCAGTCGAC	CACCGCTGAG	GTTCTCGTGA	200
	CTGGTATCAA	GGTCGTGAT	CTGCTTGCTC	CCTACGCCCC	TGGTGGTAAG	250
	ATTGGTCTGT	TTGGCGGTGC	CGGTGTTGGC	AAGACCGTGT	TCATCCAGGA	300
	GCTCATCAAC	AACATCGCCA	AGGCCACCG	TGGTTACTCC	GTCTTCACCG	350
40	GTGTCGGCGA	GCGTACCCGT	GAGGGTAACG	ATCTGTACCA	CGAAATGCAG	400
	GAGACCTCTG	TCATTTCAGCT	TGACGGTGAC	TCCAAGGTCG	CCCTGGTGTT	450
	CGGTCAGATG	AACGAGCCCC	CTGGTGCTCG	TGCCCCGTGTC	GCCTTGACCG	500
	GTTTGACTGT	CGCTGAGTAC	TTCCGTGACG	AGGAGGGCCA	GGATGGTATG	550
	TTTTGAATTA	TTTCCTTGTC	GTACAGTTCC	AAATCGAAGA	ATTACTAACT	600
45	TGTCAGTGCT	TCTCTTCATC	GACAAACATTT	TCCGCTTCAC	CCAGGCCCGT	650
	TCTGAGGTGT	CTGCCCTTCT	GGGTCGTATT	CCCTCCGCTG	TCGGTTACCA	700
	GCCCACGCTC	GCCGTGGACA	TGGGTCTGAT	GCAGGAGCGT	ATTACCACCA	750
	CCCGCAAGGG	CTCAATTACC	TCCGTCCAGG	CCGTCTACGT	GCCCGCTGAC	800
	GATCTGACGG	ATCCCGCCCC	CGCCACCACC	TTCGCCCATC	TGGACGCCAC	850
50	CACTGTGCTG	TCCCGAGGTA	TCTCTGAGCT	GGGTATCTAC	CCCGCTGTCG	900
	ACCCCTCGA	CTCCAAGTCG	CGTATGCTGG	ACCCCGTAT	TGTCGGTGAC	950
	GACCACTACG	AGACCGCCAC	TCGCGTCCAG	CAGATCCTCC	AAGAGTACAA	1000
	GTCGCTGCAG	GACATCATCG	CCATTCTGGG	TATGGACGAG	CTGTCTGAGG	1050
	CCGACAAGCT	TACAGTCGAG	CGTGCTCGTA	AGATCCAGCG	TTTCCTGAGC	1100
55	CAGCCGTTCA	CGGTCGCGCA	GGTCTTCACT	GGTATCGAAG	GCCAGCTGGT	1150
	CGATCTGAAG	GACACTATCG	CTTCGTTCAA	GGCTATCCTG	AGCGGTGAGG	1200
	GTGACAGCCT	T				1211

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2) INFORMATION FOR SEQ ID NO: 494

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1133 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
 (B) STRAIN: ATCC 52550

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494

TCTTGTTAGA GGCACCCCAG TCAAGGACAC TGGTGCTCCA ATTACCATTC 50
 CAGTTGGTAA CGGCACTTTG GGCCGTATCG TCAACGTTCT CGGTGAGCCA 100
 ATTGATGAGC GTGGACCAGT CAAGGCTGAC AAGTTCAGAC CTATTCACGC 150
 20 TGAGCCACCA ACCTTCGCTG ACCAGTCCAC CTCTGCCGAG GTTCTTGAGA 200
 CCGGTATTAA GGTTGTCGAC TTGCTTGCCC CTTATGCCAG AGGTGGTAAG 250
 ATTGGTCTTT TCGGTGGTGC CGGTGTCGGT AAGACTGTGT TCATTCAGGA 300
 GCTTATTAAC AACATTGCTA AGGCCACCGG TGGTTACTCT GTCTTCACTG 350
 GTGTCGGTGA GCGAACTCGT GAAGGTAACG ATTTGTACCA CGAAATGATG 400
 25 GAGACCGGTG TCATCAACCT TGAGGGTGAC TCCAAGGTGT CTCTTGTTGT 450
 CGGTCAGATG AACGAGCCTC CAGGAGCCCG TGCCCGTGTT GCCTTGACCG 500
 GTTTGACCAT TGCCGAGTAC TTCAGAGATG AGGAGGGCCA GGATGTCTTG 550
 TTGTTCAATTG ACAACATTTT CCGATTCACC CAGGCCGGTT CTGAGGTCTC 600
 TGCCTTGTTG GGTCGTATCC CATCTGCCGT CGGTTACCAA CCAACCTTGG 650
 30 CTACTGATAT GGGTGGTCTT CAAGAACGTA TTACCACCAC TCAAAAGGGT 700
 TCCGTCACCT CTGTCCAGGC TGTCTACGTC CCAGCTGACG ATTTGACTGA 750
 TCCTGCCCCA GCTACCACCT TCGCCCATT TGGACGCCACC ACCGAATTGT 800
 CCCGATCTAT CTCTGAGTTG GGTATCTACC CAGCTGTGCA CCCTCTTGGT 850
 TCCAAGTCCC GTCTTTTGGG TGCCTCCGTC GTCGGCCAAG AGCACTACGA 900
 35 CGTTGCCGCC AACGTCCAAC AGACCTTGCA GGCCTACAAG TCTCTCCAGG 950
 ATATCATTGC CATTTTGGGT ATGGACGAAT TGTCTGAGGC TGATAAGCTC 1000
 ACTGTCGAGC GTGCTCGTAA GATGCAGAGA TTCCTTTCTC AGCCATTAC 1050
 CGTCGCTGAG GTCTTCACTG GTCTCGAGGG TAGACTCGTT TCTTTGAAGG 1100
 ACACCATCCG ATCCTTCAAG GAGATCCTTG ACG 1133
 40

2) INFORMATION FOR SEQ ID NO: 495

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 55 (B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAAGAAA CAGAAGCTAG 50
 60 GCGAAAATTG GACAATTGAG CAATTTAGCC ATTGGAGAAA AGAAATTTCG 100

	AGTATTAATT	GTTTTTATAG	AACAACATTG	CCAAGGCTCA	CGGTGGTTAC	150
	TCTGTCTTCA	CTGGTGTCGG	AGAGCGTACC	CGTGAAGGAA	ACGATCTCTA	200
	CCATGAAATG	CAGGAGACCC	GTGTCATTCA	GCTTGATGGC	GAGTCCAAGG	250
	TCGCCCTGGT	CTTCGGCCAG	ATGAACGAGC	CCCCAGGTGC	CCGTGCCCCGT	300
5	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAG	TACTTCCGTG	ATGAGGAAGG	350
	TCAAGACGGT	GAGTTTCTTA	TGGATAAAAA	AAAATTTTTT	TTTTTTTTTT	400
	TTTTTTTCAA	GAAATTCATG	TTCTAACAAA	GTGTATTCTA	GTGCTTCTCT	450
	TCATCGACAA	CATTTTCCGT	TTCCTCAGG	CTGGTTCCGA	AGTGTCTGCC	500
	CTGCTTGGTC	GTATCCCATC	TGCCGTCGGT	TACCAACCCA	CTCTTGCCGT	550
10	CGACATGGGT	GGTATGCAGG	AACGTATTAC	CACCACCAAG	AAGGGATCCA	600
	TTACCTCC					608

15 2) INFORMATION FOR SEQ ID NO: 496

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 794 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
(B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496

30	GTTTATTCAA	GAATCATTG	TGGGTGGCAT	TCTCATAATG	TTTCGGCCAC	50
	AATTACTGAT	TGAAAATAGA	ACAACATTGC	AAAGGCTCAT	GGTGGTTACT	100
	CCGTGTTCAC	TGGTGTCGGC	GAGCGAACTC	GTGAGGGTAA	CGACTTGTAC	150
	CACGAAATGC	AGGAGACCTC	TGTCATTGAG	CTCGATGGCG	AGTCCAAGGT	200
35	CGCGCTGGTG	TTTGGTCAAA	TGAACGAACC	TCCTGGTGCT	CGTGCTCGTG	250
	TTGCTCTGAC	TGGGTAAGTT	GTTCTTTCGC	TTCTTGCGCG	TATCCACATC	300
	CCCATCTTGA	GAATACGTCT	GCCACCATGT	CATGTGATGT	TGGGCTGGTT	350
	CTGGTTTTTG	GGAGGCCCTC	AAGTTCAATT	TTTGGATGAC	AGCACCAGCT	400
	TTACAAGATT	ATGCTAACTT	AATGGAGTCT	TACGGTGGCT	GAGTTCTTCA	450
40	GGGATGAGGA	GGGACAGGAT	GGTAAGTTTG	ATAACAATCT	CGTCGGTGTC	500
	AATATCGACG	GCGTACTCTT	CGCATCAAAA	AACCAAAGAG	GTGGTTTGGT	550
	GTGAGAAGTG	CGCCGGAAAT	AATGGCAACC	ACGTGACAAT	GACCACGTGT	600
	GGGGCTCCCG	TGCTAACACG	TGACAGTCTT	GCTCTTCATC	GACAACATTT	650
	TCCGATTAC	TCAASCCGGT	TCTGARGTGT	CTGCCTTGCT	TGGTCGTATT	700
45	CCATCTGCCG	TCGGTTACCA	ACCCACACTC	GCCGTCGACA	TGGGTCTCAT	750
	GCAGGAACGT	ATCACCACCA	CCCGGAAGGG	ATCCATCACA	TCTG	794

50 2) INFORMATION FOR SEQ ID NO: 497

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1148 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*
 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497

5
 TCTTGTCCGA GGCACCGCCG TCGCTGACAC CGGTGCTCCC ATCACTATCC 50
 CCGTCGGCCG AGGTACCCTT GGTCTGAATCA TCAACGTCTG TGGTGAGCCC 100
 ATTGACGAGC GAGGACCCAT CGAGGCTTCC AAGTACCTCC CCATCCACGC 150
 TGACCCCCCT ACCTTCGCTG AGCAGTCTAC CTCCGCTGAG GTTCTCGAGA 200
 10 CCGGTATTAA GGTCGTGCGAC CTCCTCGCCC CTTACGCCCC AGGTGGTAAG 250
 ATTGGTCTCT TCGGTGGTGC CGGTGTCGGT AAGACTGTCT TCATCCAGGA 300
 GCTGATTAAAC AACATTGCCA AGGCCCATGG TGGTTTCTCC GTTTTCTGCG 350
 GTGTCGGTGA GCGAACCCGA GAGGGTAACG ATCTTTACCG AGAGATGAAG 400
 GAGACTGGTG TCATCAACCT CGAGGGTGAG TCTAAGGTCA CCCTCGTCTT 450
 15 CCGTCAGATG AACGAGCCTC CCGGAGCCCG TGCCCGAGTC GCCCTTACTG 500
 GTCTGACCAT TGCCGAGTAC TTCCGAGACG AGGAGGGTCA GGATGTGTTG 550
 CTCTTCGTTG ACAACATTTT CCGATTCACC CAGGCCGGTT CCGAGGTGTC 600
 CGCTCTGCTT GGTCGAATTC CCTCCGCTGT CGGTTACCAG CCCACTCTGG 650
 CCACCGATAT GGGTGCCCTC CAGGAGCGAA TTACCACCAC CCAGAAGGGT 700
 20 TCCGTCACCT CCGTCCAGGC CGTCTACGTG CCTGCCGATG ATTTGACCGA 750
 TCCTGCTCCC GCCACCACCT TCGCCCATCT TGACGCCACC ACCGTCCTGT 800
 CCCGAGGTAT TTCCGAGCTG GGTATCTACC CCGCTGTCGA TCCCCTTGAT 850
 TCCAAGTCTC GACTTCTGGA TATCGATGTT GTCGGAAAGG AGCACTACGA 900
 TGTTGCTTCC AACGTCCAGC AGACCCTCCA GGCTTACAAG TCTCTCCAGG 950
 25 ATATCATTGC CATTCTTGGT ATGGATGAGC TGTCCGAGCA GGACAAGCTG 1000
 ACCGTCGAGC GAGCTCGAAA GATCCAGCGA TTCCTGTCTC AGCCCTTCAC 1050
 CGTCGCCGAG GTTTTCACCG GTATTGAGGG ACGACTTGTC TCTCTCAAGG 1100
 ACACTGTCCG ATCCTTCAAG GAGATCCTTG ACGGTAAGCA CGATGCTC 1148

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2) INFORMATION FOR SEQ ID NO: 498

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 966 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: WSA-172

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498

GCGCTATTGT CGTTGTTGCT GCCTCCGACG GTCAGATGTA GGTGGAACAT 50
 CTTGGGAAAT ACGTCGTAAA ACACGTCGCT TACGTTTTCG CGAATAGGCC 100
 50 CCAGACTCGT GAGCATTTGC TGCTCGCCCG CCAGGTTGGT GTCCAGAAGA 150
 TCGTTGTCTT CGTCAACAAA ATCGATGCTA TTGATGATCC GGAGATGCTG 200
 GAACTGGTCG AACTCGAGAT GCGTGAGCTG CTGAACAGCT ACGGTTTCGA 250
 GGGTGAAGAG ACTCCGATCA TTTTCGGTTC CGCTCTCTGT GCTCTCGAAG 300
 GACGCCGTGA CGACATCGGT AAAGACAGAA TTGAGCAGCT TATGAACGCT 350
 55 GTCGACACCT GGATCCCCAC TCCTCAGCGT GACCTCGACA AACCTTTCTT 400
 GATGTCTGTC GAGGAAGTGT TCTCTATCGC CGGCCGTGGT ACCGTGGCTT 450
 CTGGTCGTGT CGAGCGTGGT ATCTTGAAGA AGGACTCTGA GGTTGAGATT 500
 GTTGGAGGCT CCTTCGAACC CAAGAAGACC AAAGTCACCG ACATTGAAAC 550
 CTTCAGAAG AGCTGTGATG AATCGCGTGC TGGTGACAAC TCTGGTCTCC 600
 60 TCCTGCGTGG TATCCGACGT GAAGACGTCA AGCGTGGTAT GGTCATTGCT 650

	GTTCCCGGCA	GCACCAAGGC	TCACGACAAG	TTCCTCGTCT	CCATGTACGT	700
	CCTGACCGAG	GCGGAGGGTG	GTCGTCGTAC	TGGCTTCGGT	GCCAACTACC	750
	GTCCCCAAGT	CTTCATCCGT	ACTGCAGGTA	AGTTCCCGCA	CACCGTGTCC	800
	AGATCTTCCG	AGAGATTAGC	GATATATGCT	AATGATTCAT	CAGACGAGGC	850
5	TGCTGACCTC	AGCTTCCCTG	ACGGCGACCA	ATCTCGCAGA	GTTATGCCTG	900
	GTGACAACGT	CGAGATGATC	CTGAAGACCC	ACCACCCTGT	TGCTGCTGAG	950
	GCTGGTCAAC	GCTTCA				966

10

2) INFORMATION FOR SEQ ID NO: 499

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 846 bases
15	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Blastoschizomyces capitatus</i>
	(B)	STRAIN: ATCC 10663

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499

	TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCCCAAACCC	50
	GTGAGCACTT	GCTTCTTGCT	CGTCAAGTTG	GTGTTAAGCA	CATTGTTGTT	100
	TTCGTTAACA	AGATTGATAC	TATTGATGAT	CCTGAAATGT	TGGAACCTTG	150
30	CGAAATGGAA	ATGAGAGAAC	TTCTTTCTTC	TTACGGTTTT	GATGGCGATA	200
	ACACCCCTGT	CATTATGGGT	TCTGCTCTCT	GTGCTCTTGA	AGGTCGTGAA	250
	CCAGAAATTG	GTGAACAAAG	AATCAACCAA	CTCCTTGATG	CTATCGATGA	300
	ATACATTCCT	ACCCAGTTC	GTGATATGGA	CCAACCTTTC	TTGATGCCAC	350
	TTGAAGGTGT	TTTCTCTATT	CCAGGTCGTG	GTACTGTTGC	CACTGGACGT	400
35	GTCTATCGTG	GTACTTTGAA	GAGAGGTGAA	GAAGTTGAAG	TTGTTGGCTA	450
	CAATGATGCT	CCAATCAAGA	CCACCGTTAC	TGGTATTGAA	ATGTTCAAGA	500
	AGGAACTTGA	TCAAGCTCAA	GCTGGTGACA	ACGCTGGTAT	TCTTTTGAGA	550
	GGTGTTAAGC	GTGAAGACCT	TAAGCGTGGT	ATGGTTGTTG	CTAAACCAGG	600
	TACCGTTAAG	CCACACACCA	AGTTCCTTGC	CTCCATCTAT	GTTTTGACTA	650
40	AGGAAGAAGG	TGGCAGACAC	TCTGGCTTTG	GTCTTAACCTA	CAGACCTCAA	700
	CTTTTCCTTG	GTTCTGCTGA	TGTTACCACT	GTCTTGACCT	TCCCAGAGGG	750
	TGTTGACCAA	AGCACTCAAG	TCATGCCAGG	TGACAACACT	GAAATGGTTT	800
	GCGAACTTGT	TCACCCAGTT	GCTGTCGAAC	AAGGCCAACG	TTTCAA	846

45

2) INFORMATION FOR SEQ ID NO: 500

(i) SEQUENCE CHARACTERISTICS:

50	(A)	LENGTH: 846 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Candida rugosa</i>
	(B)	STRAIN: ATCC 96275

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500

	GGTGCCATTA	TTGTTGTTGC	TGCCTCTGAT	GGACAGATGC	CCCAGACCCG	50
	TGAGCATCTT	TTGCTTGCCC	GCCAAGTCGG	TATGCAAAAG	GTCGTTGTGT	100
5	TTGTTAACAA	GATTGATACC	ATTGATGACC	CTGAAATGCT	TGATCTTGTC	150
	GAGATGGAGA	TGCGTGAAC	GTTGAATGAA	TATGACTTCG	ATGGAGATAA	200
	CTCTCCTGTC	ATTATGGGCT	CTGCTCTTGC	TGCTCTTGAG	GACAAGAACC	250
	CCGAGATTGG	TAAGGACCGT	ATCATGCAGC	TCTTGGACGC	TGTTGATGAA	300
	TGGATCCCTA	CCCCCGAGCG	TGACCTTGAC	AAGCCTTTCA	TGATGCCTAT	350
10	TGAGGCCTCT	TTCTCCATTT	CTGGTCGTGG	TACTGTTGCC	ACTGGCCGTG	400
	TCGAGCGTGG	TATTCTCAAG	AAGGGTGAGG	AAGTCGAGAT	CGTTGGTTTC	450
	AACAAGCAGC	CCCTGAAATC	TGTTGTTACT	GGTATTGAAA	TGTTCAAGAA	500
	GGAACCTGAT	CAGGCCCAGG	GCGGTGATAA	TGCTGGTATC	TTGCTTCGTG	550
	GTATTCGTCG	TGAGGACTTG	CAGCGTGATA	TGGTTTTGGC	CAAGCCTGGA	600
15	ACTGTTAAGG	CTCACACCAA	GTTCTTTTCC	TCCATCTACG	TTCTCTCCAA	650
	GGAAGAGGGC	GGCCGTCACT	CTCCTTTTCG	TATGAACTAT	CGTCCCCAGA	700
	TGTTTCGTTT	TGCAGCTGAT	GTCACCGTTA	CTCTTACTTT	CCCTGAGGGT	750
	GTTGAACAGC	ACACTCAGGT	CTTCCCTGGT	GAGAACACCG	AGATGGTTGG	800
20	CGAGCTCGTT	CACCCTACTG	CTATTGAGGT	TGGTCAACGC	TTCAAC	846

2) INFORMATION FOR SEQ ID NO: 501

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 944 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 35 (B) STRAIN: Silveira

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501

	AGTTGTCGTC	GTTGCTGCTT	CAGACGGTCA	AATGTATGCA	ACCGAGAGCA	50
40	CTCCCGGATC	TTGGTTTAAA	TGGCACTAAT	ATAAGACAGG	CCTCAAACCTC	100
	GAGAGCATTT	ACTTCTCGCC	CGTCAGATCG	GTATCCAAAA	AATCGTCGTC	150
	TTCGTGAACA	AGGTTGATGC	CATCGAGGAC	AAAGAGATGT	TGGAGCTTGT	200
	TGAATTGGAG	ATGCGTGAAC	TCCTAACCAG	CTACGGTTTC	GAGGGTGAAG	250
	AAACTCCCAT	CATTTTTTGGC	TCTGCTCTCT	GTGCCCTCGA	AGGAAGACAA	300
45	CCCGAGATCG	GTGTTACCAA	GATTGATGAG	CTCTTGACAG	CCGTCGACAC	350
	CTGGATTCCC	ACTCCTCAGC	GTGAGACTGA	CAAGCCCTTC	TTGATGTCCA	400
	TTGAGGAAGT	GTTCTCTATT	TCCGGACGAG	GAACCGTTGT	CTCCGGCCGT	450
	GTGGAGCGTG	GTATCCTCAA	GAAGGACTCC	GAAGTTGAAA	TTGTCGGCGG	500
	TTCGCCCCGAG	CCAATCAAAA	CCAAGGTTAC	CGATATCGAA	ACCTTTAAGA	550
50	AGTCTTGCGA	CGAGTCTCGC	GCTGGTGATA	ACTCCGGCTT	GCTCCTACGA	600
	GGCGTTAAGC	GTGAAGATAT	TAGCCGTGGC	ATGGTCGTCG	CTGTACCAGG	650
	AAGTGTC AAG	GCCCACTACTG	AATTCTTAGT	TTCGCTTTAC	GTCCTCACCG	700
	AAGCTGAGGG	TGGGCGCAAA	TCTGGATTCA	GCAGCAAGTA	CCGCCCACAG	750
	ATGTTTATT	GCACTGCCGG	TATGTAATAC	TGTGATAATT	TCGTTGACAT	800
55	GGTACTGATT	GAATTCTATA	GACGAAGCGG	CTCAGCTCAG	CTGGCCCGGA	850
	GAAGATCAAG	ACAAGATGGC	TATGCCAGGA	GACAATATCG	AAATGATTTG	900
	CACCACCTTG	CACCCAGTTG	CCGCCGAGGC	TGGCCAGCGA	TTCA	944

2) INFORMATION FOR SEQ ID NO: 502

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium oxysporum*
 (B) STRAIN: WSA-212

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502

GCTATCATCG TCGTTGCTGC CTCCGATGGA CAGATGCCCC AGACCCGTGA 50
 ACACTTGCTC CTCGCTCGTC AGGTCGGTGT CCAGCGAATT GTCGTCTTCG 100
 TCAACAAGGT CGATGCCATT GATGACCCCG AGATGCTTGA GCTCGTCGAG 150
 20 ATGGAGATGC GCGAGCTTCT TAACACCTAC GGCTTCGAAG GCGACGACAC 200
 TCCCGTCATC ATGGGCTCTG CTCTTATGTC TCTCCAGAAC CAGCGCCCCG 250
 AGATTGGCAC CGAGAAGATC GATGAGCTCC TTGCTGCCGT CGACGAGTGG 300
 ATCCCAACCC CCGAGCGTGA CCTTGACAAG CCCTTCCTTA TGTCCGTCGA 350
 GGATGTCTTC TCCATTGCCG GCCGTGGTAC CGTCGTGTCT GGCCGTGTGG 400
 25 AGCGTGGTAT TCTGAAGCGT GATCAGGAGA TCGAGCTTGT CGGAAAGGGG 450
 CAGGAGGTTA TCAAGACCAA GGTTACCGAC ATTGAGACCT TCAAGAAGTC 500
 TTGTGAGCAG TCCCAGGCTG GTGACAACCTC TGGTCTCCTC ATCCGAGGTG 550
 TTCGCCGTGA GGATGTCCGC CGTGGTATGG TTGTCTGCGC TCCTGGCACC 600
 GTCAAGTCTC ATACCCAGTT TCTCGCTTCC CTCTACGTCC TCACCAAGGA 650
 30 GGAGGGTGGC CGACACACCG GTTTCCAGGA GCACTACCGA CCCCAGCTCT 700
 ATCTCCGAAC TGCAGATGAG TCCATTGACC TGACTTTCCC CGAGGGTACT 750
 GAGGATGCCT CCAGTAAGAT GGTCATGCCT GGTGACAACA CCGAGATGGT 800
 TGTCACCATG GGTCACCCCA ATGCCATCGA GGTGAGTCAG CGATTCAAC 849

35

2) INFORMATION FOR SEQ ID NO: 503

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1064 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G186A5

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503

TGGTGCTATT GTCGTTGTTG CTGCTGCTGA CGGCCAAATG TAAGACGCCG 50
 CGAGGGACTG CTGAGGGTTT TATGCTTTT AGGCCCCCTT GTTTCTGAGA 100
 55 GCATGATGAT ACTAATATTC GGAAACGTAT CTATTAGGCC TCAAACACGT 150
 GAGCATTTCG TCCTTGCCCG ACAGGTCGGT GTCCAAAAGA TCGTCGTTTT 200
 CGTGAACAAA GTCGACGCCC TTGAGGACAA GGAGATGTTG GAGCTTGTCG 250
 AGTTAGAAAT GAGAGAGCTC TTAAACACCT ACGGCTTCGA GGGTGAAGAG 300
 ACACCCATCA TCTTTGGTTC TGCCCTTTGC GCCATGGAAG GCCGTGAGCC 350
 60 TGAGTTGGGA GAAAAGAAAA TTGATGAATT GCTGGAGGCT GTTGATACTT 400

	GGATCCCCAC	ACCACAACGT	GATACCGAAA	AACCTTTCTT	GATGTCCGTT	450
	GAGGAAGTAT	TCTCTATCTC	CGGCCGTGGA	ACCGTTGCCT	CCGGTCGTGT	500
	TGAGCGCGGT	GTCCTCAAGA	AGGATTCAGA	AGTCGAGCTA	ATTGGGGGCG	550
	GCTCCACCCC	CATCAGGACG	AAGGTAACGT	ATATCGAAAC	TTTCAAGAAA	600
5	TCCTGTGACG	AGTCTAGAGC	TGGGGACAAC	TCCGGTCTTT	TATTGCGTGG	650
	TATCAAGCGT	GAAGATATCC	GCCGTGGTAT	GGTAGTTGCC	GTTCCCTGGCA	700
	GCGTCAAGGC	CCACGACAAG	TTCTTGGTGT	CGATGTATGT	CCTGACCGAA	750
	GCTGAGGGTG	GTCGCCGAAC	CGGATTCGGC	CAGAACTATC	GTCCTCAAAT	800
	GTTTCATCCGC	ACAGCTGGTA	TGTCAAAATG	GGACCCCTTT	TCATAATCCT	850
10	TTCTTTTTTT	CCTTTTCCTC	TCTATCTCTC	TTTCTGTTTC	CTTTCAACTC	900
	GCCTGATTCA	CGAAATTAAC	TAACCCGTTT	GATTATAGAC	GAAGCCGCCC	950
	ATCTCAGCTT	CCCTAGTGGA	GCAGATGAAA	GCAAACCTCGT	TATGCCTGGT	1000
	GACAACGTCG	AGATGATCCT	CCAGACACAC	CGCCCCGTGG	CTGCTGAGGC	1050
	CGGCCAGCGA	TTCA				1064
15						

2) INFORMATION FOR SEQ ID NO: 504

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 32071

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504

	TGGTGCTATC	GTCGTTGTTG	CTGCCTCTGA	CGGCCAAATG	TAGGGATTTT	50
35	GCAAGACTGG	TGAAAAAATC	TAAAGAAAAT	AGAAAAGATT	GTGCTGATGT	100
	TTGGTATCAG	GCCCCAAACA	CGCGAGCATC	TGCTTCTTGC	CAGACAAGTC	150
	GGTGTTTACA	AAATCGTTGT	TTTCGTCAAC	AAGGTCGATG	CTGTAGAGGA	200
	TAAGGAGATG	TTGGAGCTTG	TCGAATTGGA	GATGAGAGAG	CTCTTGACCA	250
	CCTATGGGTT	CGAGGGTGAG	AAGACACCTA	TCATCTTTGG	TTCTGCGCTC	300
40	TGTGCTATGG	AGGGCCGTCA	GCCCGAGTTG	GGAGAGCAGA	AAATTGATGA	350
	ATTACTCGAG	GCTGTGGATA	CTTGGATCCC	TACGCCACAG	CGTGATACTG	400
	ACAAGCCCTT	CCTGATGTCC	ATTGAGGAGG	TGTTCTCTAT	CTCTGGACGA	450
	GGAACCGTTG	CCTCCGGCCG	CGTTGAGCGT	GGTATCCTCA	AGAAGGACTC	500
	CGAAGTTGAA	ATTATTGGCG	GCGGTGTTCC	CACAATCCTG	ACCAAGGTGA	550
45	CTGATATCGA	AACCTTCAAG	AAGTCTTGCG	ACGAGTCCAG	AGCCGGGGAC	600
	AACTCCGGCC	TCTTGTTGCG	CGGTGTCAAG	CGTGAGGATA	TCCGCCGTGG	650
	TATGGTCGTT	GCAGTTCCCG	GAAGCGTCAA	AGCACATGAC	AGATTCTTGG	700
	TGTCGATGTA	CGTTCTGACC	GAGGCTGAGG	GTGGTCGCCG	CACTGGCTTC	750
	GGTCAGAACT	ATCGTCCTCA	AATGTTTCATC	CGCACAGCTG	GTACGTTTCAT	800
50	TCTTTCACCTA	TATTCCTATA	TGCATAGCCC	GATCCTCCCA	TTAACTAATT	850
	GACACAGACG	AGGCTGCTGA	ACTCAGCTGG	CCTGATGGAG	ACGACGAAGC	900
	CAAAATGGTC	ATGCCCGGTG	ACAATGTTGA	AATGGTCCTG	AAGTCACACC	950
	GCCCCGGGGCC	GCTGAGGCTG	GACAGCGATT	CA		982

55

2) INFORMATION FOR SEQ ID NO: 505

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases

60

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 58950

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505

	CGCTGTTGTT	GTCGTCGCTG	CTTCTGATGG	TCAAATGTAA	CATATCCACG	50
	AGCTGCCAAT	TATGGACACT	GCTGATAAGA	ATAGGCCCCA	AACCCGTGAG	100
15	CACTTGCTCC	TCGCCCCGTC	GGTCGGTGTT	CAAAAGATCG	TCGTCTTCGT	150
	CAACAAGGTT	GATGCCGTCG	AGGACCCCGA	GATGTTGGAA	CTTGTCGAAT	200
	TGGAAATGCG	TGAACTCTTG	ACCACCTACG	GTTTCGAGGG	TGAAGAGACC	250
	CCTATCATTT	TCGGATCCGC	TCTTTGCGCC	TTGGAAGGCC	GCAAGCCCGA	300
	GATTGGCGAA	CAGAAGATTG	ACGAGCTCAT	GAACGCCGTT	GATACCTGGA	350
20	TCCCCACCCC	CCAGCGTGAC	CTTGACAAGC	CCTTCTTGAT	GTCCGTTGAG	400
	GAAGTTTTCT	CCATCTCTGG	TCGTGGTACC	GTTGCATCTG	GTCGTGTTGA	450
	GCGTGGTATT	TTGCGCAAGG	ATTCTGAGGT	TGAGATTATC	GGATAACCAGA	500
	AGAACCCTAT	CAAGACCAAG	GTTACCGACA	TTGAGACCTT	CAAGAAGTCT	550
	TGCGATGAAT	CTCGTGCTGG	TGACAACTCT	GGCTTGCTTC	TCCGTGGTAT	600
25	CAAGCGTGAG	GACATTCGTC	GTGGTATGGT	TATCGCTGCT	CCTGGAACCA	650
	CCAAGGCTCA	TGACAACTTC	TTGGTCTCCA	TGTATGTCTT	GACTGAGGCT	700
	GAAGGTGGTC	GTCGTAAGTG	ATTCGGCGCC	AACTACCGTC	CTCAAGCTTT	750
	CATCCGTACT	GCCGGTATGT	TCCCTTTCAA	AGTCAATTAA	TGAGCGATTT	800
	GCTAACGAGT	TATAGATGAG	GCTGCTACTC	TCAGCTTCCC	CGGTGACGAT	850
30	CAGTCCAAGC	AGGTCATGCC	CGGTGACAAC	GTTGAGATGA	TCTTGAAGAC	900
	ACACCGTCCC	GTTGCCGCCG	AAGCTGGTCA	G		931

35 2) INFORMATION FOR SEQ ID NO: 506

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506

50

	TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCTCAAACCA	50
	GAGAACATTT	RTTATTGGCT	AGACAAGTTG	GTGTTCAACA	CATTGTTGTC	100
	TTTGTTAACA	AAGTTGATAC	TATTGATGAC	CCAGAAATGT	TGGAATTAGT	150
	TGAAATGGAA	ATGAGAGAAT	TGTTAAGTAC	TTATGGTTTT	GATGGTGATA	200
55	ACGTCCCAGT	TGTTATGGGT	TCTGCTTTAT	GTGCCTTGGA	AGGTCGTGAA	250
	GAAGAAATTG	GTGTCAAAGC	TATTGATAAA	TTATTAGCTG	CTGTTGATGA	300
	ATATATCCCA	ACCCACAAA	GAGATTTAGA	AAAACCATTC	TTGATGGGTG	350
	TTGAAGATGT	CTTYTCAATC	TCAGGTAGAG	GTACCGTTGT	TACTGGTCGT	400
	GTTGAACGTG	GTAACCTGAA	GAAAGGTGAT	GAAGTTGAAA	TTGTTGGTTT	450
60	AAACAAACT	CCATTGAAAA	CTACTGTYAC	NGGTATTGAA	ATGTTCAAAA	500

	AAGAATTGGA	CCAAGCTATG	GCTGGTGATA	ACTGTGGTAT	CTTATTACGT	550
	GGTATCAAAA	GAGATGACAT	YAAAAGAGGT	ATGGTTATTG	CTAAAACCGG	600
	TACCATCTCW	GCTCACACTA	AATTCTTAGC	CTCAATGTAT	ATTTTGACTA	650
	AAGAAGAAGG	TGGTCGTCAC	TCAGGTTTTG	GTGAACATTA	CAGACCTCAA	700
5	TTATTCATCA	GAAGTGGTGA	TGTTACCGTT	GTTTTAACCT	TYCCAGAAGG	750
	TGGTGATTCA	TCTCAACAAA	TCTTACCAGG	TGACAATGTC	GAAATGGTTT	800
	GTGAATTGGT	TCACCCAAC	GCTTTAGAAG	CTGGTCAAAG	ATTCAA	846

10

2) INFORMATION FOR SEQ ID NO: 507

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 964 bases
15	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Trichophyton mentagrophytes</i>
	(B)	STRAIN: WSA-225

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507

	GGAGCTGTTG	TCGTTGTCGC	AGCTTCTGAC	GGTCAAATGT	AATTGAATGC	50
	CCGCCCAGAC	GGATGAAAGG	ATTTGACGTT	TCTAACATCA	GTCTAGGCCT	100
	CAGACCAGAG	AACATTTGCT	CCTTGCCCGC	CAGGTCGGTG	TCCAGAAGCT	150
30	GGTCGTTTTC	GTTAACAAGG	TCGATGCCGT	TGAGGACCCA	GAGATGTTGG	200
	AGCTTGTCGA	ACTTGAAATG	CGTGAAGTCC	TCAGCCACTA	CAGTTTTGAG	250
	GGTGAGGAGA	CCCCCATCAT	TTTTGGCTCT	GCTCTCTGTG	CCCTCGAGTC	300
	CCGTCGACCT	GAGCTTGGTG	TCGAGAAGAT	TGACGAGCTA	TTGAACGCCG	350
	TCGACACCTG	GATCCCCACC	CCCGAGCGCG	CCACTGATAA	GCCTTTCCTC	400
35	ATGTCCATTG	AGGAAGTGTT	CTCTATCTCT	GGTCGTGGTA	CCGTCGTCTC	450
	CGGTCGTGTT	GAGCGTGGTA	TCCTCAAGAA	GGATTCCGAC	GTCGAAATTG	500
	TTGGTGGCTC	TACCACCCCT	ATCAAGACCA	AGGTCACAGA	TATCGAAACC	550
	TTCAAGAAGT	CCTGCGATGA	ATCTCGAGCT	GGTGACAAC	CTGGTCTCCT	600
	TCTCCGAGGT	ATCAAGCGTG	AGGACTTGAA	GCGTGGAATG	GTTGTTGCTG	650
40	CCCCCGGATC	CACCAAGGCT	CACACCGACT	TCATGGTCTC	CCTCTACGTC	700
	CTGACTGAGG	CTGAGGGTGG	TCGTTCCAAC	GGCTTCACCC	ACAAGTACCG	750
	CCCTCAAATG	TTCATCCGTA	CTGCTGGTAT	GTAACCAAAG	TTTCCGCTAT	800
	TTACTAAGTA	GATCATTGCT	AACTTGTATT	CCCTTCCGTA	GACGAAGCCG	850
	CATCTTTCAG	CTGGCCTGGA	GAAGACCAAG	ACAAGAAGGC	TATGCCTGGT	900
45	GACAACGTCG	AGATGATTTG	CAAAACCCTC	CACCCCATTG	CTGCCGAGGC	950
	TGGCCAACGA	TTCA				964

50

2) INFORMATION FOR SEQ ID NO: 508

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 844 bases
	(B)	TYPE: Nucleic acid
55	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*
 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508

5	GGTGCTATCA	TTGTCGTTGC	TGCTGGAGAC	GGTTCCAAGC	CCCAGACCCG	50
	AGAGCATCTG	CTGCTTGCTC	GACAGGTCGG	TGTCCAGAAC	CTGGTTGTGT	100
	TTGTTAACAA	GGTTGATCAG	ATTGATGATA	AGGAGATTCT	TGAGCTCGTT	150
	GACATGGAGA	TGCGAGATCT	GCTGACCCAG	TACGGTTTTG	ATGGTGACAA	200
10	CACCCCCGTT	GTCATGGGCT	CTGCTCTGTG	CGCTCTTGAG	GGCAAGCAGA	250
	AGGATATTGG	AGAGGACGCC	ATCATGGCCC	TTATGGATGC	CGTTGATGAG	300
	CACATCCCTA	CCCCTAACCG	TGACCTTGAG	AAGCCCTTCC	TGATGCCCCG	350
	TGAGGACGTT	TTCTCCATCT	CTGGCCGAGG	AACTGTTGTT	ACTGGCCGAG	400
	TCGAGCGAGG	AAACCTGAAG	AAGGGTGAGG	AAATCGAGAT	TGTTGGCTAC	450
15	AACAACAAGC	CCATCAAGGC	TGTTGTTACC	GGTATTGAGA	TGTTCAAGAA	500
	GGAGCTCGAG	TCCGCCATGG	CCGGTGACAA	CGCCGGTATC	CTGCTCCGAG	550
	GTATCAAGCG	AGACGAGATC	AAGCGAGGTA	TGGTCATGTG	CAAGCCTGGC	600
	ACCGTCAACG	CCCACACCAA	GTCCTTGCT	TCTCTTTACA	TCATCCCCAC	650
	CGAGGAGGGT	GGTCGAACCA	GCTCTTTCGG	CGCCAACACT	CGACCCCGAG	700
20	TGTTTCATCCG	AACTTCTTCC	GTCACCGCCA	CTCTCACCTT	CCCCGAGGGT	750
	ACCGACGAGT	CCCAGACCGT	CAACCCCGGT	GACAACACTG	AGATGGTTCT	800
	CGAGCTTGTT	CACCCTACCG	CCATTGAGGT	CAACCAGCGA	TTCA	844

25

2) INFORMATION FOR SEQ ID NO: 509

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1067 bases
30	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bigemina*
 (B) STRAIN: Suarez-2

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509

	CTTGACAAG	CTGAAGAGCG	AGCGTGAGCG	TGGTATCACC	ATTGACATTA	50
	CCCTGTGGAA	GTTCGAAACT	GGCAAGTACT	ACTACACCGT	CATTGACGCC	100
	CCCGGTCACC	GTGACTTCAT	TAAGAACATG	ATTACGGGTA	CCTCCCAGGC	150
45	CGATGTTGCT	ATGCTTGTCG	TGCCCCGCCA	GGCTGGTGGT	TTCGAAGCTG	200
	CCTTCTCTAA	GGAAGGTCAG	ACCCGTGAGC	ACGCTCTTTT	GGCCTTCACC	250
	CTTGGTGTCA	AGCAGATCAT	TTGCGCCATC	AACAAGATGG	ACAAGTGCGA	300
	CTACAAGGAG	GACCGTTACA	GCGAAATCCA	GAAGGAAGTT	CAGGGTTACC	350
	TGAAGAAGGT	CGGTTACAAC	ATCGAGAAGG	TGCCTTTCGT	CGCCATCTCC	400
50	GGTTTCATGG	GTGACAACAT	GGTTGAGCGC	TCCACCAACA	TGCCGTGGTA	450
	CAAGGGCAAG	ACCTTGGTCG	AGGCCCTCGA	CATGATGGAG	CCCCCGAAGA	500
	GGCCCGTCGA	CAAGCCCCTG	CGTCTTCCCC	TCCAGGGTGT	GTACAAGATC	550
	GGTGGTATCG	GTACCGTCCC	TGTCGGTCGT	GTGGAGACTG	GTCAGCTCAA	600
	GGCCGGTATG	GTCCTCACCT	TCGCCCCCAA	CCCGATCACT	ACTGAGTGCA	650
55	AATCCGTCGA	AATGCACCAC	GAAGTTATCG	ATGTTGCCAG	CCCTGGTGAC	700
	AACGTTGGTT	TCAACGTGAA	GAACGTGTCC	ACCTCTGACA	TCCGCACTGG	750
	TCACGTCGCT	TCTGACTCCA	AGAACGACCC	CGCCAAGGCC	GCCGTGTCCT	800
	TCACCGCCCA	GGTCATCATC	TTGAACCACC	CTGGTACCAT	CAAGGCCGGT	850
	TACTCCCCTG	TGGTTGACTG	CCACACTGCC	CACATCTCGT	GCAAATTCTG	900
60	CGAGATCACC	AGCCGTATGG	ACAAGCGTAC	CGGTAAGGCC	CTTGAGGAGA	950

ACCCCAAGAC	CATCAAGAAC	GGCGACGCCG	CTATGGTCGT	CCTGAAGCCG	1000
TGCAAGCCCA	TGGTCGTCGA	GGCCTTCACT	GAATACGCTC	CCCTTGGTCG	1050
TTTCGCCGTG	CGTGACG				1067

5

2) INFORMATION FOR SEQ ID NO: 510

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1049 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510

GTGAACGTGA	ACGTGGTATT	ACTATTGATA	TTACCTTATG	GAAGTTCGAG	50
ACCACCAAGT	ACTACTACAC	CGTCATTGAT	GCCCCTGGTC	ACCGTGACTT	100
25 CATCAAGAAC	ATGATTACGG	GTA CTCTCTCA	AGCCGATGTT	GCTATGCTTG	150
TTGTACCAGC	TGAGGCTGGT	GGTTTCGAGG	CCGCTTTCTC	CAAGGAAGGA	200
CAGACCCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTTGGTG	TCAAACAGAT	250
CATCTGTGCC	ATTAACAAGA	TGGACAAGTG	CGACTACAAG	GAGGACCGTT	300
ACAGTGAAAT	CCAGAAGGAA	GTCCAGGGTT	ACCTCAAGAA	GGTCGGTTAC	350
30 AATATTGAGA	AGGTGCCCTT	CGTTGCCATC	TCCGGTTTCA	TGGGAGACAA	400
CATGGTTGAG	CGTTCCACCA	ACATGCCCTG	GTATAAGGGA	AAGACATTGG	450
TCGAGGCCCT	TGATCAGATG	GAACCCCCAA	AGAGGCCCGT	TGACAAGCCA	500
CTTCGTCTTC	CCCTCCAGGG	TGTCTACAAG	ATCGGTGGTA	TCGGTACCGT	550
CCCCGTCGGT	CGTGTTGAAA	CTGGTATGTT	GAAGGCTGGT	ATGATTCTAA	600
35 CCTTTGCTCC	TAACCCAATC	ACCACTGAAT	GCAAATCCGT	TGAAATGCAC	650
CACGAAACCG	TTGAGGTTGC	TTACCCCGGT	GACAACGTCG	GTTTCAACGT	700
AAAGAACGTT	TCTACTTCTG	ACATTCGCAG	TGGTCACGTT	GCCTCTGATT	750
CTAAGAACGA	CCCTGCCAAG	GCTGCTGTTT	CCTTCACTGC	CCAGGTCATT	800
GTGCTCAACC	ACCCTGGTAC	CATTAAGGCC	GGT TACTGCC	CCGTCGTCGA	850
40 TTGCCACACC	GCTCACATTT	CATGTAAATT	CGAAGAGATC	ACCAGCCGTA	900
TGGACAAGCG	TACCGGTAAA	TCTCTTGAGG	AAAACCCCAA	GACCATCAAG	950
AACGGTGACG	CTGCCATGGT	TGTGCTCAAG	CCAATGAAGC	CCATGGTTGT	1000
CGAATCCTTC	ACTGAGTATG	CTCCTCTTGG	TCGTTTCGCT	GTTTCGTGAC	1049

45

2) INFORMATION FOR SEQ ID NO: 511

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Crithidia fasciculata*
 (B) STRAIN: ATCC 11745

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511

	TGGACAAGCT	GAAGGCGGAG	CGCGAGCGCG	GTATCACGAT	CGATATTGCC	50
	CTGTGGAAGT	TCGAGTCGCC	CAAGTCCGTG	TTCACGATCA	TCGATGCCCC	100
5	CGGCCACCGC	GACTTCATCA	AGAACATGAT	CACCGGCACC	TCCCAGGCCG	150
	ATGCCGCCAT	TCTGATGATT	GACTCGACCC	AGGGTGGCTT	CGAGGCTGGC	200
	ATCTCCAAGG	ACGGCCAGAC	CCGCGAGCAC	GCCCTGCTTG	CCTTCACGCT	250
	GGGCGTGAAG	CAGATGGTTG	TGTGCTGCAA	CAAGATGGAC	GACAAGACGG	300
	TGCAGTACGC	CCAGGCCCGC	TACGAGGAGA	TCAGCAAGGA	GGTCGGCGCG	350
10	TACCTGAAGC	GCGTGGGCTA	CAACCCGGAG	AAGGTGCGCT	TCATCCCGAT	400
	CTCGGGCTGG	CAGGGCGACA	ACATGATCGA	GAAGTCCGAC	AACATGTTCG	450
	GGTACAAGGG	TCCCACGCTG	CTGGAGGCGC	TCGACCTGCT	GGAGGCCCCC	500
	GTGCGTCCGG	TGGACAAGCC	GCTGCGCCTG	CCCCTGCAGG	ACGTGTACAA	550
	GATCGGCGGT	ATCGGCACTG	TGCCCCGTGG	CCGTGTGGAG	ACCGGCGTGA	600
15	TGAAGCCGGG	CGACGTTGTG	GTGTTTCGCG	CTGCCAACGT	GACGACCGAG	650
	GTGAAGTCGA	TCGAGATGCA	CCACGAGCAG	CTGGCTGAGG	CCGTGCCCCG	700
	CGACAACGTG	GGCTTCAACG	TGAAGAACGT	GTCCGTGAAG	GATATCCGCC	750
	GTGGTAACGT	GTGCGGCAAC	ACGAAGAGCG	ACCCCCCGAA	GGAGGCGGCC	800
	GACTTCACTG	CCCAGGTGAT	CGTGCTGAAC	CACCCCGGCC	AGATCAGCAA	850
20	CGGCTACGCG	CCGGTGCTGG	ACTGCCACAC	GAGCCACATC	GCGTGCAAGT	900
	TCGCGGACAT	CGAGTCCAAG	ATCGACCGCC	GCTCTGGCAA	GGAGCTGGAG	950
	AAGAGCCCGA	AGGCCATCAA	GTCCGGCGAT	GCGGCCATCG	TGAAGATGAT	1000
	CCCGCAGAAG	CCGATGTGCG	TGGAGGTGTT	CAACGACTAC	CCGCCGCTGG	1050
	GCCGCTTCGC	TGTCCGCGAT				1070
25						

2) INFORMATION FOR SEQ ID NO: 512

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Entamoeba histolytica*
 - 40 (B) STRAIN: HM1-IMMS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512

	GCTGAAAGAG	AAAGAGGAAT	TACTATTGAT	ATTTTCATTAT	GGAAATTTCGA	50
45	AACATCTAAA	TACTACTTCA	CTATTATTGA	TGCCCCAGGT	CAYAGAGATT	100
	TCATTAAGAA	CATGATTACT	GGAACCTCAC	AAGCTGATGT	TGCCATCCTT	150
	ATTGTTGCTG	CTGGTACTGG	WGAATTTGAA	GCTGGTATTT	CAAAGAATGG	200
	ACAAACCAGA	GAACAYATTC	TTCTTTCATA	CACTCTTGGA	GTTAAACAAA	250
	TGATTGTTGG	WGTTAACAAG	ATGGATGCTA	TTCAATATAA	ACAAGAAAGA	300
50	TATGAAGAAA	TTAAGAAAGA	AATTAGTGCA	TTCCTTAAGA	AGACWGGATA	350
	TAATCCAGAC	AAGATTCCAT	TTGTCCCAAT	TTCAGGATTC	CAAGGAGATA	400
	ATATGATTGA	ACCATCAACC	AACATGCCAT	GGTACAAAGG	ACCAACATTA	450
	ATTGGAGCAC	TTGATTCAAG	CACACCACCA	GAAAGACCAG	TTGATAAACC	500
	ACTTAGACTT	CCACTTCAAG	ATGTTTAYAA	GATTTCAAGT	ATTGGAAGCTG	550
55	TACCATGTGG	AAGAGTTGAA	ACTGGAGTTC	TTAGACCAGG	AACTATTGTT	600
	CAATTTGCAC	CATCAGGAGT	TTCATCTGAA	TGTAAATCAG	TTGAAATGCA	650
	TCACACAGCA	CTTGCTCAAG	CTATTCCAGG	TGATAATGTT	GGATTCAATG	700
	TTAGAAAYTT	AACAGTTAAA	GATATTAAGA	GAGGAAATGT	AGCATCAGAT	750
	GCTAAGAATC	AACCAGCTGT	TGGATGTGAA	GATTTCACTG	CTCAAGTCAT	800
60	TGTCATGAAC	CATCCAGGAC	AAATTAGAAA	GGGATATACA	CCAGTTCTTG	850

	ATTGCCATAC	ATCACACATT	GCATGTAAAT	TCGAAGAATT	ATTAAGCAAG	900
	ATTGATAGAA	GAACAGGTAA	ATCCATGGAA	GGAGGAGAAC	CAGAATATAT	950
	TAAGAATGGA	GATTCAGCAC	TTGTTAAGAT	TGTTCCAAC	AAACCACTTT	1000
	GTGTTGAAGA	ATTTGCTAAA	TTCCCACCAT	TGGGAAGATT	TGCTGTTAGA	1050
5	GA					1052

2) INFORMATION FOR SEQ ID NO: 513

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Giardia lamblia*
 (B) STRAIN: Faubert-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513

25	GACGAGCGCG	AGCGCGGGAT	CACGATCAAC	ATCGCGCTCT	GGAAGTTCGA	50
	GACGAAGAAG	TACATCGTCA	CGATCATCGA	CGCCCCGGGC	CACCGCGACT	100
	TCATCAAGAA	CATGATCACG	GGGACGTCCC	AGGCCGACGT	CGCGATCCTC	150
	GTCGTCGCGG	CGGGCCAGGG	CGAGTTCGAG	GCCGGGATCT	CGAAGGACGG	200
	CCAGACGCGC	GAGCACGCGA	CCCTTGCGAA	CACGCTCGGG	ATCAAGACGA	250
30	TGATCATCTG	CGTCAACAAG	ATGGACGACG	GCCAGGTCAA	GTACTCGAAG	300
	GAGCGCTACG	ACGAGATCAA	GGGCGAGATG	ATGAAGCAGC	TCAAGAACAT	350
	CGGCTGGAAG	AAGGCCGAGG	AGTTCGACTA	CATCCCGACG	TCCGGCTGGA	400
	CCGGGGACAA	CATCATGGAG	AAGTCCGACA	AGATGCCCTG	GTACGAGGGC	450
	CCGTGCCTGA	TCGACGCGAT	CGACGGGCTC	AAGGCCCCGA	AGCGCCCGAC	500
35	CGACAAGCCC	CTCCGCCTCC	CGATCCAGGA	CGTCTACAAG	ATCTCGGGCG	550
	TCGGGACCGT	CCCCGCGGGC	CGCGTCGAGA	CGGGCGAGCT	CGCGCCCGGG	600
	ATGAAGGTCG	TCTTCGCCCC	GACGTCCCAG	GTCTCGGAGG	TCAAGTCCGT	650
	CGAGATGCAC	CACGAGGAGC	TCAAGAAGGC	CGGGCCCGGG	GACAACGTCG	700
	GCTTCAACGT	CCGCGGGCTC	GCCGTCAAGG	ACCTCAAGAA	GGGCTACGTC	750
40	GTCGGGGACG	TGACGAACGA	CCCGCCCGTC	GGCTGCAAGA	GCTTCACCGC	800
	CCAGGTCATC	GTCATGAACC	ACCCGAAGAA	GATCCAGCCC	GGCTACACGC	850
	CCGTCATCGA	CTGCCACACC	GCGCACATCG	CGTGCCAGTT	CCAGCTCTTC	900
	CTCCAGAAGC	TCGACAAGCG	CACGCTCAAG	CCCGAGATGG	AGAACCCGCC	950
	CGACGCAGGC	CGCGGCGATT	GCATCATCGT	CAAGATGGTC	CCCCAGAAGC	1000
45	CCCTGTGCTG	CGAGACGTTC	AACGACTACG	CGCCCCCTCGG	CCGCTTCGCC	1050
	GTCCGCGACA	TGCGCCAAAC	CGTTGCCGTC	GG		1082

50 2) INFORMATION FOR SEQ ID NO: 514

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514

5
 ACGCGTGGGT GCTCGACAAG CTGAAGGCGG AGCGCGAGCG CGGCATCACG 50
 ATCGACATTG CGCTGTGGAA GTTCGAGTCG CCCAAGTCCG TGTTCACGAT 100
 CATCGATGCG CCCGGCCACC GCGACTTCAT CAAGAACATG ATCACGGGCA 150
 CGTCGCAGGC GGACGCCGCC ATCCTGATGA TCGACTCGAC GCATGGTGGC 200
 10 TTCGAGGCTG GCATCTCGAA GGACGGCCAG ACCCGCGAGC ACGCGCTGCT 250
 TGCCTTCACT CTTGGCGTGA AGCAGATGGT GGTGTGCTGC AACAAAGATGG 300
 ACGACAAGAC GGTGACGTAC GCGCAGTCGC GCTACGATGA GATCAGCAAG 350
 GAGGTGGGCG CGTACCTGAA GCGCGTGGGC TACAACCCGG AGAAGGTGCG 400
 CTTCATCCCG ATCTCGGGCT GGCAGGGCGA CAACATGATC GAGAAGTCGG 450
 15 ACAACATGCC GTGGTACAAG GGTCCCACGC TGCTGGACGC GCTCGACATG 500
 CTGGAGCCGC CCGTGCGCCC GGTGGACAAG CCGCTGCGCC TGCCCCCTGCA 550
 GGACGTGTAC AAGATCGGCG GTATCGGGAC GGTGCCCCGTG GGGCGCGTGG 600
 AGACCGGCAT CATGAAGCCG GCGCAGCTGG TGACGTTCGC GCCCGCCAAC 650
 GTGACGACTG AGGTGAAGTC GATCGAGATG CACCACGAGC AGCTGGCGGA 700
 20 GGCGCAGCCC GGCGACAACG TCGGCTTCAA CGTGAAGAAC GTGTCGGTGA 750
 AGGACATCCG CCGTGGTAAC GTGTGCGGCA ACTCGAAGAA CGACCCGCCG 800
 AAGGAGGCGG CCGACTTCAC GGCGCAGGTG ATCGTGCTGA ACCACCCCGG 850
 CCAGATCAGC AACGGCTACG CGCCGGTGCT GGACTGCCAC ACGAGCCACA 900
 TTGCGTGCCG CTTGCGGGAA ATCGAGTCCA AGATCGACCG CCGCTCCGGC 950
 25 AAGGAGCTGG AGAAGAACCC CAAGGCGATC AAGTCTGGCG ATGCCGCGAT 1000
 CGTGAAGATG GTGCCGAGA AGCCGATGTG CGTGGAGGTG TTCAACGACT 1050
 ACGCGCCGCT GGGCCGCTTT GCCGTGCGCG ACATGCGCCA AACCGTTG 1098

30

2) INFORMATION FOR SEQ ID NO: 515

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 1104 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTCACGA 100
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
 50 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
 CTTGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
 TTGCCTTCAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
 GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGAGG AGATCAGCAA 350
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
 55 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG 450
 GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT 500
 GCTGGAGCCG CCGGTGCGCC CCGTGGACAA GCCGCTGCGC CTGCCCCCTGC 550
 AGGACGTGTA CAAGATCGGC GGTATCGGGA CCGTGCCCGT GGGCCGCGTG 600
 GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTTCG CGCCCGCCAA 650
 60 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700

AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTGCGTG -750
 AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
 GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
 GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
 5 ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG 950
 CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA 1000
 TCGTGAAGAT GGTGCCGCGA AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
 TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC 1100
 CGTC 1104
 10

2) INFORMATION FOR SEQ ID NO: 516

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania tropica*
 25 (B) STRAIN: ATCC 30815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
 30 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTCACGA 100
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
 CTTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
 TTGCCTTCAC KCTTGCGGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
 35 GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG 450
 GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT 500
 GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC 550
 40 AGGACGTGTA CAAGATCGGC GGTATCGGGA CCGTGCCCGT GGGGCGCGTG 600
 GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA 650
 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700
 AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTGCGTG 750
 AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
 45 GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
 GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
 ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG 950
 CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA 1000
 TCGTGAAGAT GGTGCCGCGA AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
 50 TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC 1100
 CGTCGG 1106

55 2) INFORMATION FOR SEQ ID NO: 517

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania donovani*

(B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517

10 TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA 100
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
 15 CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
 TTGCCTTCAC GCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
 GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTGC 450
 20 GACAACATGC CGTGGTACAA GGGTCCACG CTGCTGGACG CGCTCGACAT 500
 GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC 550
 AGGACGTGTA CAAGATCGGC GGTATCGGGA CTGTGCCCGT GGGCCGCGTG 600
 GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA 650
 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700
 25 AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG 750
 AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
 GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
 GCCAGATCAG CAACGGCTAC GCGCCGCTGC TGGACTGCCA CACGAGCCAC 900
 ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG 950
 30 CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA 1000
 TCGTGAAGAT GGTGCCGCGA AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
 TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTG 1099

35

2) INFORMATION FOR SEQ ID NO: 518

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*

(B) STRAIN: MOU

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518

55 TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA 100
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
 CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
 TTGCCTTCAC GCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
 GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
 60 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTGC 450

	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTGGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CTGTGCCCGT	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCG	CGCCCGCCAA	650
5	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
10	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

15

2) INFORMATION FOR SEQ ID NO: 519

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania enriettii*
 (B) STRAIN: ATCC 50120

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519

	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	500
	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCTGT	GTTACGATC	ATCGATGCGC	100
35	CCGGCCACCG	CGACTTCATC	AAGAACATGA	TCACCGGCAC	GTCGCAGGCC	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACC	CAGGGCGGCT	TCGAGGCTGG	200
	CATCTCGAAG	GACGGCCAGA	CCCGCGAGCA	CGCGCTGCTC	GCCTTCACGC	250
	TTGGTGTGAA	GCAGATGGTG	GTGTGCTGCA	ACAAGATGGA	CGACAAGACG	300
	GTGCAGTACT	CGCAGGCGCG	CTACGAGGAG	ATCAGCAAGG	AGGTGGGCGC	350
40	GTACCTGAAG	CGCGTCGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	GCAGGGCGAC	AACATGATCG	ACAAGTCGGA	CAGCATGCCG	450
	TGGTACAAGG	GGCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGGCGCC	500
	GGTGCGCCCG	GTGGACAAGC	CGCTGCGCCT	GCCCCTGCAG	GACGTGTACA	550
	AGATCGGCGG	TATCGGGACG	GTGCCCCTGG	GCCGCGTGGA	GACCGGCATC	600
45	ATGAAGCCTG	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGGTGCCCG	700
	GCGACAACGT	CGGCTTCAAC	GTGAAGAACG	TGTCCGGTGA	GGACATCCGC	750
	CGTGGTAACG	TGTGCGGCAA	CTCGAAGAAC	GACCCGCCGA	AGGAGGCGGC	800
	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCTGGC	CAGATCAGCA	850
50	ACGGCTACGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	CGCGTGCCGC	900
	TTCGCGGATA	TCGAGTCCAA	GATCGACCGC	CGCTCTGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCCGGCGA	TGCGGCCATC	GTGAAGATGG	1000
	TGCCGCAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CCCGCCGCTG	1050
	GGGCGCTTCG	CTGTGCGCGA	C			1071

55

2) INFORMATION FOR SEQ ID NO: 520

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 320

(A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*
 (B) STRAIN: ATCC 50121

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520

	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	50
15	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCCGT	GTTACGATC	ATCGATGCGC	100
	CCGGCCACCG	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCGCAGGCG	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACG	CATGGTGGCT	TCGAGGCTGG	200
	CATCTCGAAG	GACGGCCAGA	CCCGCGAGCA	CGCGCTGCTT	GCCTTCACTC	250
	TTGGCGTGAA	GCAGATGGTG	GTGTGCTGCA	ACAAGATGGA	CGACAAGACG	300
20	GTGACGTACG	CGCAGTCGCG	CTACGATGAG	ATCAGCAAGG	AGGTGGGCGC	350
	GTACCTGAAG	CGCGTGGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	GCAGGGCGAC	AACATGATCG	AGAAGTCGGA	CAACATGCCG	450
	TGGTACAAGG	GTCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGCCGCC	500
	GGTGCGCCCG	GTGGACAAGC	CGCTGCGCCT	GCCCCTGCAG	GACGTGTACA	550
25	AGATCGGCGG	TATCGGGACG	GTGCCCCTGG	GCCGCGTGGA	GACCGGCATC	600
	ATGAAGCCCG	GCGACGTGGT	GACGTTGCGC	CCCGCCAACG	TGACGACTGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGCAGCCCG	700
	GCGACAACGT	CGGCTTCAAC	GTGAAGAACG	TGTCGGTGAA	GGACATCCGC	750
	CGTGGAACG	TGTGCGGCAA	CTCGAAGAAC	GACCCGCCGA	AGGAGGCGGC	800
30	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCCGGC	CAGATCAGCA	850
	ACGGCTATGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	TGCGTGCCGC	900
	TTGCGGAAA	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCTGGCGA	TGCCGCGATC	GTGAAGATGG	1000
	TGCCGCAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CGCGCCGCTG	1050
35	GGCCGCTTTG	CCGTGCGCGA	C			1071

2) INFORMATION FOR SEQ ID NO: 521

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1114 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521

55	TCGTTCAAGT	ACGCGTGGGT	GCTCGACAAG	CTGAAGGCGG	AGCGCGAGCG	50
	CGGTATCACG	ATCGACATTG	CGCTGTGGAA	GTTGAGTCG	CCCAAGTCGG	100
	TGTTACGAT	CATCGATGCG	CCCGGCCACC	GCGACTTCAT	CAAGAACATG	150
	ATCACC GGCA	CGTCGCAGGC	GGATGCTGCC	ATTCTGATGA	TCGATTGAC	200
	GCAGGGTGGC	TTCGAGGCTG	GCATCTCGAA	GGACGGCCAG	ACGCGCGAGC	250
60	ACGCGCTGCT	GGCCTTCACG	CTGGGCGTGA	AGCAGATGGT	TGTGTGCTGC	300

	AACAAGATGG	ACGACAAGAC	GGTGCAGTAC	GCGCAGGCGC	GCTACGAGGA	350
	GATCAGCAAG	GAGGTGGGCG	CGTACCTGAA	GCGCGTGGGC	TACAACCCGG	400
	AGAAGGTGCG	CTTCATCCCG	ATCTCGGGCT	GGCAGGGCGA	CAACATGATC	450
	GAGAAGTCCG	ACAACATGTC	GTGGTACAAG	GGTCCCACGC	TGCTGGAGGC	500
5	GCTGGACATG	CTGGAGGCGC	CGGTGCGCCC	GGTGGACAAG	CCGCTGCGCC	550
	TGCCCCCTGCA	GGACGTGTAC	AAGATCGGCG	GCATTGGCAC	GGTGCCGGTG	600
	GGCCGTGTGG	AGACCGGCAT	CATGAAGCCC	GGCGACGTGG	TGACGTTCGC	650
	GCCCGCCAAC	GTGACGACGG	AGGTGAAGTC	GATCGAGATG	CACCACGAGC	700
	AGCTGCAGGA	GGCTGTGCCC	GGCGACAACG	TCGGCTTCAA	CGTGAAGAAC	750
10	GTGTCGGTGA	AGGACATCCG	CCGTGGTAAC	GTGTGTGGCA	ACTCGAAGAA	800
	CGACCCGCCG	AAGGAGGCGG	CTGACTTCAC	GGCGCAGGTG	ATCGTGCTGA	850
	ACCACCCCGG	CCAGATCAGC	AACGGCTACG	CGCCGGTGCT	GGACTGCCAC	900
	ACCAGCCACA	TCGCGTGCCG	CTTCGCGGAC	ATCGAGTCGA	AGATCGACCG	950
	CCGCTCCGGC	AAGGAGCTGG	AGAAGAACCC	CAAGTCCATC	AAGTCCGGCG	1000
15	ACGCCGCCAT	CGTGAAGATG	GTGCCGCAGA	AGCCGATGTG	CGTGGAGGTG	1050
	TTCAACGACT	ACCCGCCGCT	GGGCCGCTTT	GCGGTGCGCG	ACATGCGCCA	1100
	AACCGTTGCC	GTCG				1114

20

2) INFORMATION FOR SEQ ID NO: 522

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTCACGA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
40	ACGTCGCAGG	CGGACGCCGC	CATTCTGATG	ATCGACTCGA	CGCATGGCGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGACGTA	CGCGCAGTCR	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
45	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCG	CGCCCGCCAA	650
50	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAT	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
55	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCCG					1106

60

2) INFORMATION FOR SEQ ID NO: 523

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
 15 (B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
20	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCGAAGTCC	GTGTTCACGA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGCGGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
25	GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
30	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCG	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
35	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
40	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCG					1105

45 2) INFORMATION FOR SEQ ID NO: 524

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524

60

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCGAAGTCC	GTGTTACGA	100
	TCATCGATGC	GCCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
5	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
10	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCGT	GGGCCGCGTG	600
	GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCCGCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
15	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
20	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

25

2) INFORMATION FOR SEQ ID NO: 525

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1081 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: II WT

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525

	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	GATCGACATT	GCGCTGTGGA	50
	AGTTCGAGTC	GCCCAAGTCG	GTGTTACGA	TCATCGATGC	GCCCCGGCCAC	100
	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	ACGTCGCAGG	CGGACGCGGC	150
45	CATCCTGATG	ATCGACTCGA	CGCACGGTGG	GTTCGAGGCT	GGCATCTCGA	200
	AGGACGGGCA	GACGCGCGAG	CACGCGCTGC	TTGCCTTCAC	TCTTGGCGTG	250
	AAGCAGATGG	TTGTGTGCTG	CAACAAGATG	GACGACAAGA	CGGTGATGTA	300
	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	GGAGGTGGGC	GCGTACCTGA	350
	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	GCTTCATCCC	GATCTCGGGC	400
50	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	GACAACATGC	CGTGGTACAA	450
	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	GCTGGAGGCG	CCGGTGCGCC	500
	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	AGGACGTGTA	CAAGATCGGC	550
	GGCATCGGCA	CGGTGCCCCGT	GGGCCGCGTG	GAGACCGGCA	TCATGAAGCC	600
	GGGCGACGTG	GTGACGTTTCG	CGCCCCGCGAA	CGTGACGACG	GAGGTGAAGT	650
55	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	AGGCGCAGCC	CGGCGACAAC	700
	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	AAGGACATCC	GCCGTGGGAA	750
	CGTGTGCGGT	AACTCGAAGA	ACGACCCGCC	GAAGGAGGCC	GCCGACTTCA	800
	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	GCCAGATCAG	CAACGGCTAC	850
	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	ATCGCGTGCC	GGTTCGCGGA	900
60	CATCGAGTCC	AAGATTGACC	GCCGCTCCGG	CAAGGAGCTG	GAGAAGAACC	950

CCAAGGCGAT	CAAGTCCGGC	GATGCCGCGA	TCGTGAAGAT	GGTGC CG CAG	1000
AAGCCGATGT	GCGTGGAGAT	GTTCAACGAC	TACGCGCCGC	TTGGCCGCTT	1050
TGCTGTGCGC	GACATGCGCC	AAACCGTTGC	C		1081

5

2) INFORMATION FOR SEQ ID NO: 526

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526

AAATACGCGT	GGGTGCTCGA	CAAGCTGAAG	GCGGAGCGCG	AGCGCGGCAT	50
CACGATCGAC	ATTGCGCTGT	GGAAGTTCGA	GTCGCCCAAG	TCCGTGTTCA	100
25 CGATCATCGA	TGCGCCCGGC	CACCGCGACT	TCATCAAGAA	CATGATCACG	150
GGCACGTCGC	AGGCGGACGC	CGCCATCCTG	ATGATCGACT	CGACGCATGG	200
TGGCTTCGAG	GCTGGCATCT	CGAAGGACGG	CCAGACCCGC	GAGCACGCGC	250
TGCTTGCTT	CACKCTTGGC	GTGAAGCAGA	TGGTGGTGTG	CTGCAACAAG	300
ATGGACGACA	AGACGGTGAC	GTACGCGCAG	TCGCGCTACG	ATGAGATCAG	350
30 CAAGGAGGTG	GGCGCGTACC	TGAAGCGCGT	GGGCTACAAC	CCGGAGAAGG	400
TGCGCTTCAT	CCCGATCTCG	GGCTGGCAGG	GCGACAACAT	GATCGAGAAG	450
TCGGACAACA	TGCCGTGGTA	CAAGGGTCCC	ACGCTGCTGG	ACGCGCTCGA	500
CATGCTGGAG	CCGCCGGTGC	GCCCGGTGGA	CAAGCCGCTG	CGCCTGCCCC	550
TGCAGGACGT	GTACAAGATC	GGCGGTATCG	GGACGGTGCC	CGTGGGGCGC	600
35 GTGGAGACCG	GCATCATGAA	GCCGGGCGAC	GTGGTGACGT	TCGCGCCCGC	650
CAACGTGACG	ACTGAGGTGA	AGTCGATCGA	GATGCACCAC	GAGCAGCTGG	700
CGGAGGCGCA	GCCCGGCGAC	AACGTCGGCT	TCAACGTGAA	GAACGTGTCG	750
GTGAAGGACA	TCCGCCGTGG	TAACGTGTGC	GGCAACTCGA	AGAACGACCC	800
GCCGAAGGAG	GCGGCCGACT	TCACGGCGCA	GGTGATCGTG	CTGAACCACC	850
40 CCGGCCAGAT	CAGCAACGGC	TACGCGCCGG	TGCTGGACTG	CCACACGAGC	900
CACATTGCGT	GCCGCTTCGC	GGAAATCGAG	TCCAAGATCG	ACCGCCGCTC	950
CGGCAAGGAG	CTGGAGAAGA	ACCCCAAGGC	GATCAAGTCT	GGCGATGCCG	1000
CGATCGTGAA	GATGGTGCCG	CAGAAGCCGA	TGTGCGTGGA	GGTGTTCAAC	1050
GACTACGCGC	CGCTGGGCCG	CTTTGCCGTG	CGCGACATGC	GCCAAACCGT	1100
45 TG					1102

2) INFORMATION FOR SEQ ID NO: 527

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Neospora caninum*
 325

(B) STRAIN: Suarez-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527

5	GGACRAACTT	AAAGCTGAAC	GTGAGCGTGG	TATCACCATT	GATATCTCCC	50
	TGTGGAAATT	TGAGACCAGC	AAGTACTATG	TTACCATCAT	TGATGCCCCA	100
	GGACACAGAG	ACTTCATCAA	AAACATGATT	ACAGGCACAT	CCCAGGCTGA	150
	CTGTGCTGTC	CTGATTGTTG	CTGCTGGTGT	TGGTGAATTT	GAAGCCGGTA	200
	TCTCCAAGAA	CGGGCAGACC	CGTGAGCATG	CCCTTNTGGC	TTACACCCTG	250
10	GGTGTGAAAC	AACTAATTGT	TGGCGTTAAC	AAAAGKGATT	CCACTGAGCC	300
	ACCCTATAGC	CARAAGAGAT	ACGARGAAAT	TGTTAAGGAA	GTCAGCMCCT	350
	AYNTTAAAAA	AATTGGYTAC	AACCCCGACA	CAGTANCATT	TGKGCCAATT	400
	TNTGGCTGGA	ATGGTGACAA	CATGCTGGAN	CCAAGTGCTA	ATATGCCATG	450
	GTTCAAGGGA	TGGAAAGTCM	CCCGTAAGGA	CGGCAATGCC	AGKGGAACCM	500
15	CCCTGCTTGA	AGCTYTGGAT	TGCATTYTGC	CACCAAYTTG	CCCAACTGAC	550
	AAACCCTTGC	GTTTGCCTYT	CCAGGATGTC	TATAAAATTG	GKGGTATTGG	600
	TACTGTCCCT	GTGGGTCGTG	TGGAGACTGG	TGTTCTCAAA	CCTGGCATGG	650
	TGGTCACCTT	TGCTCCAGTC	AATGTAACAA	CTGAAGTGAA	GTCTGTAGAA	700
	ATGCACCATG	AAGCATTGAG	TGAAGCCCTT	CCTGGGGACA	ATGTGGGCTT	750
20	CAATGTCAAG	AACGTGTCTG	TCAAAGATGT	CCGTCGTGGC	AATGTGGCTG	800
	GTGACAGCAA	AAATGATCCA	CCCATGGAAG	CTGCTGGCTT	CACAGCTCAG	850
	GTGATTATTT	TGAACCATCC	AGGCCAAATC	AGTGCTGGAT	ATGCACCTGT	900
	GCTGGATTGT	CACACAGCTC	ACATTGCTTG	CAAGTTTGCT	GAGCTGAAGG	950
	AGAAGATTGA	TCGTCGTTCT	GGGAAAAGC	TGGAAGATGG	CCCTAAATTC	1000
25	TTGAAATCTG	GTGACGCTGC	CATCGTTGAT	ATGGTTCCTG	GCAAGCCCAT	1050
	GTGTGTCGAG	AGCTTCTCTG	ATTATCCTCC	CCTGGGCCGT	TTTGCTGTGC	1100
	GTGAC					1105

30

2) INFORMATION FOR SEQ ID NO: 528

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 935 bases
35	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Trichomonas vaginalis</i>
	(B)	STRAIN: ATCC 30001

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528

	GCACATCCCA	GGCTGATGCT	GCTATCCTTG	TCATCGACTC	CACACTCGGT	50
	GGYTTCGAAG	CCGGTATCGC	TGAACAAGGC	CAGACACGTG	AACACGCTCT	100
	TCTTGCCTTC	ACACTCGGCA	TCAAGCAGGT	CATTGTCGCC	GTCAACAAGA	150
50	TGGATGACAA	GACAGTCAAC	TACAACAAGG	CYCGTTTCGA	CGAAATCACA	200
	GCCGAAATGA	CACGCATCCT	TACAGGCATC	GGCTACAAGC	CAGAAATGTT	250
	CCGCTTCGTC	CCAATCTCCG	GCTGGGCTGG	CGACAACATG	ACAGAGAAGT	300
	CTCCAAACAT	GCCATGGTAC	AATGGCCCAT	ACCTTCTTGA	AGCCCTCGAT	350
	TCCCTTCAGC	CACCAAAGCG	CCCATTTCGAC	AAGCCACTCC	GTCTTCCACT	400
55	CCAGGATGTC	TACAAGATCA	ACGGTATCGG	TACAGTTCCA	GTCGGCCGTG	450
	TCGAATCCGG	CACAATGAAG	CCAGGCATGA	TCGTAACTT	CGCCCCATCC	500
	ACAGTTACAG	CTGAAGTTAA	GTCCATCGAA	ATGCACCACG	AATCCCTTCC	550
	AGAGGCTCTT	CCAGGTGACA	ACATCGGCTT	CAACGTCAAG	AACGTTTCCA	600
	CAGCTGATGT	CAAGCGTGGC	TACGTCGTTG	GTGATACAAA	GCGTGACCCA	650
60	CCAGTCGAAT	GCGCTTCCTT	CACAGCTCAR	ATGATCATCT	CCAACCACCC	700

	AGGCAAGATC	CACGCCGGCT	ACCAGCCAGT	TTTCGACTGC	CACACAGCTC	750
	ACATCGCCTG	CAAGTTCGAC	AAGCTCATCC	AGCGTATCGA	TCGTCGSCAC	800
	GGCAAGAAGG	CTACAGAGAA	CCCAGAATAC	ATTCAGAAGG	ATGATGCCGC	850
	TATCGTCGAG	GTTGTCCCAT	CCAAGCCACT	CGTCGTCGAG	TCCTTCCAGG	900
5	AGTACCCACC	ACTCGGCCGT	TTCGCCATCC	GTGAT		935

2) INFORMATION FOR SEQ ID NO: 529

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
 (B) STRAIN: EATRO795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529

25	AAGCTGAAGG	CTGAGCGCGA	ACGTGGTATC	ACGATCGACA	TTGCACTGTG	50
	GAAATTTCGAG	TCACCCAAGT	CTGTCTTCAC	TATTATTGAT	GCTCCTGGGC	100
	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GCACATCGCA	AGCCGACGCA	150
	GCCATCCTCA	TCATTGCCTC	TGCGCAGGGT	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGA	CAGACCCGCG	AGCACGCGTT	GCTGGCCTTC	ACTTTGGGTG	250
30	TGAAGCAGAT	GGTTGTGTGC	TGCAACAAGA	TGGACGACAA	GACTGTGAAC	300
	TACGGACAGG	AGCGGTATGA	CGAGATTGTG	AAGGAGGTGT	CTGCTTACAT	350
	CAAGAAGGTT	GGGTACAACG	TGGAGAAGGT	GCGCTTCGTC	CCCATCTCCG	400
	GATGGCAGGG	CGACAACATG	ATTGAGAAAT	CCGAGAAGAT	GCCATGGTAC	450
	AAGGGTCCAA	CGCTCCTGGA	GGCACTAGAC	ATGCTGGAGC	CACCAGTGCG	500
35	TCCGAGCGAC	AAGCCCCTGC	GTCTGCCACT	GCAGGACGTG	TACAAGATCG	550
	GTGGTATTGG	CACCGTGCCC	GTTGGTTCGTG	TGGAGACCGG	CGTGATGAAG	600
	CCTGGTGATG	TGGTGACGTT	TGCCCCCGCC	AACGTGACGA	CCGAGGTGAA	650
	ATCGATCGAG	ATGCACCACG	AGCAGCTCGC	TGAGGCGACC	CCCGGTGACA	700
	ACGTCGGCTT	TAACGTGAAG	AACGTTTCTG	TAAAGGACAT	CCGCCGTGGC	750
40	AACGTCTGCG	GTAACACCAA	GAACGACCCC	CCAAAGGAGG	CCGCCGACTT	800
	CACGGCACAG	GTGATCATCC	TGAACCACCC	CGGACAGATT	GGAAACGGTT	850
	ATGCGCCCGT	GCTGGACTGC	CACACATCGC	ACATTGCCTG	CAAGTTCGCG	900
	GAGATCGAGT	CGAAGATCGA	CCGTCGCTCT	GGCAAGGAGC	TGGAGAAGGC	950
	TCCCAAGTCG	ATCAAGTCTG	GCGACGCCGC	GATCGTGCGC	ATGGTGCCGC	1000
45	AGAAGCCTAT	GTGCGTGGAG	GTCTTCAACG	ACTACGCGCC	ACTCGGCCGC	1050
	TTTGCCGTGC	GTGAC				1065

50 2) INFORMATION FOR SEQ ID NO: 530

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Crithidia rasciculata*
 (B) STRAIN: ATCC 11745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530

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TTCGCGGAGG	GCGTGCCGCC	GGTGCTGACG	GCGCTGGACG	TGACGGAGGA	50
CCTCGGCCGC	GACGAGCCGC	TGACGCTGGA	GATTGTGCAG	CACTTGGACG	100
CGAACACCGG	CCGCTGCATT	GCCATGCAGA	CGACGGATCT	GCTGAAGCTG	150
AAGTCGAAGG	TTGTGTTCGAC	GGGCGGCAAC	ATCTCCGTGC	CGGTTGGCCG	200
CGAGACGCTG	GGCCGCATCT	TCAACGTGCT	CGGCGACGCG	ATCGACCAGC	250
GCGGTGTGGT	GGGCGAGAAG	ATGCGCATGC	CGATCCACGC	CGAGGCGCCG	300
AAGCTGGCGG	ACCAGGCCGC	GGAGGACGCG	ATTCTGACGA	CCGGCATCAA	350
GGTGATCGAC	CTGATTCTGC	CGTACTGCAA	GGGTGGCAAG	ATCGGGCTGT	400
TCGGCGGTGC	TGGTGTGGGC	AAGACTGTGA	TCATCATGGA	GCTGATCAAC	450
AACGTGGCCA	AGGGCCACGG	TGGTTTCTCC	GTGTTTCGCCG	GCGTTGGCGA	500
GCGCACCCGC	GAGGGCACGG	ATCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
TCATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTGGTGTA	CGGCCAGATG	600
AACGAGCCCC	CGGGTGCGCG	TGCGCGTGTT	GCGCAGTCTG	CGCTGACGAT	650
GGCGGAGTAC	TTCCGTGACG	TGGAGGGCCA	GAACGTGCTG	CTGTTTCATCG	700
ACAACATCTT	CCGCTTCACC	CAGGCCAACT	CCGAGGTGTC	CGCCCTGCTG	750
GGCCGCATTC	CCGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CCGAGGATCT	800
TGGTATGCTG	CAGGAGCGCA	TTACGTTCGAC	GACGAAGGGC	TCGATTACGT	850
CTGTGCAGGC	CGTGTACGTG	CCGGCCGATG	ATATCACGGA	TCCGGCGCCG	900
GCGACGACCT	TCTCGCACCT	GGATGCGACG	ACGGTGCTGG	ACCGCGCGGT	950
TGCCGAGTCT	GGCATCTACC	CCGCCGTGAA	CCCCTGAGG	TGCGCGTCGC	1000
GTATCATGGA	CCCCGATGTG	ATCGACGTGG	ACCACTACAA	CGTTGCGCAG	1050
GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTGC	1100
CGTGCTGGGT	ATCGACGAGC	TGAGCGAGGA	GGACAAGCTT	GTGGTGGACC	1150
GCGCTCGCAA	GGTGACGCGC	TTCCTGTCGC	AGCCGTTCCA	GGTGGCCGAG	1200
GTGTTACCG	GCATGACGGG	CCACTACGTG	CAGCTGGAGG	ACACAGTGGA	1250
GTCGTTCTCT	GGCCTGCTGA	TGGGCTCGTA	CGACCAGATC	CCGGAGA	1297

35 2) INFORMATION FOR SEQ ID NO: 531

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531

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CTTCTCGGAG	GGCGTGCCGC	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	50
ACCTTGGCCG	CGATGAGCCG	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	100
GCGAACACGG	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
GAAGTCGAAG	GTCGTGTCGA	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	200
GTGAGACGCT	GGGCCGCATC	TTCAAYGTTC	TGGGCGACGC	GATCGACCAG	250
CGCGGCCCCG	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	300
GAAGCTGGCG	GATCAGGCCG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	350
AGGTGATCGA	CCTGATTCTG	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	400
TTCGGCGGTG	CCGGTGTGGG	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	450
CAACGTCGCG	AAGGGCCACG	GCGGTTTCTC	CGTGTTTGCC	GCGGTTGGCG	500

	AGCGCACGCG	CGAGGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTGAAG	550
	GTGATTGACC	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCGGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATC	700
5	GACAAATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGCCGCATT	CCGGCCGCCC	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TTGGTATGCT	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	850
	TCCGTGCAGG	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	900
	CGCGACGACG	TTCTCGCACG	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	950
10	TGGCGGAGTC	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	1150
	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGCG	CAGCCGTTCC	AGGTTGCGGA	1200
15	GGTGTTCACG	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	1250
	AGTCGTTCTC	TGGCCTGCTG	ATGGGGTCGT	ACGACCAGAT	CCCGGAGA	1298

20 2) INFORMATION FOR SEQ ID NO: 532

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532

35	TTCTCGGAGG	GCGTGCCGCC	CGTGCTGACG	GCGCTGGATG	TGACGGAGGA	50
	CCTTGGCCGC	GATGAGCCGC	TGACGCTGGA	GATCGTGCAG	CACTTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCGATGCAGA	CGACGGACCT	GCTGAAGCTG	150
	AAGTCGAAGG	TTGTGTGCGAC	CGGCGGCAAC	ATCTCTGTGC	CGGTGGGCCG	200
40	TGAGACGCTG	GGCCGCATCT	TCAACGTTCT	GGGCGACGCG	ATCGACCAGC	250
	GCGGCCCCGT	GGGCGAGAAG	ATGCGCATGG	CGATCCACGC	CGAGGCCCCA	300
	AAGCTGGCGG	ATCAGGCCGC	GGAGGACACG	ATCCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CCTACTGCAA	GGGTGGCAAG	ATCGGCCTGT	400
	TCGGCGGTGC	CGGTGTGGGC	AAGACTGTGA	TCATCATGGA	GCTGATCAAC	450
45	AACGTCGCGA	AGGGCCACGG	TGGTTTCTCC	GTGTTTGCCG	GCGTTGGCGA	500
	GCGCACGCGC	GAGGGCACGG	ACCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
	TGATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTTGTGTA	CGGGCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	GCGCGCGGTT	GCGCAGTCTG	CGCTGACGAT	650
	GGCGGAGTAC	TTCCGCGACG	TGGAGGGCCA	GAACGTGCTG	CTGTTCATCG	700
50	ACAACATCTT	CCGCTTCACG	CAGGCGAACT	CCGAGGTGTC	TGCGCTGCTG	750
	GGCCGCATTC	CAGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CGGAGGATCT	800
	TGGTATGCTG	CAGGAGCGCA	TCACGTGCGC	AACGAAGGGG	TCGATCACGT	850
	CCGTGCAGGC	CGTGTACGTG	CCAGCGGATG	ATATCACGGA	TCCCGCGCCC	900
	GCGACGACGT	TCTCGCACCT	GGACGCGACG	ACTGTGCTGG	ACCGCGCGGT	950
55	GGCGGAGTCG	GGCATCTACC	CTGCCGTGAA	CCCGCTGGAG	TGCGCGTTCG	1000
	GTATCATGGA	CCCCGACGTG	ATCGATGTGG	ACCACTACAA	CGTTGCGCAG	1050
	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTTG	1100
	GGTGCTTGGC	ATCGACGAGC	TGAGCGAGGA	AGACAAGGTT	GTTGTGGACC	1150
	GCGCGCGCAA	GGTGACCCGG	TTCCTGTGCG	AGCCGTTCCA	GGTTGCGGAG	1200
60	GTGTTCACGG	GCATGACGGG	CCACTACGTG	CAGCTGGTCG	ACACGGTGGA	1250

GTCGTTCTCT GGCCTGCTGA TGGGGTCGTA CGACCAGATC CCGGAGA 1297.

5 2) INFORMATION FOR SEQ ID NO: 533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533

20 CTTCTCGGAG GCGGTGCCGC CCGTACTGAC GCGCTGGAT GTGACGGAGG 50
 ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT 100
 GCGAACACCG GCCGCTGCAT TCGATGCAG ACGACGGACC TGCTGAAGCT 150
 GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
 25 GTGAGACGCT GGGCCGCATC TTCAACGTTC TGGGCGACGC GATCGACCAG 250
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
 GAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA 350
 AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCTG 400
 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
 30 CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTTGCC GGCGTTGGCG 500
 AGCGCACGCG CGAGGGCACG GACCTATAAC TGGAGATGAT GCAGTCGAAG 550
 GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
 GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TGCAGTCT GCGCTGACGA 650
 TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC 700
 35 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT 750
 GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCCGAGGATC 800
 TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG 850
 TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACGG ATCCCGCGCC 900
 CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG 950
 40 TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000
 CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
 GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG 1100
 CGGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC 1150
 CGCGCGCGCA AGGTGACCCG GTTCCTGTCG CAGCCGTTCC AGGTTGCGGA 1200
 45 GGTGTTACG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG 1250
 AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAGA 1298

50 2) INFORMATION FOR SEQ ID NO: 534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534

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5      CTTCTCGGAG GCGGTGCCGC CCGTACTGAC GCGCTGGAT GTGACGGAGG      50
      ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT      100
      GCGAACACCG GCCGCTGCAT TCGATGCAG ACGACGGACC TGCTGAAGCT      150
      GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC      200
10     GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG      250
      CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC      300
      AAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA      350
      AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCTG      400
      TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA      450
15     CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTTGCC GGCGTTGGCG      500
      AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG      550
      GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT      600
      GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TCGCGAGTCT GCGCTGACGA      650
      TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC      700
20     GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT      750
      GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCCGAGGATC      800
      TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG      850
      TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACTG ATCCCGCGCC      900
      CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG      950
25     TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG      1000
      CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA      1050
      GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG      1100
      CCGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC      1150
      CGCGCGCGCA AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA      1200
30     GGTGTTACAG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG      1250
      AGTCGTTCTC TGGCCTGCTG ATGGGGTCTG ACGACCAGAT CCCGGAGA      1298
  
```

35 2) INFORMATION FOR SEQ ID NO: 535

(i) SEQUENCE CHARACTERISTICS:

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      (A) LENGTH: 1301 bases
      (B) TYPE: Nucleic acid
40     (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
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(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*
 (B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535

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50     GCACTTCTCG GAGGGCGTGC CGCCCGTGCT GACGGCGCTG GATGTGACGG      50
      AGGACCTTGG CCGCGATGAG CCGCTGACGC TGGAGATCGT GCAGCACTTG      100
      GACGCGAACA CCGGCCGCTG CATTGCGATG CAGACGACGG ACCTGCTGAA      150
      GCTGAAGTCG AAGGTTGTGT CGACCGGTGG CAACATCTCT GTGCCGGTGG      200
55     GCCGTGAGAC GCTGGGCCGC ATCTTCAACG TTCTGGGCGA TCGATCGAC      250
      CAGCGCGGCC CCGTGGGCGA GAAGATGCGC ATGGCGATCC ACGCCGAGGC      300
      CCCGAAGCTG GCGGATCAGG CCGCGGAGGA CACGATCCTG ACGACCGGCA      350
      TCAAGGTGAT CGACCTGATT CTGCCCTACT GCAAGGGTGG CAAGATCGGY      400
      CTGTTTCGGCG GTGCCGGTGT GGGCAAGACT GTGATCATCA TGGAGCTGAT      450
60     CAACAACGTC GCGAAGGGCC ACGGTGGTTT CTCCGTGTTT GCCGGCGTTG      500
  
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	GCGAGCGCAC	GCGCGAGGGC	ACGGACCTGT	ACCTGGAGAT	GATGCAAGTCG	550
	AAGGTGATTG	ACCTGAAGGG	CGAGTCGAAG	TGCGTGCTTG	TGTACGGGCA	600
	GATGAACGAG	CCCCCGGGTG	CGCGCGCGCG	CGTTGCGCAG	TCTGCGCTGA	650
	CGATGGCGGA	GTACTTCCGC	GACGTGGAGG	GCCAGAACGT	GCTGCTGTTC	700
5	ATCGACAACA	TCTTCCGCTT	CACGCAGGCG	AACTCCGAGG	TGTCCGCGCT	750
	GCTGGGCCGC	ATTCCGGCCG	CCGTGGGCTA	CCAGCCGACG	CTTGCGGAGG	800
	ATCTTGGTAT	GCTGCAGGAG	CGCATCACGT	CGACAACGAA	GGGGTCGATC	850
	ACGTCCGTGC	AGGCCGTGTA	CGTGCCAGCG	GATGATATCA	CGGATCCCGC	900
	GCCCGCGACG	ACGTTCTCGC	ACCTTGACGC	GACGACTGTG	CTGGACCGCG	950
10	CGGTGGCGGA	GTCGGGCATC	TACCCTGCCG	TGAACCCGCT	GGAGTGCGCG	1000
	TCGCGTATCA	TGGACCCCGA	TGTGATCGAT	GTGGACCACT	ACAACGTTGC	1050
	GCAGGATATC	GTGCAGATGC	TGACCAAGTA	CAAGGAGCTG	CAGGACATCA	1100
	TTGCGGTGCT	TGGCATCGAC	GAGCTGAGCG	AGGAAGACAA	GGTTGTGGTG	1150
	GACCGCGCGC	GCAAGGTGAC	CCGGTTCCTG	TCGCAGCCGT	TCCAGGTTGC	1200
15	GGAGGTGTTC	ACGGGCATGA	CGGGCCACTA	CGTGCAGCTG	GTCGACACGG	1250
	TGGAGTCGTT	CTCTGGCTTG	CTGATGGGGT	CGTACGACCA	GATCCCGGAG	1300
	A					1301

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2) INFORMATION FOR SEQ ID NO: 536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536

	CTTCGCGGAG	GGCGTGCCGC	CGGTGCTGAC	GTCGCTGGAT	GTGACGGAGA	50
	ACCTCGGCCG	CGATGAGCCG	CTGACGCTGG	AGATTGTGCA	GCACTTGGAC	100
	GCGAACACCG	GTCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
40	GAAGTCGAAG	GTCGTGTCGA	CCGGTGGCAA	CATCTCTGTG	CCTGTTGGCC	200
	GCGAGACGCT	GGGTCGCATC	TTCAACGTGC	TTGGCGATGC	GATTGACCAG	250
	CGCGGCCCTG	TGGGTGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCGCC	300
	GAAGCTGGCG	GATCAGGCGG	CAGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AGGTGATCGA	TCTTATTCTG	CCGTACTGCA	AGGGTGGTAA	GATCGGTCTG	400
45	TTCGGTGGTG	CCGGTGTAGG	CAAGACTGTG	ATTATTATGG	AGCTGATCAA	450
	TAACGTGGCG	AAGGGCCACG	GTGGGTTTTC	CGTGTTTGCT	GGCGTGCGCG	500
	AGCGCACGCG	CGAGGGCACT	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	550
	GTGATTGACC	TGAAGGGCGA	ATCAAAGTGC	GTGCTTGTGT	ACGGACAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GTGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
50	TGGCCGAGTA	CTTCCGCGAT	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATT	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGTCGCATT	CCTGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TGGGCATGCT	GCAGGAGCGC	ATTACGTCGA	CGACGAAGGG	CTCGATTACG	850
	TCTGTGCAGG	CCGTGTACGT	GCCTGCGGAT	GATATCACGG	ACCCGGCGCC	900
55	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGTGCGG	950
	TGGCAGAGTC	GGGCATTTAC	CCTGCGGTGA	ACCCGCTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCCGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CCGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
60	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGCG	CAGCCGTTCC	AGGTTGCGGA	1200

GGTGTTCAC T GGCATGACGG GTCAC TACGT TCAGCTGGAG GACACGGTGG 1250
 AGTCGTTCTC TGGCCTACTG ATGGGGTCAT ACGACCAGAT CCCGGAGA 1298

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2) INFORMATION FOR SEQ ID NO: 537

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537

CTTCTCGGAG GCGGTGCCGC CCGTGCTGAC GCGCTGGAT GTGACGGAGG 50
 ACCTTGGCCG TGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC 100
 GCGAACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT 150
 25 GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
 GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGATGC GATCGACCAG 250
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
 GAAGCTGGCG GATCAGGCCG CAGAGGACAC GATCCTGACG ACCGGCATCA 350
 AGGTGATCGA CTTGATCCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG 400
 30 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
 CAATGTCGCG AAGGGCCACG GTGGTTTCTC CGTGTTTGCC GCGGTTGGCG 500
 AGCGCACGCG CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG 550
 GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
 GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TCGCGAGTCT GCGCTGACGA 650
 35 TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC 700
 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CCGCGCTGCT 750
 GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC 800
 TTGGTATGCT GCAGGAGCGC ATCACGTCGA CAACGAAGGG GTCGATCACG 850
 TCCGTGCAGG CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC 900
 40 CGCGACGACG TTCTCGCACC TGGATGCGAC GACTGTGCTG GACCGCGCGG 950
 TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000
 CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
 GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GACATCATTG 1100
 CCGTGCTTGG CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTGGTGGAC 1150
 45 CGCGCGCGCA AGGTGACCCG GTTCCTGTCG CAGCCGTTCC AGGTTGCGGA 1200
 GGTGTTCACG GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG 1250
 AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAG 1297

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2) INFORMATION FOR SEQ ID NO: 538

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
(B) STRAIN: ATCC 50131

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538

	TTCTCGGAGG	GCGTGCCGCC	CGTGCTGACG	GCGCTGGATG	TGACGGAGGA	50
	CCTTGGCCGC	GATGAGCCGC	TGACGCTGGA	GATCGTGCAG	CACCTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCGATGCAGA	CGACGGACCT	GTTGAAGCTG	150
10	AAGTCGAAGG	TTGTGTCGAC	CGGCGGCAAC	ATCTCTGTGC	CGGTGGGCCG	200
	TGAGACGCTG	GGCCGCATCT	TCAACGTGCT	GGGCGACGCG	ATCGACCAGC	250
	GCGGCCCCGT	GGGTGAGAAG	ATGCGCATGG	CGATCCACGC	CGAGGCCCCG	300
	AAGCTGGCGG	ATCAGGCCGC	GGAGGACACG	ATCCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CCTACTGCAA	GGGTGGCAAG	ATCGGCCTGT	400
15	TTGGTGGCGC	CGGTGTGGGC	AAGACCGTGA	TCATCATGGA	GTTGATTAAC	450
	AACGTCGCGA	AGGGCCACGG	TGGTTTCTCG	GTGTTTGCCG	GCGTTGGCGA	500
	GCGCACGCGC	GAGGGCACGG	ACCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
	TGATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTTGTGTA	CGGGCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	CGCGCGCGTT	GCGCAGTCTG	CGCTGACGAT	650
20	GGCGGAGTAC	TTCCGAGACG	TGGAGGGCCA	GAATGTGCTG	CTGTTCATCG	700
	ACAACATCTT	CCGCTTCACG	CAGGCGAACT	CCGAGGTGTC	TGCGCTGCTG	750
	GGCCGCATTC	CGGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CGGAGGATCT	800
	TGGTATGCTG	CAGGAGCGCA	TCACGTCGAC	GACGAAGGGG	TCGATCACGT	850
	CCGTGCAGGC	CGTGACGTG	CCTGCGGATG	ATATCACGGA	TCCGGCGCCC	900
25	GCGACGACGT	TCTCGCACCT	GGACGCGACG	ACTGTGCTGG	ACCGCGCGGT	950
	GGCGGAGTCG	GGGATCTACC	CTGCCGTGAA	CCCGCTGGAG	TGCGCGTCGC	1000
	GTATCATGGA	CCCCGATGTG	ATCGACGTGG	ACCACTACAA	CGTTGCGCAG	1050
	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTGC	1100
	GGTGCTTGGT	ATCGACGAGC	TGAGCGAGGA	GGACAAGGTC	GTGGTGGACC	1150
30	GCGCGCGCAA	GGTGACCCGG	TTCCTGTTCG	AGCCGTTCCA	GGTTGCGGAG	1200
	GTGTTACCGG	GCATGACGGG	CCACTACGTG	CAGCTGGCCG	ACACGGTGGA	1250
	GTCGTTCTCT	GGGCTGCTGA	TGGGGTCGTA	CGACCAGATC	CCGGAGA	1297

35

2) INFORMATION FOR SEQ ID NO: 539

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539

CCITACATCC TBGTYGCICT IAACAAG

27

50

2) INFORMATION FOR SEQ ID NO: 540

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540

GGDGCITCYT CRTCGWAITC CTG

23

5

2) INFORMATION FOR SEQ ID NO: 541

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541

20 GTKGAAATGT TCCGCAAGCT GCT

23

2) INFORMATION FOR SEQ ID NO: 542

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542

35

CGGAARTAGA ACTGSGGACG GTAG

24

40 2) INFORMATION FOR SEQ ID NO: 543

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543

ATCTTAGTAG TTTCTGCTGC TGA

23

55

2) INFORMATION FOR SEQ ID NO: 544

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

60

(B) TYPE: Nucleic acid

335

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544

AYGTTGTCGC CMGGCATTMC CAT

23

10

2) INFORMATION FOR SEQ ID NO: 545

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545

TACATCCTBG TYGCICTIAA CAAGTG

26

25

2) INFORMATION FOR SEQ ID NO: 546

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546

40

CCRCGICCGG TRATGGTGAA GAT

23

2) INFORMATION FOR SEQ ID NO: 547

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547

55

GTACAGTTGC TTCAGGACGT ATC

23

60

2) INFORMATION FOR SEQ ID NO: 548

336

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548

ACGTTTCGATT TCATCACGTT G 21

15 2) INFORMATION FOR SEQ ID NO: 549

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549

GAACGTGATA CTGACAAACC TTTA 24

30 2) INFORMATION FOR SEQ ID NO: 550

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550

GAAGAAGAAC ACCAACGTTG 20

45 2) INFORMATION FOR SEQ ID NO: 551

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551

60 GAAGAAAAAA TCTTCGAACT GGCTA 25

2) INFORMATION FOR SEQ ID NO: 552

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552

15

TACACGGCCG GTGACTACG

19

20 2) INFORMATION FOR SEQ ID NO: 553

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553

GGCCGTGTTG AACGTGGTCA AATCA

25

35

2) INFORMATION FOR SEQ ID NO: 554

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554

GTTCTTACA TCGTTGTTTT TCTC

24

50

2) INFORMATION FOR SEQ ID NO: 555

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555

5 TCTCGAACTT TCTCTATGTA TGCA 24

2) INFORMATION FOR SEQ ID NO: 556

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556

20

CGGCGCNATC YTSGTTGTTG C 21

25 2) INFORMATION FOR SEQ ID NO: 557

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557

CCMAGGCATR ACCATCTCGG TG 22

40

2) INFORMATION FOR SEQ ID NO: 558

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558

TCITTYAART AYGCTGGGT 20

55

2) INFORMATION FOR SEQ ID NO: 559

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 bases

339

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559

10 CCGACRGCRA YIGTYTGICK CAT 23

2) INFORMATION FOR SEQ ID NO: 560

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560

25 GAYTTCATYA ARAAYATGAT YAC 23

2) INFORMATION FOR SEQ ID NO: 561

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561

40 ACIGTICGGC CRCCCTCACG GAT 23

45 2) INFORMATION FOR SEQ ID NO: 562

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562

CARATGRAYG ARCCICCIGG IGYIMGIATG 30

60

2) INFORMATION FOR SEQ ID NO: 563

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563

GGYTGRTAIC CIACIGCIGA IGGCAT

26

15

2) INFORMATION FOR SEQ ID NO: 564

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564

TAYGGICARA TGAAYGARCC ICCIGGIAA

29

30

2) INFORMATION FOR SEQ ID NO: 565

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565

45 GGYTGRTAIC CIACIGCIGA IGGDAT

26

2) INFORMATION FOR SEQ ID NO: 566

50

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566

60

5 2) INFORMATION FOR SEQ ID NO: 567

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567

TCRTCIGCIG GIACRTAIAY IGCTG

26

20 2) INFORMATION FOR SEQ ID NO: 568

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
25 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568

RTIATIGGIG CIGTIRTIGA YGT

23

35 2) INFORMATION FOR SEQ ID NO: 569

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
40 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569

RTIRTIGGIS CIGTIRTIGA TAT

23

50 2) INFORMATION FOR SEQ ID NO: 570

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570

5 RTIRYIGGIC CIGTIRTIGA YGT

23

2) INFORMATION FOR SEQ ID NO: 571

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571

20

RTIRTIGGIC CIGTIRTIGA TGT

23

25 2) INFORMATION FOR SEQ ID NO: 572

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572

RTIRTIGGIS CIGTIRTIGA

20

40

2) INFORMATION FOR SEQ ID NO: 573

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573

CCICCIACCA TRTARAAIGC

20

55

2) INFORMATION FOR SEQ ID NO: 574

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 bases

343

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574

10 ATIGCIATGG AYGGIACIGA RGG 23

2) INFORMATION FOR SEQ ID NO: 575

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575

25 TIACCATTTC AGTACCTTCT GGTA 25

2) INFORMATION FOR SEQ ID NO: 576

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576

40 AACTTCRTCA AGAAGGTYGG TTACAA 26

45 2) INFORMATION FOR SEQ ID NO: 577

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577

CATGATTGAA CCATCCACCA 20

60

2) INFORMATION FOR SEQ ID NO: 578

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578

CATGATTGAA GCTTCCACCA 20

15

2) INFORMATION FOR SEQ ID NO: 579

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579

30 GAAGGCCGTG CTGGTGAGAA 20

2) INFORMATION FOR SEQ ID NO: 580

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580

45 GCTAAACCAG CTACAATCAC TCCAC 25

2) INFORMATION FOR SEQ ID NO: 581

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581

60

5 2) INFORMATION FOR SEQ ID NO: 582

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582

TTTCAACTTC GTCGTTGACA CGAACAGT 28

20

2) INFORMATION FOR SEQ ID NO: 583

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583

CAACTGCTTT TTGGATATCT TCTTTAATAC CAACG 35

35

2) INFORMATION FOR SEQ ID NO: 584

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584

ACATGACACA TCTAAAACAA 20

50

2) INFORMATION FOR SEQ ID NO: 585

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585

5 ACCACATACT GAATTCAAAG 20

2) INFORMATION FOR SEQ ID NO: 586

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586

20

CAGAAGTATA CGTATTATCA 20

25 2) INFORMATION FOR SEQ ID NO: 587

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587

CGTATTATCA AAAGACGAAG 20

40

2) INFORMATION FOR SEQ ID NO: 588

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588

TCTTCTCAAA CTATCGTCCA 20

55

2) INFORMATION FOR SEQ ID NO: 589

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 20 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589

GCACGAAACT TCTAAAACAA

20

10

2) INFORMATION FOR SEQ ID NO: 590

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590

25 TATACGTATT ATCTAAAGAT

20

2) INFORMATION FOR SEQ ID NO: 591

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591

40

TCCTGGTTCT ATTACACCAC

20

2) INFORMATION FOR SEQ ID NO: 592

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592

55

CAAAGCTGAA GTATACGTAT

20

60

2) INFORMATION FOR SEQ ID NO: 593

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593

TTCACTAACT ATCGCCCACA 20

2) INFORMATION FOR SEQ ID NO: 594

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594

ATTGGTATCC ATGACACTTC 20

2) INFORMATION FOR SEQ ID NO: 595 :

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595

45 TTAAAGCAGA CGTATACGTT 20

2) INFORMATION FOR SEQ ID NO: 596

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596

60

5 2) INFORMATION FOR SEQ ID NO: 597

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597

ATTGGTATCA AAGAAACTTC 20

20

2) INFORMATION FOR SEQ ID NO: 598

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598

AATTACACCT CACACAAAAT 20

35

2) INFORMATION FOR SEQ ID NO: 599

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599

CGGTGAAGAA ATCGAAATCA 20

50

2) INFORMATION FOR SEQ ID NO: 600

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600

5 ATGCAAGAAG AATCAAGCAA 20

2) INFORMATION FOR SEQ ID NO: 601

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601

20

GTTTCACGTG ATGATGTACA 20

25 2) INFORMATION FOR SEQ ID NO: 602

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602

AAGTTGAAGT TGTTGGTATT 20

40

2) INFORMATION FOR SEQ ID NO: 603

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603

GGTATTAAAG ACGAAACATC 20

55

2) INFORMATION FOR SEQ ID NO: 604

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 20 bases

351

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604

GGTGATGAAG TAGAAATCGT 20
10

2) INFORMATION FOR SEQ ID NO:605

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605

25 GAAATGTTCC GTAAATTATT 20

2) INFORMATION FOR SEQ ID NO:606

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606

40 ATTAGACTAC GCTGAAGCTG 20

45 2) INFORMATION FOR SEQ ID NO: 607

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 821 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 55 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus faecalis*
 - (B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607
60

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACAC	50
	GTGAACATAT	CTTATTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
5	ATGTTCCAGT	TATCGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGACGAG	250
	TCTTATGAAG	AAAAAATCTT	AGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGTGAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
10	CGAAACATCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GACAACTTCG	GTGCTTTATT	ACGTGGTGTA	550
	GCACGTGAAG	ATATCGAACG	TGGACAAGTA	TTAGCTAAAC	CAGCTACAAT	600
	CACTCCACAC	ACAAAATTCA	AAGCTGAAGT	ATACGTATTA	TCAAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
15	TTCCGTACAA	CAGACGTTAC	TGGTGTGTA	GAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTTGCTAT	GGACGTTGAA	TTAATTCACC	800
	CAATCGCTAT	CGAAGACGGA	A			821

20

2) INFORMATION FOR SEQ ID NO: 608

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608

	CGGAGCTATC	TTGGTAGTTT	CTGCTGCTGA	CGGCCCAATG	CCTCAAACATC	50
	GTGAACACAT	CCTATTGTCT	CGTCAAGTTG	GTGTTCCCTTA	CATCGTTGTA	100
	TTCTTGAACA	AAGTAGACAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
40	TGAAATGGAA	GTTCGTGACC	TATTAACAGA	ATACRAATTC	CCTGGTGRCG	200
	ATGTTCCCTGT	AGTTGCTGGA	TCAGCTTTGA	AAGCTCTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATTCT	TGAATTAATG	GCTGCAGTTG	ACGAATACAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATTACTGGA	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
45	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAGTTGTTG	GTATTGCTGA	450
	AGAAACTTCA	AAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACYACGC	TGAAGCTGGA	GACRACATTG	GTGCTTTACT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCRT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
50	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	A					751

55

2) INFORMATION FOR SEQ ID NO: 609

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: ATCC 49573

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609

	CGGTGCGATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GCGWACCATA	CATCGTTGTT	100
	TTCTTGAACA	AAATGGATAT	GGTTGAYGAC	GAAGAATTGC	TAGAATTAGT	150
15	TGAAATGGAA	GTTCGTGACC	TATTGTCTGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCCCTGT	AATCGCCGGT	TCTGCTTTGA	AAGCTCTTGA	AGGAGATCCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTGATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
20	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	GAAATCGTTG	GTATTGCTGA	450
	CGAAACTGCT	AAAACAACCTG	TAACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACRAT	600
	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	TTATGTTTTG	ACAAAAGAAG	650
25	AAGGTGGRCG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTT	GAATTACCAG	AAGGAACTGA	750
	A					751

30

2) INFORMATION FOR SEQ ID NO: 610

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae* Rd
(B) STRAIN: KW20
(C) ACCESSION NUMBER: extracted from U32739

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610

	AATATGATTA	CTGGTGCGGC	ACAAATGGAT	GGTGCTATTT	TAGTAGTAGC	50
	AGCAACAGAT	GGTCCTATGC	CACAAACTCG	TGAACACATC	TTATTAGGTC	100
50	GCCAAGTAGG	TGTTCCATAC	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	150
	GTAGATGACG	AAGAGTTATT	AGAATTAGTC	GAAATGGAAG	TTCGTGAACT	200
	TCTATCTCAA	TATGACTTCC	CAGGTGACGA	TACACCAATC	GTACGTGGTT	250
	CAGCATTACA	AGCGTTAAAC	GGCGTAGCAG	AATGGGAAGA	AAAAATCCTT	300
	GAGTTAGCAA	ACCACTTAGA	TACTTACATC	CCAGAACCAG	AACGTGCGAT	350
55	TGACCAACCG	TTCCTTCTTC	CAATCGAAGA	TGTGTTCTCA	ATCTCAGGTC	400
	GTGGTACTGT	AGTAACAGGT	CGTGTAGAAC	GAGGTATTAT	CCGTACAGGT	450
	GATGAAGTAG	AAATCGTCGG	TATCAAAGAT	ACAGCGAAAA	CTACTGTAAC	500
	GGGTGTTGAA	ATGTTCCGTA	AATTACTTGA	CGAAGGTCGT	GCAGGTGAAA	550
	ACATCGGTGC	ATTATTACGT	GGTACCAAAC	GTGAAGAAAT	CGAACGTGGT	600
60	CAAGTATTAG	CGAAACCAGG	TTCAATCACA	CCACACACTG	ACTTCGAATC	650

	AGAAGTGTAC	GTATTATCAA	AAGATGAAGG	TGGTCGTCAT	ACTCCATCTCT	700
	TCAAAGGTTA	CCGTCCACAA	TTCTATTTCC	GTACAACAGA	CGTGACTGGT	750
	ACAATCGAAT	TACCAGAAGG	CGTGGAAATG	GTAATGCCAG	GCGATAACAT	800
	CAAGATGACA	GTAAGCTTAA	TCCACCCAAT	TGCGATGGAT	CAAGGTTTAC	850
5	GTTTCGCAAT	CCGTGAAGGT	GGCCGTACAG	TAGGTGCAGG	C	891

2) INFORMATION FOR SEQ ID NO: 611

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611

25	CGGCGGTATC	TTAGTTGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCTGCATTAA	AAGCATTAGA	AGGCGATGCT	250
30	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCAGTTG	ATGATTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTATGCACGA	450
	AACTTCTAAA	ACAACGTGTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
35	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCA	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCTATTAC	600
	ACCACACACA	AAATTCAAAG	CTGAAGTATA	CGTATTATCT	AAAGATGAAG	650
	GTGGACGTCA	CACTCCATTC	TTCATAACT	ATCGCCCACA	ATTCTATTTC	700
	CGTACTACTG	ACGTAACCTG	TGTTGTAAAC	TTACCAGAAG	GTACAGAAAT	750
40	GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
	TCGCTATCGA	AGACGGAA				818

45 2) INFORMATION FOR SEQ ID NO: 612

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi A
 (B) STRAIN: ATCC 9150

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612

355

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
5	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAACTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	400
10	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTCAGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	650
15	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTC			825

20

2) INFORMATION FOR SEQ ID NO: 613

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 778 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia ficaria*

(B) STRAIN: ATCC 33105

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613

	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GYCAGGTTGG	CGTTCCTTTC	ATCATCGTRT	100
40	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGCGAACT	GCTGTCCGCT	TACGACTTCC	CTGGCGATGA	200
	CCTGCCGGTG	ATTCGCGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	TAAAATCATC	GAGCTGGCTG	AMCMSCTGGA	TACTTACATC	300
	CCAGAACCAG	AGCGCGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	GGTTACCGGT	CGTGTTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTCAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCCATCAAG	600
50	CCGCACACCC	AGTTCGATTC	AGAAGTGTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACKCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCTG	GCGACAACGT	GAACATGA			778

55

2) INFORMATION FOR SEQ ID NO: 614

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 653 bases

356

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614

	GTGCGATCTT	AGTAGTATCA	GCTACTGATG	GTCCAATGCC	TCAAACCTCGT	50
	GAACACATTT	TGTTATCACG	TCAAGTTGGT	GTTAAGCACT	TGATCGTTTT	100
15	CTTGAACAAA	GTAGATTTAG	TTGATGACGA	AGAATTGATC	GACTTAGTTG	150
	AAATGGAAGT	ACGTGAATTA	CTTTCTGAAT	ATGGTTTCCC	AGGTGATGAT	200
	ATTCCAGTGC	TTAAAGGTTC	TGCTTTGAAA	GCATTAGAAG	GCGATCCAGA	250
	ACAAGAACAA	GTTATTCTTG	ATTTGATGGA	TACCGTTGAT	GAATATATCC	300
	CAACACCTGA	ACGTGACAAT	GACAAACCGT	TCTTGTTACC	AGTTGAGGAT	350
20	GTTTTCTCGA	TCACAGGACG	TGGTACTGTA	GCTTCTGGTC	GTATCGACCG	400
	TGGCGAAGTT	AAAGTCGGCG	ATGAAATTGA	AATCATCGGG	ATCAAACCTG	450
	AAGTTCAAAA	AGCAATCGTT	ACTGGACTTG	AAATGTTCCG	TAAAACATTG	500
	GATTATGGTG	AAGCTGGCGA	TAACGTTGGG	GTTCTATTAC	GTGGGATTAC	550
	ACGTGATGAA	ATCGAACGTG	GCCAAGTATT	AGCTAAACCA	GGTTCAATCA	600
25	CACCACATAC	TAAGTTCAAA	GCCGAAGTAT	ATGTGTTGAC	GAAAGAAGAA	650
	GGT					653

30 2) INFORMATION FOR SEQ ID NO: 615

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus durans*
 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615

45	CCATTCTAGT	TGTATCTGCA	ACAGATGGAC	CAATGCCACA	AACACGTGAA	50
	CATATTTTAT	TGTCACGTCA	AGTAGGTGTT	AAATATTTGA	TCGTCTTCTT	100
	GAACAAAATC	GACTTAGTAG	ATGATGAAGA	ATTGATTGAT	CTTGTCGAAA	150
	TGGAAGTTCG	TGAATTATTA	AGCGAATATG	GTTTCCCAGG	TGACGATACA	200
50	CCAGTCATCA	AAGGTTTCAGC	ATTAAAAGCT	TTACAAGGAG	ATCCTGATGC	250
	AGAAGCAGCT	ATCATGGAAT	TGATGGATAC	TGTTGATGAA	TATATCCCAA	300
	CACCAGAACG	TGATACAGAC	AAACCATTAT	TGTTACCAGT	GGAAGATGTC	350
	TTCTCAATCA	CAGGTCGTGG	GACTGTTGCT	TCAGGTCGTA	TCGATCGTGG	400
	TGCAGTTCGT	GTAGGTGATG	AAATCGAAAT	CGTCGGTATC	AAACCTGAAA	450
55	CACAAAAGC	TGTTGTAACT	GGGGTCGAAA	TGTTCCGCAA	GACATTAGAC	500
	TATGGTGAAG	CAGGAGATAA	CGTTGGGGTA	TTGTTACGTG	GTATCCAACG	550
	TGAAGATATC	GAACGTGGAC	AAGTAATCGC	AAAACCAGGT	TCAATCACAC	600
	CACATACAAA	ATTCAAAGCA	GAAGTGACG	TATTGACAAA	AGAAGAAGGT	650
	GGACGTCATA	CACCATTCTT	CAATAACTAT	CGTCCACAAT	TCTACTTCCG	700
60	TACAACTGAC	GTAAGTGGAA	CAATCGTTTT	ACCTGGAGGC	ACTGAAATGG	750

TTATGCCTGG AGATAACGTA ACGATCGACG TTGAATTGAT CCATCAGTT 890
GCCATCGAAA ACGGAACAAC TTTCTCTAT 829

5

2) INFORMATION FOR SEQ ID NO: 616

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
(B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616

GGTGCAATTT TAGTAGTATC TGCTACTGAT GGCCCAATGC CACAAACACG 50
TGAACATATC TTGTTATCAC GTCAAGTAGG GGTTAAACAC TTAATCGTCT 100
TCTTGAACAA AGTTGATTTA GTTGATGATG AAGAATTGAT CGATTTAGTT 150
25 GAAATGGAAG TTCGGGAATT GCTTTCTGAA TATGGTTTCC CAGGCGATGA 200
TATTCCAGTA CTTAAAGGTT CTGCTTTGAA AGCTTTAGAA GGCGATCCTG 250
AACAAGAACA AGTAATCCTT GACTTGATGG ATACGGTTGA TGAATACATC 300
CCAACGCCTG AACGTGATAC TGACAAACCA TTCTTGTTAC CAGTCGAAGA 350
TGCTTTCTCA ATCACAGGAC GTGGTACGGT TGCATCTGGT CGTATCGATC 400
30 GTGGGGAAGT TAAAGTCGGT GATGAAGTTG AAATCATCGG GATCAAACCT 450
GAAGTGCAA AAGCTGTCGT AACTGGACTA GAAATGTTCC GTAAGACATT 500
GGATTACGGT GAAGCTGGCG ATAACGTTGG GGTTCATTAT CGTGGGATTA 550
CTCGTGATGA AATCGAACGT GGACAAGTAT TAGCTAAACC AGGTTCAATC 600
ACTCCACATA CGAAATTCAG TGCAGAAGTT TATGTATTGA CGAAAGAAGA 650
35 AGGTGGCCGT CATACGCCA 669

2) INFORMATION FOR SEQ ID NO: 617

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
(B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617

55 CGGGGCAATT TTAGTTGTAT CTGCAACTGA TGGCCCAATG CCACAAACAC 50
GTGAACACAT TTTGTTAGCT CGTCAAGTAG GGGTTAAATA TTTAATCGTC 100
TTCTTGAACA AAACAGATTT AGTTGATGAT GAAGAATTAT TGGAAC TAGT 150
TGAAATGGAA GTTCGTGAAT TATTAAATGA ATACAATTTC CCTGGCGATG 200
ATATTCCTGT TATTCGCGGA TCTGCTTTAA AAGCATTAGA AGGCGATCCA 250
60 GAACAAGAAG AAGTAATTAT GAACTTGATG GATACTGTGG ATGAATATAT 300

	CCCAACTCCA	GAACGTGACA	ATGATAAACC	ATTCTTGTTA	CCAGTGGGAAG	350
	ATGTCTTCAC	AATTACTGGT	CGTGGTACTG	TTGCTTCAGG	TCGTATCGAC	400
	CGTGGTAAAG	TCAACGTTGG	TGATGAAATT	GAAATTATCG	GAATTAAACC	450
	AGAAACACAA	AAAGCTGTTG	TAACCGGTTT	GGAAATGTTC	CGTAAACTT	500
5	TGGATTATGG	TGAAGCTGGT	GATAACGTTG	GGGTCTTATT	ACGTGGGATT	550
	ACTCGTGATG	AAGTAGAACG	TGGTCAAGTA	TTAGCAAAAC	CAGGTTCCAT	600
	TACACCGCAT	ACCAAATTTA	AAGGTGAAGT	TTATATCTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCATACTCCT	TTCTTTAATA	ACTATCGTCC	TCAATTTTAT	700
	TTCCGTACAA	CTGATGTGAC	TGGTAACATC	GCATTACCTG	AAGGAACTGA	750
10	AATGGTAATG	CCTGGTGATA	ATGTAACAAT	TGAAGTTGAA	TTGATTCATC	800
	CAATCGCCGT	TGAAAAAGGG	ACTACTTTCT	CAATT		835

15 2) INFORMATION FOR SEQ ID NO: 618

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618

30	GGTGCAATCC	TAGTAGTATC	AGCTACTGAT	GGTCCAATGC	CGCAAACACG	50
	TGAACATATT	TTGCTATCAC	GGCAAGTGGG	TGTAAACAC	TTAATCGTAT	100
	TTTTAAACAA	AGTTGATTTA	GTCGATGATG	AAGAATTGAT	CGATCTAGTT	150
	GAAATGGAAG	TCCGTGAATT	ACTTTCTGAA	TATGGTTTCC	CAGGTGACGA	200
35	TATTCCAGTT	CTCAAAGGTT	CAGCTTTGAA	AGCATTAGAA	GGCGATCCTG	250
	AACAAGAACA	AGTAATCCTT	GATTTAATGG	ATACAGTTGA	CGAATATATC	300
	CCAACTCCAG	AACGTGACAC	TGACAAGCCA	TTCTTGTTAC	CAGTCGAAGA	350
	TGTATTTTCT	ATCACTGGTC	GTGGGACTGT	AGCGTCTGGA	CGGATTGATC	400
	GTGGTGAAGT	TAAAGTCGGC	GATGAAGTTG	AAATCATCGG	GATCAAACCT	450
40	GAAATTCAAA	AAGCAGTCGT	AACTGGACTT	GAAATGTTCC	GTAAACTTTT	500
	AGATTATGGT	GAAGCTGGCG	ATAACGTTGG	GGTTCTATTA	CGTGGGATTA	550
	CACGTGATGA	AATCGAACGT	GGTCAAGTCT	TAGCTAAACC	AGGTTCAATC	600
	ACACCACATA	CAAAATTTCAG	TGCAGAAGTT	TACGTATTGA	CGAAAGAAGA	650
	AGGTGGACGT	CATACACCAT	CTT			673

45

2) INFORMATION FOR SEQ ID NO: 619

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1713 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 60 (C) ACCESSION NUMBER: K00428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619

	TTTCATATTT	TTAAGGATTT	TGTTTTAGCA	CCCATCCGAC	CTCAGTCAAT	50
5	ATATCCTTTC	GCGACCAGGC	TTTCCTCCCT	TTTGCTGCTA	ACTGGTTACA	100
	GATTTTCCTA	TTTTTGGTCA	TTTTTATCTT	TGAAACTGAT	TAAGCTGAAA	150
	AAATTTGAGC	TTCTTTGTTG	TAAACTATTT	TGTGCTTTCA	GTTTTATTCT	200
	AGCTCGACAA	AGGTAACAGA	CAAAAATGTC	AGCTTTATTA	CCAAGATTAC	250
	TCACAAGAAC	AGCTTTTAAA	GCTTCTGGGA	AACTTCTGAG	GCTCTCTTCA	300
10	GTAATTTCTA	GGACCTTTTC	TCAAACACT	ACTTCCTATG	CAGCTGCTTT	350
	TGATCGTTCC	AAACCGCATG	TAAATATAGG	TACGATCGGC	CATGTTGATC	400
	ATGGGAAGAC	AACTTTAACC	GCAGCCATTA	CGAAAACGTT	AGCCGCAAAA	450
	GGTGGTGCCA	ACTTCTTGGA	CTATGCTGCC	ATCGATAAGG	CTCCGGAAGA	500
	AAGAGCTCGT	GGTATTACAA	TTTCTACTGC	ACACGTGGAA	TACGAAACGG	550
15	CCAAGAGACA	TTATTCTCAC	GTCGACTGTC	CAGGCCACGC	TGATTACATC	600
	AAGAATATGA	TTACCGGTGC	TGCTCAAATG	GATGGTGCTA	TCATTGTTGT	650
	AGCTGCTACC	GATGGACAAA	TGCCCCAAAC	TAGAGAACAT	TTACTTTTGG	700
	CCAGACAAGT	TGGTGTCCAA	CATATTGTCG	TTTTTGT TAA	CAAGGTTGAT	750
	ACCATTGATG	ATCCAGAAAT	GTTAGAGTTA	GTCGAAATGG	AAATGAGAGA	800
20	ACTTTTAAAC	GAATATGGGT	TTGACGGTGA	TAATGCTCCA	ATTATCATGG	850
	GTTCTGCCCT	TTGCGCTTTG	GAAGGTCGCC	AACCTGAAAT	TGGGGAGCAG	900
	GCCATCATGA	AACTTTTGGA	TGCAGTGGAT	GAGTATATTC	CTACACCTGA	950
	AAGAGATTTG	AACAAGCCTT	TCTTGATGCC	CGTTGAAGAT	ATCTTCTCTA	1000
	TCTCCGGTAG	AGGTACTGTG	GTCACTGGTC	GTGTGGAAAG	GGGTAATTTA	1050
25	AAGAAAGGTG	AGGAATTGGA	AATTGTTGGT	CACAACTCCA	CCCCATTGAA	1100
	AACAACAGTT	ACTGGTATTG	AAATGTTTAG	AAAGGAATTG	GACTCTGCTA	1150
	TGGCAGGTGA	CAATGCCGGT	GTTTTACTTA	GAGGTATCAG	GAGAGATCAA	1200
	TTGAAGAGAG	GTATGGTCTT	AGCTAAGCCA	GGTACCGTTA	AAGCCCATAC	1250
	AAAGATTCTA	GCCTCTTTGT	ACATTTTATC	CAAAGAGGAA	GGTGGTAGAC	1300
30	ATTCTGGGTT	TGGTGAAAAC	TACAGACCAC	AAATGTTTAT	AAGAACAGCT	1350
	GATGTTACAG	TTGTGATGAG	ATTTCTTAAG	GAGGTGGAAG	ATCATTCTAT	1400
	GCAAGTTATG	CCAGGTGACA	ATGTTGAAAT	GGAATGTGAT	TTGATCCATC	1450
	CTACCCCATT	AGAAGTTGGT	CAACGTTTCA	ATATCAGAGA	GGGTGGAAGA	1500
	ACTGTTGGTA	CCGGTCTAAT	CACACGTATT	ATTGAATAGA	CTTATTGATG	1550
35	CAACTGGAGT	ATATTTCTAT	ATATTCTGTT	CATTTCCCCT	CTCATAATAT	1600
	ATACTTGTTT	CGTTAAAATT	TTATACGTGT	AAATAAAGTG	CCATAAATTT	1650
	TTCAGCTTTA	CTTTTGGTAG	AGTCCTGCTA	GCACTAGATT	TTACAATTTT	1700
	ATGTGCACAC	ACC				1713

40

2) INFORMATION FOR SEQ ID NO: 620

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| 45 | (A) | LENGTH: 18 bases |
| | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Single |
| | (D) | TOPOLOGY: Linear |

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620

55 ATTGGTGCAT TGCTACGT

18

2) INFORMATION FOR SEQ ID NO: 621

60 (i) SEQUENCE CHARACTERISTICS:

360

- (A) LENGTH: 751 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: ATCC 19434

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621

15 TGGTGCAATC TTAGTTGTTT CTGCAACTGA CGGTCCGATG CCTCAAACAC 50
GTGAACACAT TTTATTGTCA CGCCAAGTTG GTGTAAAATA CCTGATTGTT 100
TTCTTGAACA AAGTTGATTT AGTCGATGAT GAAGAATTGA TCGATTTGGT 150
AGAAATGGAA GTTCGCGAGT TATTGAGCGA ATATGGTTTC CCAGGCGATG 200
ACACTCCTGT GATCAAAGGT TCCGCATTAA AAGCATTGCA AGGCGATCCA 250
GATGCTGAAG CTGCTATTAT GGAATTGATG GATACAGTAG ATGAATATAT 300
20 CCCAACACCA GAACGTGATA CAGATAAACC ATTACTATTG CCAGTGGAAG 350
ACGTCTTCTC AATTACAGGT CGAGGAACTG TTGCCTCAGG TCGTATTGAT 400
CGTGGTGCTG TTCGTGTCGG TGATGAGGTA GAGATCGTAG GGATCAAACC 450
TGAAACACAA AAAGCAGTTG TAACAGGTGT AGAAATGTTC CGTAAAACGT 500
TAGATTACGG GGAAGCTGGG GATAACGTAG GCGTGTTGTT ACGGGGGATC 550
25 CAACGTGACG ATATCGAACG TGGACAAGTA CTTGCTAAAC CAGGTTCCAT 600
TACTCCACAT ACAAATTCA AAGCAGAAGT GTACGTGTTG ACAAAGAAG 650
AAGGTGGACG TCATACTCCA TTCTTCAACA ACTATCGTCC ACAGTTCTAC 700
TTCCGCACAA CTGATGTTAC AGGAACAATC ACATTGCCAG AAGATACAGA 750
A 751

30

2) INFORMATION FOR SEQ ID NO: 622

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
(B) STRAIN: ATCC 13264

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622

50 GTCAAATGGG ACGAATCCAG ATTCCAAGAA ATTGTCAAGG AAACCTCCAA 50
CTTTATCAAG AAGGTTGGTT ACAACCCAAA GACTGTTCCA TTCGTCCCAA 100
TCTCTGGTTG GAACGGTGAC AACATGATTG AAGCTACCAC CAACGCTCCA 150
TGGTACAAGG GTTGGGAAAA GGAAACCAAG GCCGGTGTCTG TCAAGGGTAA 200
GACTTTGTTG GAAGCCATTG ACGCCATTGA ACAACCATCT AGACCAACTG 250
ACAAGCCATT GAGATTGCCA TTGCAAGATG TTTACAAGAT TGGTGGTATT 300
55 GGTACTGTGC CAGTCGGTAG AGTTGAAACC GGTGTCATCA AGCCAGGTAT 350
GGTTGTTACT TTCGCCCCAG CTGGTGTTAC CACTGAAGTC AAGTCCGTTG 400
AAATGCATCA CGAACAATTG GAACAAGGTG TTCCAGGTGA CAACGTTGGT 450
TTCAACGTCA AGAACGTTTC CGTTAAGGAA ATCAGAAGAG GTAACGTCTG 500
TGGTGACGCT AAGAACGATC CACCAAAGGG TTGCGCTTCT TTCAACGCTA 550
60 CCGTCATTGT TTTGAACCAT CCAGGTCAAA TCTCTGCTGG TTA CTCTCCA 600

361

GTTTTGGATT	GTCACACTGC	TCACATTGCT	TGTAGATTCTG	ACGAATTGTT	650
GGAAAAGAAC	GACAGAAGAT	CTGGTAAGAA	GTTGGAAGAC	CATCCAAAGT	700
TCTTGAAGTC	CGGTGACGCT	GCTTTGGTCA	AGTTCGTTCC	ATCTAAGCCA	750

5

2) INFORMATION FOR SEQ ID NO: 623

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 1269 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptococcus neoformans*
- (B) STRAIN: ATCC 44104

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623

TCTTGAAAGC	TTAAGGCCGA	GCGAGAGCGA	GGTATCACCA	TCGACATTGC	50
TCTTTGGAAG	TTCGAGACCC	CCAGGTACCA	GGTCACCGTC	ATTGACGCCC	100
25 CCGGTCACCG	AGACTTCATC	AAGAACATGA	TCACCGGTAC	CTCCCAGGCT	150
GACTGTGCCA	TCCTCATCAT	TGCCACCGGT	ATCGGTGAGT	TCGAGGCCGG	200
TATCTCCAAG	GACGGTCAGA	CCCGAGAGCA	CGCCCTCCTC	GCCTTCACCC	250
TCGGTGTCAG	GCAGCTCATT	GTTGCTTGCA	ACAAGATGGA	CACCTGCAAG	300
TGGTCCGAGG	ACCGATTCAA	CGAAATCGTC	AAGGAGACCA	ACGGTTTCAT	350
30 CAAGAAGGTT	GGTTACAACC	CCAAGGCTGT	CCCCTTCGTC	CCCATCTCTG	400
GTTGGCACGG	TGACAACATG	TTGGAGGAGA	CCACCAAGTC	AGTGAATCCG	450
CTTCTACGTG	ATGAGATGTT	TTTCTGACTT	TCCGTGCAGC	ATGCCCTGGT	500
ACAAGGGATG	GACCAAGGAG	ACCAAGTCTG	GTGTTTCCAA	GGGTAAGACC	550
CTCCTCGAGG	CCATCGACGC	CATCGAGCCC	CCTACCCGAC	CCACCGACAA	600
35 GCCCCTCCGT	CTCCCTCTCC	AGGACGTCTA	CAAGATCGGT	GGTATCGGCA	650
CAGTCCCTGT	CGGCCGAGTC	GAGACCGGTG	TCATCAAGGC	CGGTATGTTG	700
TCTCATCTCT	CTTGTCTCGT	AACATGCGTC	TCGTAACATG	CGCTTACTTC	750
ATTTTCAGGT	ATGGTCGTCA	AGTTCGCCCC	CACCAACGTC	ACCACTGAAG	800
TCAAGTCCGT	TGAGATGCAC	CACGAGCAGA	TCCCCGAGGG	TCTTCCCGGA	850
40 GACAACGTTG	GTTTCAACGT	CAAGAACGTT	TCCATCAAGG	ACATCCGACG	900
AGGTAACGTC	TGTGGTGACT	CCAAGAACGA	CCCCCCTATG	GAGGCTGCTT	950
CTTTCAACGC	CCAGGTTATC	GTCCTTAACC	ACCCTGGTCA	GATCGGTGCC	1000
GGTTACACCC	CCGTTCTCGA	CTGTCACACT	GCCCGTAAGC	CTGACCCAAT	1050
ACCTCCAACA	TACCTTTGAA	GCTGACCCTT	TCTAGACATT	GCCTGCAAGT	1100
45 TTGCTGAGTT	GATCGAGAAG	ATTGACCGAC	GAACCGGTAA	GGTCATGGAG	1150
GCCGCCCCCA	AGTTCGTCAA	GTCTGGTGAC	GCCGCCATTG	TCAAGCTTGT	1200
TGCCCAGAAG	CCCCTCTGTG	TTGAGACCTA	CGCCGACTAC	CCCCCTCTTG	1250
GTCGATTCGC	CGTCCGAGA				1269

50

2) INFORMATION FOR SEQ ID NO: 624

- (i) SEQUENCE CHARACTERISTICS:
- 55 (A) LENGTH: 753
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 60 (ii) MOLECULE TYPE: Genomic DNA

362

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(B) STRAIN: ATCC 36801

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624

	TCTGTCAAAT	GGGACAAAAA	CAGATTTGAA	GAAATCATCA	AGGAAACCTC	50
	CAACTTCGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTGTT	CCATTTCGTT	100
10	CAATCTCTGG	TTGGAATGGT	GACAACATGA	TTGAACCATC	CACCAACTGT	150
	CCATGGTACA	AGGGTTGGGA	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	200
	TAAGACCTTG	TTAGAAGCTA	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	250
	CCGACAAACC	ATTGAGATTG	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	300
	ATTGGTACTG	TGCCAGTCGG	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	350
15	TATGGTTGTT	ACTTTCGCCC	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	400
	TTGAAATGCA	TCACGAACAA	TTGGCTGAAG	GTGTTCCAGG	TGACAATGTT	450
	GGTTTCAACG	TTAAGAACGT	TTCCGTTAAA	GAAATTAGAA	GAGGTAACGT	500
	TTGTGGTGAC	TCCAAGAACG	ATCCACCAAA	GGGTTGTGAC	TCTTTCAATG	550
	CCCAAGTCAT	TGTTTTGAAC	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	600
20	CCAGTCTTGG	ATTGTCACCC	TGCCACATT	GCTTGTAAT	TCGACACTTT	650
	GGTTGAAAAG	ATTGACAGAA	GAACTGGTAA	GAAATTGGAA	GAAAATCCAA	700
	AATTCGTCAA	ATCCGGTGAT	GCTGCTATCG	TCAAGATGGT	CCCAACCAAA	750
	CCA					753

25

2) INFORMATION FOR SEQ ID NO: 625

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625

40

CGTTGAAGAC	ACGACCCAAA	GTATCC	26
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2) INFORMATION FOR SEQ ID NO: 626

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626

55

TACCACCTTT	TAAGTAAGGT	GCTAAT	26
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60

2) INFORMATION FOR SEQ ID NO: 627

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627

ATTGTCTATA AAAATGGCGA TAAGTC

2) INFORMATION FOR SEQ ID NO: 628

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628

AAAATGGCGA TAAGTCACAA AAAGTA

2) INFORMATION FOR SEQ ID NO: 629

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629

AAGTTCCATC TCAACAAGGT CAATA

2) INFORMATION FOR SEQ ID NO: 630

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630

CGGAGCTATC CTAGTCGTTT CA

2) INFORMATION FOR SEQ ID NO: 631

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631

15 CAGACCAACY GAIAARCCAT TRAGAT 26

2) INFORMATION FOR SEQ ID NO: 632

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632

30 CCCTTTGGTG GRTCSTKCTT GGA 23

35 2) INFORMATION FOR SEQ ID NO: 633

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633

CAGACCAACY GAIAARCCIT TRAGAT 26

50 2) INFORMATION FOR SEQ ID NO: 634

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634

AACACYGTCA GRRCIATTGC YATGGA

26

5

2) INFORMATION FOR SEQ ID NO: 635

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635

AAACCRGTIA RRGCRACCTCT IGCTCT

26

20

2) INFORMATION FOR SEQ ID NO: 636

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636

35 ACTGGYGTTG AIATGTTCCG YAA

23

2) INFORMATION FOR SEQ ID NO: 637

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637

50

ACGTCAGTIG TACGGAARTA GAA

23

2) INFORMATION FOR SEQ ID NO: 638

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

366

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638

CCAATGCCAC AAACICGTGA RCACAT

26

10

2) INFORMATION FOR SEQ ID NO: 639

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639

TTTACGGAAC ATTTCWACAC CWGTIACA

28

25

2) INFORMATION FOR SEQ ID NO: 640

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640

TCCATGGTIT WYGGICARAT GAA

23

40

2) INFORMATION FOR SEQ ID NO: 641

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641

55 TGATAACCWA CIGCIGAIGG CATACG

26

60

2) INFORMATION FOR SEQ ID NO: 642

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642
10 GGCGTIGGIG ARCGIACICG TGA 23

15 2) INFORMATION FOR SEQ ID NO: 643

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643

ACTGGIGTIG ARATGTTCCG YAA 23

30 2) INFORMATION FOR SEQ ID NO: 644

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644

ACGTCIGTIG TICKGAARTA GAA 23

45 2) INFORMATION FOR SEQ ID NO: 645

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645

ACGTCIGTIG TICKGAARTA RAA 23

60

2) INFORMATION FOR SEQ ID NO: 646

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646

15 ATCGACAAGC CITTCTTIAT GSC 23

2) INFORMATION FOR SEQ ID NO: 647

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647

30 ACGTCCGTSG TRCGGAAGTA GAACTG 26

35 2) INFORMATION FOR SEQ ID NO: 648

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648

ACGTCSGTSG TRCGGAAGTA GAACTG 26

50 2) INFORMATION FOR SEQ ID NO: 649

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649

GTCCTATGCC TCARACWCGI GAGCAC

26

5

2) INFORMATION FOR SEQ ID NO: 650

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650

TTACGGAACA TYTCAACACC IGT

23

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2) INFORMATION FOR SEQ ID NO: 651

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651

35 TGACGACCAC CITCYTCYTT YTTCA

25

2) INFORMATION FOR SEQ ID NO: 652

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652

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CCWAYAGTIY KICCICCYTC YCTIATA

27

2) INFORMATION FOR SEQ ID NO: 653

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
60 (C) STRANDEDNESS: Single

370

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653

GAYTTCATIA ARAAYATGAT 20

10

2) INFORMATION FOR SEQ ID NO: 654

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654

TACAARATYK GIGGTATYGG 20

25

2) INFORMATION FOR SEQ ID NO: 655

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655

CCRATACCIC MRATYTTGTA 20

40

2) INFORMATION FOR SEQ ID NO: 656

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656

55 AATTAATGGC TGCAGTTGAY GA 22

2) INFORMATION FOR SEQ ID NO: 657

60

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657

TTGTCCACGT TCGATRTCTT CA

2) INFORMATION FOR SEQ ID NO: 658

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658

GATYTAGTCG ATGATGAAGA ATT

2) INFORMATION FOR SEQ ID NO: 659

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659

GCTTTTTTGIG TTTCWGGTTT RAT

2) INFORMATION FOR SEQ ID NO: 660

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660

GTAGAATTGA GGACGGTAGT TAG

2) INFORMATION FOR SEQ ID NO: 661

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661

15 GTAGAAATGT GGWCGATART TRT

23

2) INFORMATION FOR SEQ ID NO: 662

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 30 (A) ORGANISM: *Corynebacterium diphtheriae*
 (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662

35	CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC	50
	GTGAGCACGT TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT	100
	GCTCTGAACA AGTGCGACAT GGTGATGAT GAGGAAATCA TCGAGCTCGT	150
	CGAGATGGAG ATCCRTGAGC TGCTCGCTGA GCAGGATTAC GACGAAGAGG	200
	CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG CGACGAGAAG	250
40	TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC	300
	AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA	350
	TCTTCACCAT CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT	400
	GGCTCCCTGA AGGTCAACGA GGACGTCGAG ATCATCGGTA TCCGCGAGAA	450
	KGCTACCACC ACCACCGTTA CCGGTATCGA GATGTTCCGT AAGCTTCTCG	500
45	ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG TGGCGTTAAG	550
	CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC	600
	CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCTGTCC AAGGACGAGG	650
	GTGGCCGCCA CACCCCATTC TTCGACAACCT ACCGCCACA GTTCTACTTC	700
	CGCACCACCG ACGTTACCGG TGTGTGAAG CTTCTGAGG GCACCGAGAT	750
50	GGTCATGCCT GGCGACAACG TCGACATGTC CGTCACCCTG ATCCAGCCTG	800
	TCGCTATGGA TGAGGGCCTG CGCTTCGCTA TC	832

55 2) INFORMATION FOR SEQ ID NO: 663

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1192 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Single

373

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida catenulata*

(B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663

10 AACGGCGAGC AAGACTTGGT GTTGGAGGTT TCTCAGCACT TGGGTGAGAA 50
 CACCGTGCGT ACCATTGCCA TGGACGGTAC CGAGGGTTTG GTGAGAGGTA 100
 CCGCTGTCAC TGACACCGGT GCTCCCATCT CGGTCCCCGT TGGTCAGGGT 150
 ACCTTGGGCC GGATCATCAA CGTTGTCGGT GAGCCCATCG ACGAGCGTGG 200
 15 TCCCATCCAG TGCAAGCAGA GAAACCCCAT TCACGCCGAG CCCCCGTCTT 250
 TCACCGAGCA GTCCGTCGAG GCTGAGGTGT TGGAGACCGG TATCAAGGTT 300
 GTCGACTTGT TGGCTCCCTA CGCCCGTGGT GGTAAGATTG GTCTTTTCGG 350
 TGGTGCCGGT GTCGGTAAGA CCGTGTTTCAT CCAGGAGTTG ATTAACAACA 400
 TTGCCAAGGC CCACGGTGGT TTCTCCGTGT TCACTGGTGT CGGTGAGCGT 450
 20 ACTCGTGAGG GTAACGACTT GTACCGTGAA ATGAAGGAGA CCGGTGTCAT 500
 CAACTTGGAG GGCGACTCCA AGGTGGCCTT GGTGTTCCGT CAGATGAACG 550
 AGCCCCCGGG GGCTCGTGCC CGTGTCGCCT TGACCGGTTT GACCATTGCC 600
 GAGTACTTCC GTGACGAGGA AGGCCAGGAC GTGTTGTTGT TCGTTGACAA 650
 CATTTTCAGA TTCACCCAGG CCGGTTCCGA GGTGTCGGCG TTGTTGGGTC 700
 25 GTATCCCCTC CGCCGTCGGT TACCAGCCCA CTTTGGCCAC CGACATGGGT 750
 TTGTTGCAGG AGAGAATTAC CACCACCAAG AAGGGTTCCG TCACCTCTGT 800
 GCAGGCCGTG TACGTCCCTG CCGATGACTT GACTGACCCT GCCCCCGCCA 850
 CCACTTTCGC TCACTTGGAC GCCACCACCG TGTTGTCGCG TGGTATCTCC 900
 GAGTTGGGTA TCTACCCCGC CGTCGACCCC TTGGACTCCA AGTCGAGATT 950
 30 GTTGGACGTC GAGGTTGTTG GCCAGGAGCA CTACGACGTC GCCACCGGTG 1000
 TCCAGGAGTG CTTGCAGGCC TACAAGTCGT TGCAGGACAT CATTGCCATT 1050
 TTGGGTATGG ACGAGTTGTC CGAGCAGGAC AAGTTGACCG TCGAGAGAGC 1100
 CCGTAAGATC CAGCGTTTCT TGTCGCAGCC CTTGCTGTC GCCGAGGTTT 1150
 TCACTGGTAT CCCCGGTAGA TTGGTGAGAT TGCAGGACAC CG 1192

35

2) INFORMATION FOR SEQ ID NO: 664

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664

50 AAYATGATIA CIGGIGCIGC ICARATGGA

29

2) INFORMATION FOR SEQ ID NO: 665

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from X00779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665

10	ATGGGTAAAG	AGAAGTCTCA	CATTAAACGTT	GTCGTTATCG	GTCATGTCGA	50
	TTCTGGTAAG	TCTACCACTA	CCGGTCATTT	GATTTACAAG	TGTGGTGGTA	100
	TTGACAAGAG	AACCATCGAA	AAGTTCGAAA	AGGAAGCCGC	TGAATTAGGT	150
	AAGGGTTCTT	TCAAGTACGC	TTGGGTTTTG	GACAAGTTAA	AGGCTGAAAG	200
	AGAAAGAGGT	ATCACTATCG	ATATTGCTTT	GTGGAAGTTC	GAAACTCCAA	250
15	AGTACCAAGT	TACCGTTATT	GATGCTCCAG	GTCACAGAGA	TTTCATCAAG	300
	AACATGATTA	CTGGTACTTC	TCAAGCTGAC	TGTGCTATCT	TGATTATTGC	350
	TGGTGGTGTC	GGTGAATTCG	AAGCCGGTAT	CTCTAAGGAT	GGTCAAACCA	400
	GAGAACACGC	TTTGTTGGCT	TTCACCTTGG	GTGTTAGACA	ATTGATTGTT	450
	GCTGTCAACA	AGATGGACTC	CGTCAAATGG	GACGAATCCA	GATTCCAAGA	500
20	AATTGTCAAG	GAAACCTCCA	ACTTTATCAA	GAAGGTTGGT	TACAACCCAA	550
	AGACTGTTCC	ATTCGTCCCA	ATCTCTGGTT	GGAACGGTGA	CAACATGATT	600
	GAAGCTACCA	CCAACGCTCC	ATGGTACAAG	GGTTGGGAAA	AGGAAACCAA	650
	GGCCGGTGTC	GTCAAGGGTA	AGACTTTGTT	GGAAGCCATT	GACGCCATTG	700
	AACAACCATC	TAGACCAACT	GACAAGCCAT	TGAGATTGCC	ATTGCAAGAT	750
25	GTTTACAAGA	TTGGTGGTAT	TGGTACTGTG	CCAGTCGGTA	GAGTTGAAAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	TTTTGCCCCA	GCTGGTGTTA	850
	CCACTGAAGT	CAAGTCCGTT	GAAATGCATC	ACGAACAATT	GGAACAAGGT	900
	GTTCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCGTTAAGGA	950
	AATCAGAAGA	GGTAACGTCT	GTGGTGACGC	TAAGAACGAT	CCACCAAAGG	1000
30	GTTGCGCTTC	TTTCAACGCT	ACCGTCATTG	TTTTGAACCA	TCCAGGTCAA	1050
	ATCTCTGCTG	GTTACTCTCC	AGTTTTGGAT	TGTCACACTG	CTCACATTGC	1100
	TTGTAGATTC	GACGAATTGT	TGGAAAAGAA	CGACAGAAGA	TCTGGTAAGA	1150
	AGTTGAAGA	CCATCCAAAG	TTCTTGAAGT	CCGGTGACGC	TGCTTTGGTC	1200
	AAGTTCGTTC	CATCTAAGCC	AATGTGTGTT	GAAGCTTTCA	GTGAATACCC	1250
35	ACCATTAGGT	AGATTCGCTG	TCAGAGACAT	GAGACAAACT	GTCGCTGTCG	1300
	GTGTTATCAA	GTCTGTTGAC	AAGACTGAAA	AGGCCGCTAA	GGTTACCAAG	1350
	GCTGCTCAAA	AGGCTGCTAA	GAAATAA			1377

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2) INFORMATION FOR SEQ ID NO: 666

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1536 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from M12082

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666

	ATGGTTTTGC	CAAGACTATA	TACTGCTACA	TCCCGTGCTG	CTTTTAAAGC	50
	AGCCAAACAA	TCCGCTCCGC	TTCTATCCAC	TTCGTGGAAA	AGATGTATGG	100
	CCTCAGCTGC	TCAATCTACT	CCAATCACCG	GTAAAGTTAC	CGCTGTCATT	150
60	GGTGCCATTG	TTGACGTTCA	TTTTGAACAA	TCAGAGTTGC	CCGCTATTTT	200

	GAACGCTTTA	GAAATTAAAA	CACCTCAAGG	TAAGTTGGTT	TTGGAAGTTG	250
	CTCAACATTT	GGGTGAAAAC	ACTGTCAGAA	CCATTGCTAT	GGATGGTACC	300
	GAAGGTTTGG	TCCGTGGTGA	AAAGGTTCTT	GACACTGGTG	GCCCTATCTC	350
	CGTCCCAGTT	GGGAGAGAAA	CTTTAGGGAG	AATCATCAAC	GTTATCGGTG	400
5	AACCTATTGA	TGAAAGAGGT	CCAATTAAGT	CCAAACTAAG	AAAGCCAATT	450
	CACGCAGACC	CTCCTAGTTT	TGCAGAACAA	TCTACTTCGG	CTGAAATTTT	500
	GGAAACAGGT	ATCAAAGTCG	TCGATCTATT	AGCTCCTTAT	GCCAGAGGTG	550
	GTAAGATTGG	TCTTTTCGGT	GGTGCAGGTG	TCGGTAAGAC	TGTGTTTCATT	600
	CAAGAATTGA	TTAACAATAT	CGCCAAGGCC	CATGGTGGTT	TTTCCGTTTT	650
10	CGCCGGTGTT	GGTGAAAGGA	CCAGAGAGGG	TAATGACTTG	TACCGTGAAA	700
	TGAAGGAAAC	TGGAGTCATT	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	750
	GTTTTTCGGTC	AAATGAACGA	ACCTCCAGGA	GCCAGAGCCA	GAGTCGCTTT	800
	AACTGGTTTG	ACGATCGCTG	AATATTTTCA	AGATGAAGAA	GGTCAAGACG	850
	TCTTGTTGTT	TATCGACAAT	ATCTTTTAGAT	TTACTCAAGC	TGGTTCAGAA	900
15	GTCTCTGCCC	TTTTGGGTCG	TATTCCATCT	GCCGTCGGTT	ATCAACCAAC	950
	TTTGGCCACT	GATATGGGTC	TCTTACAAGA	AAGAATTACC	ACCACAAAGA	1000
	AGGGTTCTGT	CACTTCTGTG	CAAGCCGTTT	ATGTTCCAGC	CGATGATTTA	1050
	ACAGATCCGT	CTCCGTCCAC	ATCTTTTGCC	CATTTGGACG	CATCATCCGT	1100
	CTTGTCAGA	GGTATTTTCA	AATTAGGTAT	TTACCCTGCA	GTGGATCCAT	1150
20	TGGATTCTAA	ATCAAGGTTA	TTGGATGCCG	CCGTTGTCGG	TCAAGAACAT	1200
	TATGACGTCG	CCTCCAAGGT	TCAAGAAACT	TTACAGACCT	ATAAATCTTT	1250
	ACAAGATATC	ATTGCTATTT	TGGGTATGGA	TGAATTGTCC	GAACAAGATA	1300
	AACTAACTGT	CGAAAGGGCA	AGAAAGATTC	AAAGATTCTT	ATCTCAACCA	1350
	TTTGCTGTCT	CCGAAGTCTT	TACTGGTATC	CCAGGTAAAT	TAGTGAGATT	1400
25	AAAGGACACC	GTTGCCTCGT	TCAAAGCCGT	TTTGGAAGGT	AAATACGATA	1450
	ATATACCAGA	ACATGCTTTC	TATATGGTTG	GTGGTATTGA	AGATGTTGTT	1500
	CGTAAAGCTG	AAAAGTTAGC	CCGTGAAGCC	AACTAG		1536

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2) INFORMATION FOR SEQ ID NO: 667

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: Y

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667

	CGGAAGGCGT	GCCGCCGGTG	TTAACTGCTT	TGGATGTGGT	GGAAAAACTT	50
	GGCCGTGACG	AGCCCTTGAC	ACTTGAAATT	GTACAGCACT	TGGACGCCCA	100
	CACCGGCCGT	TGCATTGCGA	TGCAGACGAC	AGATCTGCTT	AAGCTGAAAT	150
50	CGAAGGTAGT	CTCGAGTGGC	GGGAACATTT	CTGTGCCTGT	GGGTCGGGAG	200
	ACACTTGGA	GAATCTTCAA	TGTGCTGGGC	GATGCCATTG	ACCAGCGCGG	250
	CCATGTTGGA	GAGAAGCAAC	GCATGCCTAT	TCACGCTGTG	GCACCAAAGT	300
	TGGCGGATCA	GGCGGCAGAG	GACACCATTC	TCACAACGGG	TATCAAGGTG	350
	ATTGATCTGA	TTTTGCCCTA	CTGCAAGGGT	GGGAAGATTG	GTCTTTTGG	400
55	TGGTGCTGGC	GTGGGCAAGA	CGGTTATTAT	CATGGAACCT	ATTAACAACG	450
	TTGCCAAGGG	CCATGGTGGG	TTCTCCGTCT	TTGCGGGTGT	TGGTGAACGC	500
	ACGCGTGAGG	GGACGGATCT	TTACCTGGAG	ATGATGCAAT	CCAAAGTTAT	550
	TGACCTGAAG	GGTGAATCGA	AGTGTGTGTT	GGTGTATGGT	CAGATGAACG	600
	AGCCTCCGGG	TGCCCCGTGCT	CGTGTGGCGC	AGTCTGCCTT	GACAATGGCC	650
60	GAGTACTTCC	GTGATGTGGA	AGGGCAAGAC	GTGTTGCTTT	TTATCGACAA	700

	CATTTTCCGC	TTTACGCAGG	CAAACCTCTGA	GGTGTCAGCG	CTGTTGGGTC	750
	GTATTCCCGC	TGCCGTCGGC	TACCAGCCTA	CCCTTGCTGA	GGATCTTGGG	800
	CAGTTGCAGG	AGCGCATTAC	GTCCACGACA	AAAGGTTCCA	TTACCTCTGT	850
	GCAGGCTGTG	TACGTGCCAG	CCGATGATAT	TACCGACCCT	GCGCCAGCAA	900
5	CGACCTTTTC	CCACCTCGAT	GCCACGACGG	TGCTGGACCG	TGCCGTTGCC	950
	GAATCCGGCA	TTTACCCCGC	TGTCAACCCA	CTGGAGTGTG	CCTCGCGTAT	1000
	CATGGACCCG	GATGTAATCA	GCGTTGACCA	CTACAACGTG	GCGCAGGATG	1050
	TGGTGCAGAT	GCTTACCAAG	TACAAGGAGC	TGCAGGATAT	CATTGCGGTG	1100
	CTTGGCATTG	ATGAGCTCAG	TGAGGAGGAT	AAACTTATCG	TGGACCGTGC	1150
10	GCGTAAGGTG	ACAAAGTTTC	TCTCCCAGCC	TTTCCAGGTG	GCGGAGGTGT	1200
	TTACTGGCAT	GACAGGCCAC	TACGTGCAGC	TGGAGGAGAC	CATTGAGTCT	1250
	TTTTCCGGCC	TGTTGATGGG	CACATATGAT	CAGGTGCCGG	AGA	1293

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2) INFORMATION FOR SEQ ID NO: 668

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1191 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium glutamicum*

(C) ACCESSION NUMBER: X77034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668

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	GTGGCAAAGG	CGAAGTTCGA	GCGTACCAAG	CCCCACGTAA	ACATCGGCAC	50
	CATCGGTCAC	GTTGACCACG	GTAAGACCAC	CACCACCGCG	GCTATCACCA	100
	AGGTTCTGGC	TGACACTTAC	CCTGAGCTCA	ACGAGGCTTT	CGCCTTCGAC	150
35	TCCATCGATA	AGGCTCCTGA	GGAGAAGGAG	CGTGGCATCA	CGATCAACAT	200
	CTCCACGTT	GAGTACCAGA	CTGAAAAGCG	CCACTACGCA	CACGTTGACG	250
	CTCCAGGCCA	CGCCGACTAC	ATCAAGAACA	TGATTACCGG	CGCTGCTCAG	300
	ATGGACGGCG	CAATCCTCGT	TGTTGCTGCT	ACCGACGGCC	CAATGCCTCA	350
	GACCCGTGAG	CACGTTCTTC	TTGCTCGCCA	GGTTGGCGTT	CCTTACATCC	400
40	TCGTTGCTCT	TAACAAGTGC	GACATGGTTG	AGGATGAGGA	AATCATCGAG	450
	CTCGTCGAGA	TGGAAGTTCG	TGAACTTCTT	GCTGAGCAGG	ACTACGACGA	500
	AGAGGCTCCA	ATTGTTTACA	TCTCCGCTCT	GAAGGCTCTT	GAGGGCGACG	550
	AGAAGTGGGG	CAAGCAGATC	CTTGAGCTCA	TGCAGGCTTG	CGATGACAAC	600
	ATCCCTGACC	CAGTTCGTGA	GACCGACAAG	CCATTCTCTA	TGCCTATCGA	650
45	GGACATCTTC	ACCATCACCG	GTCGTGGCAC	CGTTGTTACC	GGTCGTGTTG	700
	AGCGCGGTAC	CCTGAACGTG	AACGATGATG	TTGACATCAT	CGGCATCAAG	750
	GAGAAGTCCA	CCTCCACCAC	CGTTACCGGT	ATCGAGATGT	TCCGTAAGCT	800
	TCTTGACTCC	GCTGAGGCTG	GCGACAACCTG	TGGTCTGCTT	CTCCGTGGTA	850
	TCAAGCGCGA	AGATGTTGAG	CGTGGCCAGG	TTATCGTTAA	GCCAGGCGCT	900
50	TACACCCCTC	ACACCGAGTT	CGAGGGCTCT	GTCTACGTTC	TGTCCAAGGA	950
	TGAAGGTGGC	CGCCACACCC	CATTCTTCGA	CAACTACCGT	CCTCAGTTCT	1000
	ACTTCCGCAC	CACCGACGTT	ACCGGTGTTG	TGAAGCTTCC	AGAGGGCACC	1050
	GAGATGGTCA	TGCCTGGCGA	CAACGTCGAC	ATGTCCGTCA	CCCTGATCCA	1100
	GCCTGTGCT	ATGGACGAGG	GCCTGCGTTT	CGCTATCCGC	GAAGGCTCCC	1150
55	GCACCGTTGG	CGCTGGTCGT	GTCACCAAGA	TCATCAAGTA	A	1191

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2) INFORMATION FOR SEQ ID NO: 669

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: extracted from V00267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669

15	ATGGCTACTG	GAAAGATTGT	CCAGGTAATC	GGCGCCGTAG	TTGACGTCGA	50
	ATTCCCTCAG	GATGCCGTAC	CGCGCGTGTA	CGATGCTCTT	GAGGTGCAAA	100
	ATGGTAATGA	GCGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGCGGCGGT	150
	ATCGTACGTA	CCATCGCAAT	GGGTTCCTCC	GACGGTCTGC	GTCGCGGTCT	200
	GGATGTAAAA	GACCTCGAAC	ACCCGATTGA	AGTCCCGGTA	GGTAAAGCGA	250
20	CTCTGGGCCG	TATCATGAAC	GTACTGGGTG	AACCGGTCTGA	CATGAAAGGC	300
	GAGATCGGTG	AAGAAGAGCG	TTGGGCGATT	CACCGCGCAG	CACCTTCCTA	350
	CGAAGAGCTG	TCAAACCTCT	AGGAACTGCT	GGAAACCGGT	ATCAAAGTTA	400
	TCGACCTGAT	GTGTCCGTTC	GCTAAGGGCG	GTAAAGTTGG	TCTGTTCCGT	450
	GGTGCGGGTG	TAGGTAAAC	CGTAAACATG	ATGGAGCTCA	TTCGTAACAT	500
25	CGCGATCGAG	CACTCCGGTT	ACTCTGTGTT	TGCGGGCGTA	GGTGAACGTA	550
	CTCGTGAGGG	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	600
	GACAAAGTAT	CCCTGGTGTA	TGGCCAGATG	AACGAGCCGC	CGGGAAACCG	650
	TCTGCGCGTT	GCTCTGACCG	GTCTGACCAT	GGCTGAGAAA	TTCCGTGACG	700
	AAGGTCGTGA	CGTTCTGCTG	TTCGTTGACA	ACATCTATCG	TTACACCCTG	750
30	GCCGGTACGG	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CAGCGGTAGG	800
	TTATCAGCCG	ACCCTGGCGG	AAGAGATGGG	CGTTCTGCAG	GAACGTATCA	850
	CCTCCACCAA	AACTGGTTCT	ATCACCTCCG	TACAGGCAGT	ATACGTACCT	900
	GCGGATGACT	TGACTGACCC	GTCTCCGGCA	ACCACCTTTG	CGCACCTTGA	950
	CGCAACCGTG	GTACTGAGCC	GTCAGATCGC	GTCTCTGGGT	ATCTACCCGG	1000
35	CCGTTGACCC	GCTGGACTCC	ACCAGCCGTC	AGCTGGACCC	GCTGGTGGTT	1050
	GGTCAGGAAC	ACTACGACAC	CGCGCGTGGC	GTTCAAGTCCA	TCCTGCAACG	1100
	TTATCAGGAA	CTGAAAGACA	TCATCGCCAT	CCTGGGTATG	GATGAACTGT	1150
	CTGAAGAAGA	CAAACCTGGT	GTAGCGCGTG	CTCGTAAGAT	CCAGCGCTTC	1200
	CTGTCCCAGC	CGTTCTTCGT	GGCAGAAGTA	TTCACCGGTT	CTCCGGGTAA	1250
40	ATACGTCTCC	CTGAAAGACA	CCATCCGTGG	CTTTAAAGGC	ATCATGGAAG	1300
	GCGAATACGA	TCACCTGCCG	GAGCAGGCGT	TCTACATGGT	CGGTTCCATC	1350
	GAAGAAGCTG	TGGAAAAAGC	CAAAAAACTT	TAA		1383

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2) INFORMATION FOR SEQ ID NO: 670

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*
(B) STRAIN: NCTC 11638
(C) ACCESSION NUMBER: extracted from AF004014

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670

	ATGAAAGCGA	TGGAAGGTAA	AATCATTTCAG	GTTTTAGGCC	CGGTGGTAGA	50
	TGTGGAGTTT	GAATCCTATC	TGCCGGCGAT	TTTTGAAGCA	CTAGACATTA	100
5	ATTTTGAAGT	TAATGGCGTT	CAAAAATCTT	TAGTTTTAGA	GGTGGCAGCC	150
	CATTTGGGTG	GTAATCGGGT	GCGAGCGATT	GCTATGGATA	TGACAGAAGG	200
	CTTAGTGCGT	AACCAAGCCG	TCAAAGCTCG	TGGCAAAATG	ATTGAAGTGC	250
	CTGTGGGCGA	AGAAGTGTTA	GGGCGTATTT	TTAATGTTGT	GGGCGAGAGC	300
	ATTGATAATT	TAGAGCCGCT	TAAGCCGTCC	TTAACTTGGC	CCATTCACAG	350
10	AAAAGCCCCT	AGTTTTGAGC	AGCAAAGCAC	TAAAACAGAA	ATGTTTGAAA	400
	CCGGTATTAA	AGTCATTGAC	TTGCTCGCGC	CTTATTCTAA	GGGCGGTAAA	450
	GTAGGCTTGT	TTGGTGGGGC	TGGCGTAGGC	AAAACGGTGA	TCATTATGGA	500
	GCTTATCCAC	AATGTGGCTT	ATAAGCATAA	CGGGTATTCTG	GTGTTTGCAG	550
	GTGTGGGGGA	GCGCACCAGA	GAAGGGAACG	ATCTGTATTT	TGAGATGAAA	600
15	GAAGGGGGCG	TTTTAGACAA	AGTTGCGTTG	TGCTATGGGC	AAATGAATGA	650
	GCCACCAGGT	GCAAGGAATC	GCATCGCATT	CACCGGCTTG	ACGATGGCGG	700
	AGTATTTCCG	TGATGAAAAG	GGCTTAGATG	TGTTGATGTT	TATTGATAAC	750
	ATCTTTAGAT	ACGCTCAAAG	CGGTGCGGAA	ATGAGCGCGC	TATTAGGCCG	800
	TATCCCTTCA	GCGGTGGGGT	ATCAGCCCAC	GCTAGCCGGG	GAAATGGGGA	850
20	AACTTCAAGA	GCGTATCGCT	TCCACTAAAA	ATGGCTCTAT	CACTTCGGTT	900
	CAAGCGGTGT	ATGTGCCAGC	AGACGACTTG	ACTGACCCAG	CCCCTGCTTC	950
	GGTGTTTGCG	CATTTAGATG	CGACTACGGT	GTTGAATAGA	AAGATCGCTG	1000
	AAAAAGGGAT	TTATCCGGCG	GTGGATCCTT	TGGATTCCAC	TTCAAGGATT	1050
	TTAAGCCCTC	AAATGATTGG	CGAGAAGCAC	TATGAAATCG	CCACCGGTAT	1100
25	CCAGCAAGTT	TTGCAAAAAT	ACAAGGATTT	GCAAGATATT	ATTGCGATTT	1150
	TGGGATTGGA	CGAATTGAGC	GAAGAGGATA	AAAAAACGGT	TGAAAGGGCC	1200
	AGAAAAATTG	AGAAGTTTTT	ATCCCAGCCG	TTTTTTGTGG	CTGAAGTGTT	1250
	TACAGGAAGT	CCCGGTAAGT	ATGTGACTCT	CCAAGAGACT	TTAGAGGGCT	1300
	TTGGAGGGAT	TTTAGAGGGC	AAATACGATC	ACATTCCTGA	AAACGCGTTT	1350
30	TACATGGTGG	GCAGCATTCA	AGAGGTTTTA	GAAAAAGCTA	AAAACATGAA	1400
	AAATTCCTAA					1410

35 2) INFORMATION FOR SEQ ID NO: 671

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1401 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium acetobutylicum*
 (B) STRAIN: DSM 792
 (C) ACCESSION NUMBER: extracted from AF101055

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671

	ATGCCAGAAC	ATGTAGGTAA	AATTGTTTCAG	GTAATAGGAC	CTGTTGTGGA	50
	TATTAAATTT	GATGCAGAGA	ACCTTCCTGA	CATCTATAAT	TCCATAGAAA	100
	TAGATATGGG	AGATAATAAA	AACTCATTG	CTGAAGTTGA	ACAACATGTA	150
55	GGAGATGACA	TAGTAAGAAC	AATAGCAATG	GAAGGTACTG	ACGGATTAAA	200
	AAGAGGAATG	GAAGCAGTTA	ACACTGGTAA	ACCAATATCT	GTACCAGTTG	250
	GAGAAAATGT	TTTAGGACGT	CTTTTTAATG	TTTTAGGTCA	GACAATAGAT	300
	GAAGCAGGAG	ACATGAATGC	TGATAAGTAT	TATCCAATTC	ATAGACCAGC	350
	TCCAACCTTT	GAAGAACAAT	CAGTTCAACC	AGAAATGTTT	GAAACAGGTA	400
60	TTAAGGTTAT	AGATTTACTT	GCTCCATATC	AAAAGGGTGG	AAAATCGGT	450

	TTGTTTCGGTG	GTGCCGGTGT	TGGTAAAACA	GTTCTTATTC	AGGAACTTAT	500
	AAATAATATA	GCAAAAGAAC	ACGGTGGATT	ATCAGTATTC	ACAGGTGTTG	550
	GAGAAAGAAC	AAGAGAAGGT	AATGACCTTT	ATTATGAAAT	GAAAGATTCA	600
	GGAGTTATAA	ATAAAACAGC	TCTAGTATTT	GGTCAGATGA	ATGAACCACC	650
5	TGGCGCTAGA	ATGAGAGTTG	CTTTAACAGG	ACTTACAATG	GCTGAATATT	700
	TTAGAGACAA	AGGTCAAGAT	GTGCTTCTAT	TTATAGATAA	TATATTCAGA	750
	TTTACACAAG	CTGGTTCAGA	GGTTTCAGCT	TTACTTGGTA	GAATACCTAG	800
	TGCCGTTGGT	TATCAGCCAA	CACCTGCAAA	TGAAATGGGT	GCTCTTCAAG	850
	AGAGAATAAC	ATCAACAAAA	CAGGGTTCAA	TCACATCCGT	TCAGGCTGTA	900
10	TATGTTTCCTG	CTGATGACCT	TACAGACCCA	GCTCCAGCAA	CAACATTTAC	950
	GCATCTTGAT	GCAACAACAG	TTCTTTCAAG	AGAAATATCA	AACTTAGGAA	1000
	TATATCCTGC	AGTTAGTCCT	CTTGAATCAA	CTTCAAGAAT	ACTTGATCCA	1050
	AGAATTGTTG	GAGAAGAGCA	TTATGAAGTT	GCTAACAAGG	TTAAACATAT	1100
	ACTTGAAAGA	TATCAAGAAC	TTCAAGATAT	CATAGCTATA	CTTGGTGTTG	1150
15	ATGAACTTTC	AGATGAGGAT	AGATTGTTAG	TTGGAAGAGC	AAGAAGAGTA	1200
	CAGAGATTCT	TATCTCAAGC	TTTTAGTGTT	GCTGAACAAT	TTACAGGAAT	1250
	GAAAGGTCAG	TTTGTACCTG	TAAAAGATAC	TATAAGAAGT	TTTAAAGAAA	1300
	TATTAGATGG	TAAGTGTGAT	GATCTTCCAG	AAGCTGCATT	TTTATTTGCA	1350
	GGAACAATAG	AAGATGTAAA	AGAAAAAGCT	AAAAAAATGA	TGGAAAGCTA	1400
20	A					1401

2) INFORMATION FOR SEQ ID NO: 672

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cytophaga lytica*
 (B) STRAIN: DSM 2039
 (C) ACCESSION NUMBER: M22535

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672

40

	ATGTCTAAAG	TTACAGGTAA	AGTTTCCCAA	ATTATTGGCC	CAGTTATAGA	50
	TGTGGAGTTC	CAAGCAGGGG	TAGATCTTCC	AAAAATTTAT	GATTCATTAG	100
	AAATTAAAAA	AGCAGATGGA	TCAATTTTGG	TTTTGGAAGT	ACAATCACAC	150
	ATTGGTGAGA	ACACAGTAAG	AACTATATCT	ATGGATTCTT	CTGATGGTTT	200
45	AAGTCGTGGA	GCAGAGGTTA	ATGCAACAGG	AAGCGCTATA	CAAATGCCAG	250
	TTGGAGATGA	CGTTTACGGA	CGTTTATTTA	ACGTAATTGG	AGACGCTATT	300
	GATGGTCTTG	GGAATTTACC	AAAATCTGGT	AAAGATGGTT	TGCCAATACA	350
	CAGAGAGGCA	CCAAAATTTG	AAGACTTATC	TACTTCTACA	GAAGTATTAT	400
	TTACAGGTAT	TAAAGTAATT	GACCTTATTG	AGCCTTATGC	AAAAGGTGGT	450
50	AAGATTGGTT	TATTTGGAGG	TGCCGGAGTA	GGTAAAACAG	TATTAATTCA	500
	GGAATTAATT	AACAACATTG	CAAAAGGTCA	CGGTGGACTT	TCTGTATTTG	550
	CTGGTGTAGG	TGAGCGTACT	CGTGAGGGTA	ACGATTTACT	ACGTGAGATG	600
	TTAGAGTCTG	GTATTATTAA	ATACGGAGAT	GACTTTATGC	ACTCTATGGA	650
	AGAAGGTGGT	TGGGATTTAT	CTAAAGTTGA	TAAATCTGTA	ATGAAAGATT	700
55	CTAAAGCAAC	CTTTGTATTT	GGACAAATGA	ATGAGCCACC	AGGAGCACGT	750
	GCACGTGTTG	CATTATCTGG	TTTAACTATT	GCAGAATATT	TCCGTGATGG	800
	AGCAGGTGAA	GGTCAAGGTA	AAGATGTACT	TTTCTTTGTG	GATAACATTT	850
	TCCGTTTTAC	ACAAGCTGGT	TCTGAGGTAT	CTGCATTACT	TGGTCGTATG	900
	CCATCTGCGG	TAGGTTACCA	ACCAACATTA	GCAACAGAAA	TGGGTGCTAT	950
60	GCAAGAGCGT	ATTACATCAA	CAAAAAGAGG	TTCTATTACA	TCTGTACAGG	1000

	CGGTTTACGT	ACCTGCGGAT	GATTTAACGG	ATCCAGCACC	GGCA A CTACC	1050
	TTTGCTCACT	TAGATGCAAC	AACGGTATTG	TCTCGTAAAA	TTGCAGAGTT	1100
	AGGTATTTAC	CCAGCGGTAG	ATCCATTAGA	TTCTACTTCT	AGAATCTTAG	1150
	CTCCAGAAAT	TTTAGGAAAA	GATCACTACT	CTTGTGCACA	ACGTGTAAAA	1200
5	GAGTTGTTAC	AACGTTATAA	AGAATTACAA	GATATTATTG	CTATCCTTGG	1250
	TATGGAAGAA	TTATCTGAGG	AAGATAAAAT	GGCAGTTGGT	AGAGCAAGAC	1300
	GTGTACAACG	TTTCTTATCT	CAGCCTTTCC	ACGTAGCAGA	GCAATTTACA	1350
	GGTCTTAAAG	GTGTTTTAGT	AGATATCAAG	GATACTATTA	AAGGATTTAA	1400
	TATGATTATG	GATGGTGAAT	TAGATCACTT	ACCAGAATCT	GCATTTAACC	1450
10	TTAAAGGTAC	TATTGAAGAA	GCTATAGAAG	CAGGAGAAAA	AATGCTTGCT	1500
	GAAGCATAA					1509

15 2) INFORMATION FOR SEQ ID NO: 673

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ehrlichia risticii*
(B) STRAIN: HRC-IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673

30	CCTAAAATAT	ATGATGCATT	ATATGTAAAA	CTAGATAATG	AAAATTTGTG	50
	TTTAGAAGTT	TCACAAATTA	TTGGAGATAA	TGTTGTTAGA	TGTATTGCAA	100
	TGGGAGCTAC	TTATGGATTA	AATCGTGGTT	TAGAAGTAGT	TTGTTTCAGGA	150
	AATCCAATTC	AGGTTCCCTGT	AGGTGAACAA	GTTTTAGGTA	GAATGTTTAA	200
35	TGTTGTTGGT	AAAACAATTG	ACAATCTTGA	ATCTTTAGAT	GATAAAAATA	250
	TAAAAATGAT	GCCAATTCAT	CGAAATCCAC	CATCATTTGA	AGAGCAATCC	300
	AATGAAATTG	AAATTTTTGA	AACAGGCATT	AAAGTTATTG	ATTTATTAAT	350
	TCCATATGCT	AAAGGTGGTA	AGATTGGATT	ATTTGGTGGA	GCAGGGGTTG	400
	GGAAAACGGT	TCTTGTTCAA	GAATTAATTC	ACAATATCGC	AAAAGGTCAT	450
40	GGTGGTCTAT	CTGTTTTTGC	TGGAGTTGGT	GAAAGAATCT	GTGAAGGTAA	500
	TGACTTGTAT	TATGAAATGA	TTGAAGGTGG	AGTTATAGAT	AAAACAGCCT	550
	TAGTGTTTGG	GCAAATGAAT	GAACCTCCTG	GCGCAAGAAT	GCGCGTAGCA	600
	TTAACTGCTT	TAACAATGGC	TGAATATTTT	CGTGATGTTC	AAAACCAAGA	650
	TGTTTTGTTA	TTTATTGATA	ATATCTTTAG	ATTTACACAA	GCTGGTAGTG	700
45	AAGTTTCAGC	ATTATTAGGA	AGAATGCCAT	CTGCTGTTGG	TTATCAACCA	750
	ACTTTGGCAT	ATGAAATGGG	ATTGTTACAA	GAAAGAATCA	CTTCCACTAA	800
	AAGTGGTTCT	ATAACATCT				819

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2) INFORMATION FOR SEQ ID NO: 674

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 840 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674

	AGAGCGAAGT	ACCAAGTGTT	TACGATGCTC	TGAATGTTGT	GGATTCCAAA	50
	GAACGTCTGG	TTCTGGAAGT	TCAACAGCAG	CTAGGCGGTG	GCGTGATTCTG	100
	CGCTATCGTT	ATGGGTAGCT	CGGATGGTTT	ACGTCGTGGA	ATGACAGTAC	150
10	AAAACACTGG	CGCTCCAATT	TCAGTACCAG	TAGGTACTAA	AACCCTAGGT	200
	CGTATCATGA	ACGTGCTTGG	TGATGCGATT	GACGAACGTG	GCGACATTGG	250
	CGCAGAAGAG	GTGTACTCGA	TTCACCGTCC	TGCTCCAAGC	TACGAAGAAC	300
	AGTCTAGTGC	AACTGAACTT	TTGGAAACGG	GTGTTAAGGT	TATCGACCTG	350
	ATCTGTCCGT	TTGCGAAAGG	CGGTAAAATC	GGTCTGTTCG	GTGGTGCGGG	400
15	TGTAGGTAAG	ACCGTTAACA	TGATGGAAC	TATCAACAAC	ATCGCGCTAC	450
	AGCACTCAGG	TTTGTCAGTA	TTTGCTGGGG	TAGGTGAGCG	TACTCGTGAG	500
	GGTAACGACT	TCTACCACGA	AATGCAGGAA	GCGGGCGTTG	TAAACGTTGA	550
	ACAACCAGAA	CTGTCGAAAG	TAGCGATGGT	TTACGGTCAG	ATGAACGAGC	600
	CACCAGGCAA	CCGTCTGCGT	GTAGCACTGA	CTGGTCTGAC	TATGGCGGAA	650
20	AAGTTCCGTG	ATGAAGGCCG	TGACGTACTG	CTGTTTATCG	ACAACATCTA	700
	CCGTTACACC	CTAGCGGGAA	CGGAAGTATC	TGCTCTGCTT	GGCCGTATGC	750
	CTTCAGCGGT	AGGTTACCAA	CCAACACTGG	CTGAAGAGAT	GGGTGTTCTG	800
	CAAGAACGTA	TCACGTCAAC	CAAAAAGGT	TCTATCACCT		840

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2) INFORMATION FOR SEQ ID NO: 675

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675

	CGGCGGTATC	CTAGTTGTAG	CGGCAACTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGCCAAGTAG	GTATTCCTTA	CATCATCGTA	100
45	TTCATGAACA	AGTGTGACAT	GGTTGACGAT	GAAGAGCTTC	TAGAGCTGGT	150
	AGAGATGGAA	GTTCGTGAGC	TGCTGTCTGA	GTACGATTTC	CCAGGTGATG	200
	ACCTGCCAGT	AATCCAAGGT	TCAGCACTAG	GCGCGCTAAA	CGGCGAAGCA	250
	CAGTGGGAAG	CGAAGATTGT	TGAGCTAGCA	GAAGCACTGG	ATACTTAYAT	300
	TCCAGAGCCA	GAGCGTGCAG	TAGACATGGC	ATTCCTGATG	CCAATCGAAG	350
50	ACGTATTCTC	AATCCAAGGT	CGTGGTACAG	TAGTAACTGG	CCGTATCGAG	400
	CGCGGCATCC	TGAAAGTGGG	TGACGAAGTA	GCGATCGTTG	GTATCAAAGA	450
	GACAGTAAAA	ACGACCTGTA	CAGGTGTAGA	GATGTTCCGT	AAGCTGCTTG	500
	ACGAAGGTCG	TGCAGGTGAG	AACGTAGGTG	CACTRCTACG	TGGTACTAAG	550
	CGTGAAGAAG	TAGAGCGTGG	TCAAGTACTG	GCGAAGCCAG	GTTCAATCAC	600
55	ACCACACACT	AAGTTCGAAT	CAGAAGTATA	CGTACTGTCA	AAAGATGAAG	650
	GTGGCCGTCA	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAAC	ACGTAACAGG	CAGCATTGAG	CTACCAGARG	GCGTAGAAAT	750
	GGTAATGCCA	GGCGACAACG	TGAAGATGGT	TGTAGACCTG	ATTGCACCAA	800
	TCGCGATGGA	CGAAGGTCTA	CGCTTCGC			828

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2) INFORMATION FOR SEQ ID NO: 676

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania enriettii*
 15 (B) STRAIN: ATCC 50120
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676

20	CTTCTCGGAT	GGCGTGCCGC	CGGTGCTGAC	GGCGCTGGAC	GTGACGGAGG	50
	AACTCGGGCG	CGACGAGCCG	CTGACGCTAG	AGATCGTGCA	ACACTTGGAC	100
	GCGCACACCG	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TACTGAAGCT	150
	GAAGTCGAAG	GTCGTGTCGA	CCGGCGGGAA	CATCTCTGTG	CCTGTGGGCC	200
	GCGAGACGCT	TGGCCGCATC	TTCAACGTAC	TGGGCGACGC	GATTGACCAG	250
	CGCGGCCCCG	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CGGAGGCGCC	300
25	GAAGCTGGCG	GACCAGGCGG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AAGTGATCGA	TCTGATCCTG	CCGTACTGCA	AGGGCGGCAA	GATCGGTCTG	400
	TTCGGCGGTG	CCGGTGTGGG	GAAGACTGTG	ATCATCATGG	AGCTGATCAA	450
	CAACGTCGCG	AAGGGCCACG	GTGGCTTCTC	CGTGTTCCGC	GGCGTTGGGG	500
	AGCGCACCCG	CGAGGGGACG	GATCTGTACC	TGGAGATGAT	GCAATCGAAG	550
30	GTGATCGACC	TGAAAGGTGA	GTCGAAGTGT	GTGCTTGTGT	ACGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCCGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATC	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CAGCGCTGCT	750
	GGGCCGCGATC	CCCGCCGCTG	TGGGCTACCA	ACCGACGCTT	GCGGAGGATC	800
35	TCGGCATGTT	GCAGGAGCGC	ATCACGTCTG	CGACGAAGGG	GTCGATCACG	850
	TCTGTGCAGG	CGGTGTACGT	GCCTGCGGAT	GATATCACGG	ATCCCGCGCC	900
	GGCGACGACA	TTCTCGCACC	TGGACGCGAC	GACGGTGCTG	GACCGCGCGG	950
	TGGCGGAGTC	TGGCATCTAC	CCCGCGGTCA	ACCCACTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCTGATGT	GATCGACGTG	GATCACTACA	ACGTTGCGCA	1050
40	GGACATTGTT	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTTG	1100
	CGGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
	CGTGCGCGCA	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	1200
	GGTGTTTACT	GGCATGACAG	GCCATTACGT	ACAGCTGAGC	GACACGGTGG	1250
45	AGTCGTTCTC	CGGTTTGCTG	ATGGGGTCGT	ACGACCAGAT	TCCGGAGA	1298

2) INFORMATION FOR SEQ ID NO: 677

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1083 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 55 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Babesia microtti*
 60 (B) STRAIN: Persing-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677

	CAAGCTCAAG	TCTGAGCGTG	AGAGAGGTAT	TACTATTGAC	ATTACTCTCT	50
5	GGAAATTTGA	GACCCAGAAA	TACGAGTACA	CTGTCATAGA	CGCACCTGGT	100
	CATCGTGACT	TTATCAAAAA	TATGATTACT	GGGACTTCAC	AAGCCGACGT	150
	TGCTATGCTT	GTCGTTCCCTG	CTGAATCTGG	CGGATTCGAG	GCTGCTTTTT	200
	CCAAAGAAGG	TCAGACCCGT	GAACACGCCT	TACTAGCCTT	CACACTTGGC	250
	GTCAAACAGA	TGATTGTTGC	TATTAACAAA	ATGGATTCTT	GTCAGTACAA	300
10	GGAGGATCGT	TATATGGAAA	TTTTCAAGGA	AGTACAGCAG	TACTTGAAGA	350
	AGGTGGGTTA	CAAAGTTGAA	AGCGTGCCGT	TTGTTGCTAT	TTCAGGATTC	400
	CACGGTGACA	ACATGGTTGA	AAAATCTACT	AACATGCCTT	GGTATAAGGG	450
	TAAGACCCTC	GTAGAGGCAC	TTGATCAAAT	GGAGCCTCCA	AAACGTCCGG	500
	TCGAAAAACC	TCTTAGATTG	CCCCTGCAGT	CAGTCTATAA	AATTGGAGGT	550
15	ATTGGTACGG	TACCAGTCGG	AAGGGTCGAA	ACAGGACAAC	TGAAAGCAGG	600
	AATGATCATT	ACTTTTGCCC	CCACTGGTTT	GACCACTGAA	TGTAAATCTG	650
	TTGAAATGCA	TCACGAGGTT	GTGGAAGTGG	CTAGCCCCGG	TGATAACGTT	700
	GGATTTAATG	TCAAGAATGT	GTCTGTTAAG	GATATTAAGA	GAGGAAATGT	750
	GGCTTCGGAT	TCGAAAAATG	ACCCAGCCAA	GGAAGCTACC	TCTTTCTCTG	800
20	CACAAGTCAT	TGTACTCAAT	CACCCTGGTA	CCATCAAGGC	CGGTTACTCA	850
	CCTGTGGTTG	ATTGCCATAC	TGCCCACATT	GCTTGCAAAT	TCGAATCTCT	900
	AGACACTAGG	ATTGACAAGC	GTACTGGCAA	GACTTTGGAA	GAAAATCCTA	950
	AGACTATTAA	GAATGGTGAC	GCTGCCATGG	TGACTATGAA	ACCAAATAAA	1000
	CCCATGGTTG	TGGAAACTTT	CACCGACTAC	GCCCCGTTGG	GCCGGTTCGC	1050
25	CGTGCGTGAT	ATGCGCCAAA	CCGTTGCCGT	CGG		1083

2) INFORMATION FOR SEQ ID NO: 678

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: Lev-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678

45	TGTGCTCATT	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCT	CACGGTGGTT	50
	ACTCTGTCTT	CACTGGTGTC	GGTGAGCGAA	CTCGTGAGGG	TAACGACTTG	100
	TACCACGAAA	TGAGGGAGAC	TGGTGTTATC	AACCTTGAGG	GTGACTCCAA	150
	GGTCGCTCTT	GGTGAGTTCT	TTTTTTTCTT	CAGGCTAATT	AGTCGATGAC	200
	GTGGGCCCTG	ACTAAAACCTG	TTTCTTCCAG	TCTTCGGTCA	GATGAACGAG	250
50	CCCCCTGGAG	CCCGTGCCCG	AGTTGCCCTT	ACTGGTTTGA	CCATTGCCGA	300
	GTACTTCCGT	GACGAGGAAG	GCCAGGATGT	GTTGCTTTTC	ATTGACAACA	350
	TTTTCCGATT	CACCCAGGCC	GGTTCCGAGG	TGTCTGCCTT	GCTCGGTCGT	400
	ATCCCCTCTG	CCGTCGGTTA	CCAGCCCCTT	CTTTCCACCG	ACATGGGTGG	450
	TATGCAGGAG	CGAATGTAGG	TTGCATTCTC	TGTGATTTTA	CGGCAAGCCT	500
55	TGACTTTTTT	TTTCTAGTAC	CACCACCAAG	AAGGGTTCCA	TTACCTCCGT	550
	C					551

60 2) INFORMATION FOR SEQ ID NO: 679

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 552 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: ATCC 44104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679

15	TGTGCTCATT	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCC	CACGGTGGTT	50
	ACTCCGTCTT	CACCGGTGTC	GGTGAGCGAA	CTCGTGAGGG	TAACGACTTG	100
	TACCACGAAA	TGAGGGAGAC	TGGTGTTATC	AACCTTGAGG	GTGACTCCAA	150
	GGTCGCTCTT	GGTGAGTTCT	TTTTTTTGGG	AGCTAATTAG	TCGATGACGT	200
20	GGGCCCTGAC	CAAAACCGTT	TCTTTCAGTC	TTCGGTCAGA	TGAACGAGCC	250
	CCCTGGAGCC	CGTGCCCGAG	TTGCTCTTAC	TGGTTTGACC	ATTGCCGAGT	300
	ACTTCCGTGA	CGAGGAAGGC	CAGGATGTGT	TGCTTTTCAT	TGACAAACATT	350
	TTCCGATTCA	CCCAGGCCGG	TTCCGAGGTG	TCTGCCTTGC	TCGGTCGTAT	400
	CCCCTCTGCC	GTCGGTTACC	AGCCCACTCT	TTCCACCGAT	ATGGGTGGTA	450
25	TGCAAGAGCG	AATGTAAGTT	GCATTTTTTG	TGATTTTACG	GCAAGTCTTG	500
	ACTTACATTT	TTTTCTAGCA	CCACCACCAA	GAAGGGTTCC	ATTACCTCCG	550
	TC					552

30 2) INFORMATION FOR SEQ ID NO: 680

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1018 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Cunninghamella bertholletiae*
 (B) STRAIN: ATCC 42115

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680

	TCTCCCTGCT	ATTTTAAACG	CTCTTGAAGT	TAAGGATCAT	GCTGGTGGTC	50
	GTCTTGTTCT	TGAAGTTGCT	CAACACTTGG	GTGAAAACAC	TGTACGTACT	100
	ATTGCTATGG	ATGGTACTGA	AGGTAAGTTT	ATTTTTAGAT	GATCATAAAT	150
50	AATTGATCAT	AATGATAAAA	AAAAAAGAAG	AAGAAGAACA	GGATGTATAT	200
	AATGGTTAAT	AAATAATATT	TTCATATTGK	ATATAACTAT	TTAATCTGTT	250
	TTTTTTTCTT	CATGATTATA	TATATATATG	TMCTAATATC	TAATATGAAC	300
	CTTTTTTTATA	AAATTAATCA	GGTCTTGTCC	GTGGTCAAAA	GGTTGTTGAT	350
	ACTGGTGCTC	CTATTACCAT	TCCTGTTGGT	AAGGAAGTTC	TTGGTCGTAT	400
55	CATCAACGTT	ATTGGTGAAC	CCATTGATGA	ACGTGGTCCT	ATTAAGGCCA	450
	AGTCTCACCG	TGCTATTAC	GCTGAAGCTC	CAGAATTCGT	TGATCAATCT	500
	CCTACTCCCG	AAATTCTTGA	AACTGGTATT	AAGGTTGTCG	ATTTATTAGC	550
	TCCTTATGCT	CGTGGTGGTA	AGATTGGTCT	TTTCGGTGGT	GCTGGTGTAG	600
	GTAAAACTGT	CTTGATTCAA	GAACTTATTA	ACAACATTGC	TAAAGCCCAT	650
60	GGTGGTTACT	CTATTTTCTG	TGGTGTGGT	GAACGTACTC	GTGAAGGTAA	700

	CGATTTATAC	CACGAAATGA	TGGAAACTGG	TGTCATTAAA	CTTGAAGGTG	750
	ACTCCAAGTG	TGCTCTTGTA	TTCGGTCAAA	TGAACGAACC	TCCTGGTGCT	800
	CGTGCCCGTG	TTGCTTTAAC	TGGTTTAACC	ATTGCTGAAT	ACTTCCGTGA	850
	TGAAGAAGGT	CAAGATGTGT	TACTTTTCAT	TGATAACATT	TTCCGTTTCA	900
5	CTCAAGCTGG	TTCTGAAGTA	TCTGCCCTTT	TAGGTCGTAT	TCCATCTGCT	950
	GTAGGTTACC	AACCCACTTT	ATCTACTGAT	ATGGGTGGTA	TGCAAGAACG	1000
	TATTACTACT	ACCAAGAA				1018

10

2) INFORMATION FOR SEQ ID NO: 681

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681

GGISSITTYG GIISIGGIAA RAC

23

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2) INFORMATION FOR SEQ ID NO: 682

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682

GTIACIGGYT CYTCRAARTT ICCICC

26

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2) INFORMATION FOR SEQ ID NO: 683

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683

55 GTIACIGGIT CISWIAWRTC ICCICC

26

60

2) INFORMATION FOR SEQ ID NO: 684

386

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3267 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (C) ACCESSION NUMBER: M64984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684

15	ATGGCTGGTG	CTTTAGAAAA	CGCAAGAAAA	GAAATTAAAC	GTCTTTCATT	50
	AGATGACACC	AATGAATCCC	AATATGGTCA	AATCTATTCT	GTTTCCGGTC	100
	CGGTTGTTAT	TGCCGAAAAC	ATGATTGGAT	GTGCCATGTA	CGAATTGGTT	150
	AAAGTTGGTC	ATGATAATTT	AGTTGGGGAA	GTTATTAGAA	TTAATGGTGA	200
	TAAAGCAACC	ATTCAAGTTT	ATGAAGAAAC	TGCAGGGGTC	ACTGTTGGTG	250
20	ATCCAGTTTT	AAGAACTGGT	AAACCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAATGGAAA	CTATTTATGA	TGGTATTCAA	AGACCTTTAA	AAGCCATTAA	350
	AGATGAATCC	CAATCTATTT	ATATCCCAAG	AGGTATTGAT	GTCCTGCTT	400
	TATCAAGAAC	TGTTCAATAT	GATTTCACTC	CAGGTCAATT	GAAAGTTGGT	450
	GATCATATCA	CTGGTGGGGA	CATTTTTTGGT	TCTATTTATG	AAAACCTCTT	500
25	ATTGGATGAC	CATAAGATTT	TGTTACCTCC	AAGAGCAAGA	GGTACTATTA	550
	CTTCTATTGC	TGAAGCCGGT	TCTTATAATG	TTGAAGAACC	AGTTTTTGAA	600
	GTTGAATTTG	ATGGTAAGAA	ACATAAATAC	TCTATGATGC	ATACATGGCC	650
	AGTTAGAGTT	CCAAGACCAG	TTGCTGAAAA	ATTGACTGCT	GATCATCCAT	700
	TGTTGACCGG	TCAAAGAGTC	TTGGATTCTT	TATTCCCATG	TGTTCAAGGT	750
30	GGTACTACTT	GTATCCCAGG	GGCTTTTGGT	TGTGGTAAAA	CTGTTATTTT	800
	TCAATCTTTG	TCCAAATTCT	CCAACCTCTG	TGTTATTATC	TATGTTGGTT	850
	GTTTCACTAA	AGGTACTCAA	GTCATGATGG	CTGATGGTGC	CGACAAATCT	900
	ATTGAATCTA	TTGAAGTTGG	TGACAAAGTC	ATGGGTAAAG	ATGGTATGCC	950
	AAGAGAAGTT	GTTGGCTTAC	CAAGAGGTTA	TGATGATATG	TACAAGGTTC	1000
35	GTCAACTTTC	TAGTACTAGA	CGTAATGCTA	AATCCGAAGG	CTTGATGGAT	1050
	TTCACTGTTT	CTGCTGATCA	TAAACTTATC	TTGAAAATA	AACAAGATGT	1100
	CAAGATTGCT	ACACGTAAAA	TTGGTGGCAA	CACCTATACT	GGTGTACTT	1150
	TCTATGTTTT	GGAAAAGACT	AAGACTGGTA	TTGAATTAGT	TAAAGCCAAG	1200
	ACTAAAGTTT	TCGGTCATCA	TATCCATGGT	CAAAATGGCG	CTGAAGAAAA	1250
40	AGCTGCTACT	TTTGCTGCTG	GCATTGACTC	TAAAGAATAC	ATTGATTGGA	1300
	TCATTGAAGC	TAGAGATTAT	GTACAAGTTG	ATGAAATTGT	CAAGACCAGC	1350
	ACCACTCAAA	TGATCAACCC	AGTTCATTTT	GAATCTGGTA	AACTCGGTAA	1400
	CTGGTTACAC	GAACACAAGC	AAAACAAATC	ACTTGCTCCA	CAATTGGGTT	1450
	ACTTGTTGGG	TACTTGGGCT	GGTATTGGAA	ATGTTAAATC	TTCTGCTTTC	1500
45	ACCATGAACT	CCAAAGATGA	TGTTAAATTA	GCTACAAGAA	TTATGAACTA	1550
	CTCTTCAAAA	TTGGGCATGA	CTTGTTCTTC	TACTGAATCC	GGTGAACCTA	1600
	ATGTCGCTGA	AAACGAAGAA	GAATTTTTCA	ATAACCTTGG	TGCTGAAAAG	1650
	GATGAAGCTG	GTGATTTCAC	TTTTGATGAA	TTTACCGATG	CTATGGATGA	1700
	ATTGACTATC	AATGTTTCATG	GTGCAGCTGC	AAGCAAGAAG	AACAATTTGT	1750
50	TGTGGAATGC	TTTGAAATCT	CTTGGTTTCA	GAGCCAAGTC	TACTGATATT	1800
	GTCAAGAGTA	TTCTCAACA	TATTGCTGTT	GATGATATTG	TTGTCAGAGA	1850
	ATCTTTGATT	GCCGGTTTAG	TTGATGCTGC	TGGTAATGTT	GAAACCAAAT	1900
	CCAATGGTTC	TATTGAAGCT	GTTGTTAGAA	CTTCTTTCAG	ACATGTCGCT	1950
	AGAGGTCTTG	TCAAGATTGC	TCATTCTTTG	GGTATTGAAT	CATCTATTAA	2000
55	TATTAAAGAT	ACTCACATTG	ATGCTGCTGG	TGTTAGACAA	GAATTTGCTT	2050
	GTATTGTCAA	TTTGACTGGT	GCTCCACTTG	CTGGTGTTCT	TTCTAAATGT	2100
	GCACTTGCAA	GAAACCAAAC	TCCAGTTGTC	AAATTTACCA	GAGACCCAGT	2150
	TTTGTTCAAC	TTTGATTTGA	TCAAATCTGC	AAAAGAAAAC	TATTATGGTA	2200
	TTACTTTGGC	TGAAGAAACT	GATCATCAAT	TCCTTTTATC	CAACATGGCC	2250
60	TTGGTGCACA	ACTGTGGTGA	ACGTGGTAAT	GAGATGGCTG	AAGTTTTGAT	2300

	GGAATTCCCA	GAATTGTTTA	CTGAAATTTT	TGGTAGAAAA	GAACCAATTA	2350
	TGAAACGTAC	CACTTTGGTT	GCCAATACTT	CTAATATGCC	AGTCGCTGCC	2400
	AGAGAAGCTT	CTATTTATAC	TGGTATTACA	TTGGCTGAAT	ATTTTCAGAGA	2450
	TCAAGGTAAG	AATGTTTCTA	TGATTGCTGA	TTCTTCTTCA	CGTTGGGCTG	2500
5	AAGCTTTGAG	AGAAATTTCT	GGTAGATTGG	GTGAAATGCC	TGCTGATCAA	2550
	GGTTTCCCAG	CTTATTTGGG	TGCTAAATTG	GCTTCTTTCT	ATGAGCGTGC	2600
	CGGTAAAGCC	ACTGCTTTGG	GTTCAACCAGA	TAGAGTTGGT	TCAGTTTCTA	2650
	TTGTTGCTGC	TGTTTCTCCA	GCTGGTGGTG	ATTTCTCTGA	TCCAGTTACT	2700
	ACTTCTACTT	TGGGTATTAC	TCAAGTTTTT	TGGGGGTGG	ATAAGAAATT	2750
10	GGCCCAAAGA	AAACATTTCC	CATCTATTAA	CACCAGTGTT	TCTTATTCTA	2800
	AATACACCAA	TGTTTTGAAC	AAATACTATG	ATTCCAATA	TCCAGAATTC	2850
	CCACAATTGA	GAGACAAAAT	TAGAGAAATT	TTATCTAATG	CTGAAGAATT	2900
	GGAACAAGTT	GTTCAATTAG	TTGGTAAATC	TGCATTGTCT	GATTCTGATA	2950
	AGATTACTTT	AGATGTTGCT	ACCTTGATTA	AAGAAGATTT	CTTGCAACAA	3000
15	AATGGTTATT	CTTCATATGA	TGCATTCTGT	CCAATTTGGA	AGACTTTTGA	3050
	TATGATGAGA	GCATTTATTT	CATATTATGA	TGAAGCACAA	AAAGCAATTG	3100
	CCAATGGTGC	TCAATGGTCT	AAATTAGCTG	AAAGTACTAG	TGATGTTAAA	3150
	CATGCTGTTT	CTTCAGCTAA	ATTCTTTGAA	CCATCAAGAG	GTCAAAAAGA	3200
	AGGTGAAAAA	GAATTTGGAG	ATTTATTAAC	CACTATCTCC	GAAAGATTTG	3250
20	CTGAAGCTTC	AGAATAA				3267

2) INFORMATION FOR SEQ ID NO: 685

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 9790
 (C) ACCESSION NUMBER: D17462

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685

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	TTGCAAATTG	GAAAAATCAT	AAAAGTCTCC	GGTCCTCTCG	TTATGGCAGA	50
	AAATATGTCA	GAAGCAAGTA	TTCAAGACAT	GTGTTTAGTG	GGAGATTTAG	100
	GAGTCATCGG	CGAAATCATT	GAGATGCGTC	AAGATGTGGC	GTCTATTCAA	150
	GTATATGAAG	AACTTCAGG	AATTGGTCCC	GGAGAACCTG	TTCTGTTCCAC	200
45	TGGGGAAGCA	CTATCTGTTG	AGCTAGGACC	AGGAATCATT	TCACAAATGT	250
	TTGACGGGAT	TCAAAGACCA	CTGGATACAT	TTATGGAAGT	GACTCAAAGT	300
	AACTTCTTAG	GACGTGGGGT	CCAATTACCA	GCTTTAGATC	ATGAGAAACA	350
	ATGGTGGTTT	GAAGCGACAA	TCGAAGAAGG	AACAGAAGTA	AGTGCTGGAG	400
	ACATCATTGG	GTACGTGGAT	GAAACGAAGA	TCATTCAGCA	CAAAATCATG	450
50	GTCCCTAATG	GTATCAAAGG	AACTGTACAA	AAAATTGAAT	CTGGATCATT	500
	TACGATCGAT	GATCCGATTT	GTGTGATCGA	AACGGAACAA	GGCTTAAAAG	550
	AGCTGACGAT	GATGCAAAAA	TGGCCAGTAC	GTCGTGGTCG	ACCAATCAAA	600
	CAAAAATTAA	ATCCAGATGT	ACCGATGATC	ACCGGTCAAA	GGGTCATTGA	650
	CACGTTTTTC	CCAGTAACTA	AAGGAGGAGC	GGCAGCCGTT	CCAGGTCCGT	700
55	TTGGTGCAGG	GAAGACAGTT	GTGCAACACC	AGATTGCTAA	GTGGTCGGAC	750
	GTAGATCTAG	TGGTTTACGT	TGGTTGTGGG	GAACGAGGAA	ATGAAATGAC	800
	GGATGTCGTC	AATGAATTTT	CTGAACCTGAT	CGATCCAAAT	ACAGGCGAGT	850
	CTTTGATGGA	ACGAACCTGT	TTGATCGCTA	ATACATCGAA	CATGCCAGTA	900
	GCTGCTCGAG	AAGCTTCTAT	TTATACGGGA	ATCACGATTG	CCGAGTACTT	950
60	CCGTGACATG	GGGTATGATG	TAGCAATCAT	GGCAGATTCC	ACTTCTCGTT	1000

	GGGCAGAAGC	ACTGCGTGAA	ATGAGCGGAC	GTTTAGAAGA	AATGCCCTGGT	1050
	GATGAAGGTT	ATCCCGCTTA	TCTGGGCTCT	CGTCTAGCTG	AATACTATGA	1100
	ACGTTTCAGGA	CGTGTCATTG	CTCTAGGCTC	TGACCAACGT	GAGGGCAGTA	1150
	TCACTGCCAT	CAGTGCGGTT	TCTCCTTCTG	GTGGAGATAT	CTCTGAACCA	1200
5	GTGACTCAAA	ATACCTTACG	TGTGGTGAAG	GTTTTCTGGG	GATTAGATTC	1250
	TAGTCTTGCT	CAAAAAAGAC	ATTTTCCATC	GATTAACCTG	ATCCAAAGTT	1300
	ACTCATTATA	TTCAACAGAA	GTTGGCAGAT	ATATGGATCA	AATCTTACAA	1350
	CAGGATTGGT	CTGATATGGT	AACTGAAGGC	ATGCGGATCT	TGCAAGAAGA	1400
	AGAACAATTA	AATGAAATCG	TGCGCTTGGT	AGGGATCGAT	TCGCTTTCTG	1450
10	ATAACGATCG	CTTGACCCTT	GAAGTAGCAA	AATCGATTCG	AGAAGACTAT	1500
	TTACAACAAA	ATGCTTTTGA	TGATGTAGAT	ACGTTTACTT	CAAGAGAAAA	1550
	ACAATTCAAC	ATGTTGAAAG	TTATTTTGAC	TTTTGGGAAA	GAAGCTCGAA	1600
	AAGCCTTATC	GTTGGGAGCG	TACTTCAATG	AAATCATGGA	AGGTACAGTA	1650
	GCGGTCAGAG	AACGCATTAG	TCGGAGCAAG	TATATTCCAG	AAGAAGAGTT	1700
15	AGCCAAAATT	AGTAGTATAA	ATGAAGAAAT	CAAAGAAACG	ATCCAATTGA	1750
	TTGTTTCAGA	AGGAGGGATG	ACCGATGATT	AA		1782

20 2) INFORMATION FOR SEQ ID NO: 686

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1781 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia pneumoniae*
 (B) STRAIN: CWL 029
 (C) ACCESSION NUMBER: Genome project

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686

	CAGGGACATG	TTATAGAAGC	TTATGGAAAC	TTGTTACGTG	TACGCTTTGA	50
	CGGATATGTT	AGACAAGGTG	AAGTTGCATA	TGTCAACGTA	GATAATACCT	100
	GGTTAAAAGC	AGAAGTGATT	GAAGTTGCTG	ATCAAGAAGT	CAAGGTTTCAG	150
40	GTATTTGAAG	ATACACAAGG	CGCGTGTCGA	GGAGCTCTTG	TTACGTTTTTC	200
	AGGACATCTT	TTAGAAGCCG	AGTTAGGGCC	TGGCTTGCTT	CAGGGCATTTC	250
	TCGATGGACT	TCAAAATCGT	CTTGAGGTGC	TAGCTGAAGA	TAGTTCTTTC	300
	TTGCAGAGAG	GCAAGCATGT	TAATGCTATT	TCTGATCATA	ATTTATGGAA	350
	TTATACTCCC	GTAGCTTCTG	TTGGGGATAC	TTAAGACGA	GGAGATCTTC	400
45	TAGGAACAGT	ACCTGAAGGA	CGATTTACTC	ATAAGATTAT	GGTTCCTTTT	450
	TCTTGCTTTC	AAGAGGTTAC	CCTGACTTGG	GTAATTTCTG	AAGGAACCTA	500
	TAATGCTCAT	ACTGTGGTCG	CAAAAGCTCG	AGATGCTCAG	GGTAAAGAAT	550
	GTGCCTTTAC	TATGGTGCAA	AGATGGCCGA	TCAAACAAGC	TTTTATTGAA	600
	GGAGAGAAGA	TCCCTGCGCA	TAAGATTATG	GATGTGGGTT	TGCGAATCTT	650
50	AGATACGCAA	ATTCCAGTAT	TGAAGGGGGG	AACTTTCTGT	ACCCCAGGAC	700
	CTTTTGGTGC	AGGGAAAACA	GTCTTACAAC	ACCATCTTTC	TAAGTACGCT	750
	GCTGTAGATA	TTGTGATTTT	GTGTGCGTGC	GGAGAGCGTG	CTGGTGAAGT	800
	TGTTGAGGTA	TTACAAGAGT	TCCCTCATCT	TATCGACCCC	CATACCGGAA	850
	AGTCTTTAAT	GCACAGAACA	TGTATTATTT	GTAACACATC	ATCCATGCCT	900
55	GTGGCTGCCC	GAGAGTCTTC	GATCTATTTA	GGAGTGACGA	TTGCAGAATA	950
	CTATCGCCAG	ATGGGACTAG	ATATTCTGCT	TTTAGCTGAT	TCTACATCCC	1000
	GATGGGCACA	AGCCCTTAGA	GAGATTTTCG	GACGTCTTGA	AGAAATCCCT	1050
	GGAGAGGAAG	CATTTCTGCT	ATACCTGTCT	TCTAGAATAG	CTGCTTTTTTA	1100
	TGAGCGAGGA	GGAGCTATCA	CCACGAAAGA	TGGTTCTGAA	GGATCTTTAA	1150
60	CTATATGTGG	TGCGGTGTCT	CCTGCAGGAG	GAACTTTTGA	AGAACCAGTC	1200

	ACTCAATCTA	CATTAGCTGT	AGTCGGAGCG	TTCTGTGGTC	TTTCAAAAGC	1250
	ACGAGCTGAC	GCACGTAGGT	ATCCTTCAAT	AGACCCTTTG	ATTTCTTGGT	1300
	CAAAATATTT	GAACCAGGTA	GGACAAATTT	TAGAAGAGAA	GGTTTCAGGC	1350
	TGGGGTGGTG	CTGTGAAAAA	AGCAGCACAG	TTTCTAGAGA	AAGGTTTCAGA	1400
5	AATCGGCAAG	CGTATGGAAG	TTGTCAGTGA	AGAAGGGGTT	TCTATGGAAG	1450
	ACATGGAAAT	CTACTTAAAG	GCAGAACTTT	ATGATTTTTG	TkATCTCCAG	1500
	CAGAACGCAT	TCGATCCTGT	GGACTGTTAT	TGTCCTTTTG	AGAGACAGAT	1550
	AGAGTTATTT	TCATTAATCA	GTCGTATTTT	TGATGCTAAA	TTTGTTTTTG	1600
	ATAGTCCTGA	TGATGCAAGA	AGCTTTTTTC	TTGAGCTGCA	GAGCAAGATT	1650
10	AAGACATTAA	ATGGCCTGAA	ATTTCTTTCA	GAGGAATATC	ATGAGAGTAA	1700
	AGAGGTCATA	GTTAGACTGT	TGGAAAAAAC	AATGGTACAA	ATGGCGTAAG	1750
	GATATGCAAA	CAATCTACAC	AAAAATAACT	G		1781

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2) INFORMATION FOR SEQ ID NO: 687

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1758 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Halobacterium salinarum*
- (C) ACCESSION NUMBER: S56356

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687

	ATGAGTCAAG	CTGAAGCAAT	CACTGACACC	GGCGAAATCG	AGAGCGTGAG	50
	CGGTCCGGTC	GTGACCGCCA	CGGGCCTCGA	CGCGCAGATG	AACGACGTCG	100
	TCTACGTGGG	CGACGAGGGT	CTGATGGGCG	AGGTCATCGA	GATCGAAGGC	150
35	GACGTAACCA	CCATCCAGGT	CTACGAGGAG	ACGTCCGGCA	TCGGGCCGGG	200
	CCAGCCCCTG	GACAAACACG	GCGAACCCTG	CACCGTGGAC	CTGGGCCCGG	250
	GGATGCTGGA	CTCCATCTAC	GATGGTGTGC	AGCGTCCACT	GGACGTCCTC	300
	GAAGACGAGA	TGGGGGCGTT	CCTCGATCGC	GGTGTGACG	CACCCGGCAT	350
	CGACCTCGAC	ACCGACTGGG	AGTTCGAGCC	CACCGTCGAG	GCGGGCGACG	400
40	AGGTCGCGGC	CGGCGATGTC	GTCGGCACCG	TCGACGAAAC	GGTCAGCATC	450
	GAACACAAGG	TTCTGGTGCC	CCCCCGCAGT	GACGGCGGCG	AAGTCGTCGC	500
	CGTCGAATCC	GGCACGTTCA	CCGTCGACGA	CACGGTCGTC	GAGTTGGACA	550
	CCGGCGAGGA	GATCCAGATG	CACCAGGAGT	GGCCGGTCCG	CCGCCAGCGC	600
	CCCACCGTCG	ACAAGCAGAC	GCCGACGGAG	CCGCTGGTGT	CCGGCCAGCG	650
45	CATCCTCGAC	GGCCTGTTCC	CGATCGCGAA	AGGCGGGACG	GCCGCGATCC	700
	CGGGGCCGTT	CGGGTCCGGG	AAGACGGTCA	CCCAGCAGTC	CCTCGCGAAG	750
	TTCCGCCGAC	GCGACATCGT	TGTCTACATC	GGCTGTGGTG	AGCGCGGCAA	800
	CGAGATGACG	GAAGTCATCG	AGGACTTCCC	GGAGCTGCCC	GACCCCCAGA	850
	CCGGGAACCC	GCTGATGGCC	CGCACCACGC	TCATCGCGAA	CACGTCGAAC	900
50	ATGCCGGTTG	CCGGGCGTGA	GTCCTGCATT	TACACGGGAA	TCACCATCGC	950
	GGAGTACTAC	CGCGACATGG	GCTACGACGT	GGCGCTGATG	GCCGACTCCA	1000
	CCTCGCGGTG	GGCGGAGGCC	ATGCGGGAGA	TCTCCTCGCG	ACTCGAGGAG	1050
	ATGCCCCGGC	AGGAGGGGTA	TCCCGCGTAC	CTGGCCGCCC	GCCTCTCGGA	1100
	GTTCTACGAG	CGCGCCGGCT	ACTTCGAGAA	CTTCAACGGG	ACCGAGGGCT	1150
55	CCATCTCGGT	CATCGGTGCG	GTGTCGCCGC	CCGGCGGGGA	CTTCTCCGAG	1200
	CCGGTCACCC	AGAACACGCT	GCGCATCGTG	AAGACGTTCT	GGGCGCTTGA	1250
	CTCGGACCTC	GCCGAGCGCC	GGCACTTCCC	GGCGATCAAC	TGGGACGAGT	1300
	CCTACAGCCT	CTACAAGGAC	CAACTCGACC	CGTGGTTTAC	GGACAACGTC	1350
	GTCGACGACT	GGGCCGAGCA	GCGCCAGTCG	GCGGTCGACA	TCCTCGACGA	1400
60	GGAATCCGAA	CTCGAAGAGA	TCGTGCAGCT	CGTCGGGAAG	GACGCGCTGC	1450

	CCGAGGACCA	GCAGCTCACG	CTGGAAGTCG	CGCGGTACAT	CCGCGAGGCG	1800
	TGGCTCCAGC	AGAACGCGCT	CCACGACGTG	GATCGCTACT	GCCCCGCCGA	1550
	GAAGACGTAC	GCCATCCTCT	CCGGCATCAA	GACGCTTCAC	GAGGAGTCCT	1600
	TTGAGGCGTT	GGACGCCGGT	GTGCCAGTCG	AGGAGATCAC	GTCGATCGAC	1650
5	GCCGCGCCGC	GCCTGAATCG	TCTCGGCACG	ACGCCCCGACG	ACGAGCACGA	1700
	GGCGGAGGTC	GCGGAGATCA	AACAGCAGAT	TACCGAGCAG	CTTCGGGAGC	1750
	TCTACTGA					1758

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2) INFORMATION FOR SEQ ID NO: 688

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 3118 bases
15	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human
(C) ACCESSION NUMBER: L09234

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688

	GAATTCCGGC	AGCTGACTAG	TCTTGTGATT	GGGGTCCTGG	GCTGATAAAA	50
	TCATTCCAAA	TGACGAGCAC	ATTGATAAAG	ACGTCCGATG	AGGACCGGGA	100
	GTCCAAATTC	GGCTTTGTTT	TTGCCGTATC	TGGACCTGTG	GTGACAGCTG	150
30	AACGAATGGC	CGGTTCTGCT	ATGTACGAAC	TGGTGCGTGT	CGGTTATTAT	200
	GAAGTGGTCG	GAGAGATCAT	CCGGTTGGAG	GGTGACATGG	CAACAATCCA	250
	AGTATACGAA	GACACCTCAG	GTGTGACAGT	AGGCGATCCC	GTGCTGCGCA	300
	CAGGCAAGCC	GCTGTCCGTG	GAAGTGGGAC	CCGGAATCAT	GGGCAGCATC	350
	TTCGACGGTA	TCCAGCGACC	GCTGAAGGAT	ATCAATGAAC	TGTCAAATAG	400
35	TATCTACATC	CCGAAAGGTG	TCAATGTGCC	TGCCCTGAGT	CGCACTGCAC	450
	AGTGGGACTT	CAGTCCCGTC	AGTGTCAAGG	TTGGAAGCCA	CATTACTGGT	500
	GGTGACCTGT	ACGGTTTGGT	CCACGAAAAT	ACTCTGGTGA	AACACAAGTT	550
	GCTGCTGCCG	CCCCGTGCCA	AGGGAAGTGT	CACGTACATT	GCAGAACCTG	600
	GAAACTACAC	AGTTGATGAT	GTTGTCCTGG	AGACAGAATT	TGACGGCGAG	650
40	CGATCAAAGT	TCACCATGCT	GCAAGTGTGG	CCTGTACGTC	AGCCCAGGCC	700
	TGTTACAGAA	AAGTTGCCAG	CTAACTACCC	CCTCCTTACT	GGCCAGCGTG	750
	TGCTCGACTC	CCTATTCCCG	TGTGTCCAGG	GTGGAACAAC	AGCTATTCCT	800
	GGGGCCTTCG	GATGTGGCAA	GACTGTAATA	TCACAGTCTT	TGTCAAATAA	850
	CTCAAACCTC	GATGTAATTA	TCTATGTAGG	TTGTGGTGAG	CGAGGTAATG	900
45	AAATGTCAGA	AGTACTCAGG	GATTTCCCGC	AGTTGTCGTT	GGAGATTGAT	950
	GGTGTGACTG	AATCAATCAT	GAAGAGAACA	GCCCTGGTCG	CAAACACATC	1000
	AAACATGCCT	GTGGCTGCTC	GAGAAGCATC	TATCTACACA	GGTATTACAC	1050
	TGTCAGAATA	CTTCAGGGAC	ATGGGTTACA	ATGTATCCAT	GATGGCTGAC	1100
	TCAACTTCAC	GATGGGCCGA	AGCTCTTCGA	GAAATCTCAG	GTCGATTGGC	1150
50	TGAAATGCCT	GCCGACAGCG	GTTATCCCGC	CTACCTAGGT	GCACGACTTG	1200
	CCAGTTTCTA	CGAGCGTGCC	GGCCGTGTGA	AGTGCTTGGG	TAACCCAGAC	1250
	AGGGAGGGCT	CCGTGAGTAT	AGTGGGCGCC	GTGTCGCCGC	CCGGTGGAGA	1300
	CTTCTCAGAT	CCCGTGACGA	CGGCCACACT	AGGTATCGTC	CAGGTGTTCT	1350
	GGGGTCTCGA	CAAGAACTT	GCCCAGCGAA	AGCACTTCCC	ATCCATCAAC	1400
55	TGGCTCATCT	CGTACAGTAA	ATACATGCGT	GCTCTGGATG	ACTTCTACGA	1450
	CAAGAATTTT	CCAGAGTTTG	TCCCACTGCG	TACAAAGGTG	AAGGAGATTT	1500
	TGCAGGAGGA	AGAAGACCTG	TCTGAAATTG	TGCAGTTGGT	CGGTAAAGCT	1550
	TCATTGGCAG	AAACTGACAA	GATCACACTT	GAGGTTGCCA	AACTATTAAA	1600
	GGATGATTTT	CTGCAACAGA	ACAGCTATT	ACCATATGAC	CGTTTCTGCC	1650
60	CATTCTACAA	GACAGTAGGA	ATGCTGAAAA	ATATGATTGC	TTTCTACGAT	1700

	ATGTCTCGGC	ATGCAGTTGA	ATCTACTGCT	CAGAGCGAGA	ACAAGATCAC	1750
	TTGGAATGTT	ATTAGAGATT	CTATGGGCAA	TATTCTGTAT	CAGCTTTCCT	1800
	CCATGAAATT	CAAGGATCCA	GTCAAGGATG	GAGAAGCGAA	GATCAAGGCA	1850
	GACTTTGAGC	AGCTTCATGA	AGACATTGAG	CAAGCCTTCA	GGAACCTGGA	1900
5	GGATTAAAGT	GGTAGCTGCC	AGTGGTTCTC	TCGGTGCAGT	TGTCACATTT	1950
	GGCAAGCTCT	GTAGGGTTGC	CGAGTGGCAT	CGGTGCTAGA	CACCTGAGCA	2000
	TTCCTTTGCC	ACATAAAGAC	TAAAGCAGGT	GGAATTTTCA	TTGTAAAAAG	2050
	CTGGTTCCAT	TGGTGCTAAG	ATTATGTTGT	GCCCTTTTCT	GCTTCTCACA	2100
	TTCCAACAGA	GGAATTTACT	TCCAGTTTTT	TTCCATTTTC	CTCCTCATTT	2150
10	TAAGTGTCGG	TACAGAGGCA	ATAATCTGAT	AACTCTGTAC	CGTCACTTAC	2200
	AAGCAGGGAG	AATTTGTAAT	TATTACAAAT	CCCATTATCT	CTGTGCACCA	2250
	CAGCCTTGTA	AATTCATTTG	TCCCAGGACT	CCCTCTTGTG	TGTACGTGAG	2300
	ATTGCCGTCT	GTATGTATGT	ACACACCGTA	CTGCAGTATT	TGAAGTCAGT	2350
	CAGAAGGTGA	ATTACACCAC	TTACTCATTG	TGTCACGTAG	CAAGTGTGCA	2400
15	AACTGCCATC	CATTGTCCTA	TTTATTCACA	TAAGTAGTTT	TCTTTGCATT	2450
	TCCAGTGTTG	CAAATTGTGT	TTAGAAAATT	ATGCCATCGA	GACTGGTCGA	2500
	ACCTCACATT	GTAATCAGT	ATTTACACAC	ACGTTTACTT	GCTACAGAAA	2550
	TGTAGAAAAA	ATAATTGTTG	TATATTGAAA	GTACAAGTGA	CAAAGTTGCA	2600
	TTTAAAATGG	TGAATGTATT	TTATATTTCT	TTTGTAGACA	CAAGAGTTAA	2650
20	TGCATTTTGC	TTAATGGAGA	TGTATGTAAA	CCTAAAATAG	CAGTTTGTGC	2700
	ACAAATTATG	TATATGTGAA	ATGGAGATGG	TTTCTAATTT	GCTGATTGAT	2750
	TGCCAGTATT	AATTTAAACA	ACTGTAGTTG	TGGGATGTAG	TGGGAAGATT	2800
	TTTTTTTTCC	TATAAAATTG	GTGGATGTAT	GTGTCGGAGA	TTTTGATTGT	2850
	ATGTGTAAAA	TAGTGATCCC	AGTAACTGTA	AAGCTTTAGA	ATACAGTTAC	2900
25	TGACTGTATA	GTTGTACAGG	TGTTGTTACT	TTTAAGAATT	TATTGACACA	2950
	AAGGTGAAAG	TCTATTATTG	TATTGTAATG	TTTAAAGCAT	TTAAGGTTTA	3000
	AAAATCCTAC	TTCTGTGTAT	AAATGTTACC	ATTCCTCATA	TAACATAACT	3050
	GTGTAGAAAT	ACAGTCAACT	TCATGTTTCT	TAGCATTTCA	CTGTTGTCAC	3100
	ATAAATTATG	CCCGGAAT				3118
30						

2) INFORMATION FOR SEQ ID NO: 689

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1836 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Plasmodium falciparum*
 - 45 (B) STRAIN: 3D7
 - (C) ACCESSION NUMBER: L08200
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689

50	ATGACAAAAG	TTGCTGTTGA	AAAAGAGGAA	CCAGGAGTTG	TTTATAAGGT	50
	GGCTGGTTCA	TTAGTTATTG	CTGAGAATAT	GAGTGGAACT	CGTATGTACG	100
	AGTTAGCTAA	AGTAGGATGG	AATAAATTGG	TTGGAGAAAT	TATTAGATTA	150
	GAAGGGAATT	ATGCATATAT	ACAAGTTTAT	GAAGATACTT	CAGGTTTATC	200
	TGTAGGAGAC	CCTGTTATAA	AAACAGGAAA	TGCTTTATCA	GTCGAATTGG	250
55	GTCCTGGTAT	TTTAGATAAT	ATTTATGATG	GTATTCAAAG	ACCATTAGAA	300
	AGAATAGCAA	ATGTGTGTGG	TGATGTATAT	ATATATAAAG	GTATTGATAT	350
	GACATCTTTA	GATCATGATA	AACAATGGCA	ATTTTATGCT	GATAAGAAAT	400
	TAAAATTAAA	TGATATTGTT	ACTGGTGGAG	ATATCTTTGG	ATTTGTTGAT	450
	GAAAATAAAT	TATTTAAAGA	ACACAAAATT	ATGGCTCCAC	CTAATGCTAA	500
60	AGGGAGGCTT	ACATATATTG	CTCCAGATGG	ATCATATACT	TTAAAAGATA	550

	AAATATTTGA	ATTAGAATAT	CAAGGAAAAA	AATATACATA	TGGTTTATCT	600
	CATTTATGGC	CTGTTTCGTGA	TCCTAGACCT	GTTTTAGAAA	AGGTAACAGG	650
	GGATACTTTA	TTATTAACAG	GGCAAAGAGT	TTTAGATTCTG	TTATTTCCAA	700
	CAGTTCAAGG	AGGTACTTGT	GCTATTCCTG	GTGCATTTGG	TTGTGGAAAA	750
5	ACTTGTGTTT	CTCAGGCCTT	ATCAAAATAT	TCTAATAGTG	AAGTTATTAT	800
	ATATGTAGGA	TGTGGTGAAA	GAGGTAATGA	AATGGCTGAA	ATTTTATCCG	850
	ACTTTCCTGA	ATTAACACT	AAAGTAGATA	ATGAAGATGT	AGGTATTATG	900
	CAAAGAACGT	GTTTAGTTGC	TAATACTTCT	AACATGCCTG	TCGCTGCAAG	950
	AGAAGCTAGT	ATTTATACAG	GTATTACTTT	ATGTGAATAT	TTCCGTGATA	1000
10	TGGGTTATAA	TGCTACCATG	ATGGCTGATA	GTACAAGTAG	ATGGGCAGAA	1050
	GCCTTAAGAG	AAATTTTCAGG	ACGTTTTCAGT	GAAATGCCTG	CAGATAGTGG	1100
	TTATCCAGCT	TATTTAGGTG	CTAGATTAGC	TTCCTTTTAT	GAACGTGCAG	1150
	GAAAAGTCAA	ATGTATTGGT	TCTCCATCTC	GTATAGGATC	CATTACAATT	1200
	GTGGGTGCTG	TGTCTCCACC	AGGTGGTGAT	TTCTCTGACC	CTGTAACTAC	1250
15	AGCAACCATG	TCTATTGTTC	AAGCATTTTG	GGGGTTAGAT	AAAAAACTAG	1300
	CTCAAAGAAA	ACATTTCCCT	TCTGTTAATT	GGTCTACATC	CTTTTCAAAG	1350
	TATGTCAGAC	AATTAGAACA	ATACTTTGAT	AATTTTGATC	AAGATTTCTT	1400
	ATCTTTAAGA	CAAAAAATTA	GTGATATTTT	ACAACAAGAA	AGTGACTIONGA	1450
	ATGATATTGT	TCAACTAGTA	GGAAAGGATT	CATTATCAGA	AGACCAAAAA	1500
20	GTTGTTATGG	AAGTAGCCAA	AATTATTAGA	GAAGATTTTC	TTCAACAAAA	1550
	TGCATTTAGC	GATTATGATT	ATATGTGCCC	ATTACAAAAA	ACAGTTGGTA	1600
	TGATGAGAAT	TATTTGCCAC	TTTTATGCTC	AATGCTTAAG	AACATTACAA	1650
	GAATATGACT	CAAGAGAAAG	AAAAATTGGT	TGGGGATCTA	TATATAATAC	1700
	ATTAAGACCA	ACTATAAATA	AAATTACACA	TATGAAATTT	GAAAACCCAA	1750
25	AAAATTCAGA	TGAATATTTT	AAAAAGTATT	TTAAGGCACT	TGAAGAAGAA	1800
	ATAACAGTAG	GTTTAAGAAA	CTTGATGGAA	AAATGA		1836

30 2) INFORMATION FOR SEQ ID NO: 690

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3216 bases
- (B) TYPE: Nucleic acid
- 35 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 40 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Saccharomyces cerevisiae*
- (B) STRAIN: X2180-1A
- (C) ACCESSION NUMBER: J05409

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690

	ATGGCTGGTG	CAATTGAAAA	CGCTCGTAAG	GAAATAAAAA	GAATCTCATT	50
	AGAAGACCAT	GCTGAATCTG	AATATGGTGC	CATCTATTCT	GTCTCTGGTC	100
	CGGTCGTCAT	TGCTGAAAAT	ATGATTGGTT	GTGCCATGTA	CGAATTGGTC	150
50	AAGGTCGGTC	ACGATAACCT	GGTGGGTGAA	GTCATTAGAA	TTGACGGTGA	200
	CAAGGCCACC	ATCCAAGTTT	ACGAAGAAAC	TGCAGGCCTT	ACGGTCGGTG	250
	ACCCTGTTTT	GAGAACAGGT	AAGCCTCTGT	CGGTAGAATT	GGGTCCTGGT	300
	CTGATGGAAA	CCATTTACGA	TGGTATTCAA	AGACCTTTGA	AAGCCATTAA	350
	GGAAGAATCG	CAATCGATTT	ATATCCCAAG	AGGTATTGAC	ACTCCAGCTT	400
55	TGGATAGGAC	TATCAAGTGG	CAATTTACTC	CGGGAAAGTT	TCAAGTCGGC	450
	GATCATATTT	CCGGTGGTGA	TATTTACGGT	TCCGTTTTTG	AGAATTGCT	500
	AATTTCAAGC	CATAAGATTC	TTTTGCCACC	AAGATCAAGA	GGTACAATCA	550
	CTTGGATTGC	TCCAGCTGGT	GAGTACACTT	TGGATGAGAA	GATTTTGGAA	600
	GTTGAATTTG	ATGGCAAGAA	GTCTGATTTC	ACTCTTTACC	ATACTTGGCC	650
60	TGTTCTGTGT	CCAAGACCAG	TTACTGAAAA	GTTATCTGCT	GACTATCCTT	700

	TGTTAACAGG	TCAAAGAGTT	TTGGATGCTT	TGTTTCCTTG	TGTTCAAGGT	750
	GGTACGACAT	GTATTCCAGG	TGCTTTTGGT	TGTGGTAAGA	CCGTTATCTC	800
	TCAATCTTTG	TCCAAGTACT	CCAATTCTGA	CGCCATTATC	TATGTCGGGT	850
	GCTTTGCCAA	GGGTACCAAT	GTTTTAATGG	CGGATGGGTC	TATTGAATGT	900
5	ATTGAAAACA	TTGAGGTTGG	TAATAAGGTC	ATGGGTAAAG	ATGGCAGACC	950
	TCGTGAGGTA	ATTAAATTGC	CCAGAGGAAG	AGAAACTATG	TACAGCGTCG	1000
	TGCAGAAAAG	TCAGCACAGA	GCCCACAAAA	GTGACTCAAG	TCGTGAAGTG	1050
	CCAGAATTAC	TCAAGTTTAC	GTGTAATGCG	ACCCATGAGT	TGGTTGTTAG	1100
	AACACCTCGT	AGTGTCCGCC	GTTTGTCTCG	TACCATTAAG	GGTGTCGAAT	1150
10	ATTTTGAAGT	TATTACTTTT	GAGATGGGCC	AAAAGAAAGC	CCCCGACGGT	1200
	AGAATTGTTG	AGCTTGTCAG	GGAAGTTTCA	AAGAGCTACC	CAATATCTGA	1250
	GGGGCCTGAG	AGAGCCAACG	AATTAGTAGA	ATCCTATAGA	AAGGCTTCAA	1300
	ATAAAGCTTA	TTTTGAGTGG	ACTATTGAGG	CCAGAGATCT	TTCTCTGTTG	1350
	GGTTCCCATG	TTCGTAAAGC	TACCTACCAG	ACTTACGCTC	CAATTCTTTA	1400
15	TGAGAATGAC	CACTTTTTTCG	ACTACATGCA	AAAAAGTAAG	TTTCATCTCA	1450
	CCATTGAAGG	TCCAAAAGTA	CTTGCTTATT	TACTTGGTTT	ATGGATTGGT	1500
	GATGGATTGT	CTGACAGGGC	AACTTTTTTCG	GTTGATTCCA	GAGATACTTC	1550
	TTTGATGGAA	CGTGTTACTG	AATATGCTGA	AAAGTTGAAT	TTGTGCGCCG	1600
	AGTATAAGGA	CAGAAAAGAA	CCACAAGTTG	CCAAAACGTG	TAATTTGTAC	1650
20	TCTAAAGTTG	TCAGAGGTAA	TGGTATTTCG	AATAATCTTA	ATACTGAGAA	1700
	TCCATTATGG	GACGCTATTG	TTGGCTTAGG	ATTCTTGAAG	GACGGTGTCA	1750
	AAAATATTCC	TTCTTTCTTG	TCTACGGACA	ATATCGGTAC	TCGTGAAACA	1800
	TTTCTTGCTG	GTCTAATTGA	TTCTGATGGC	TATGTTACTG	ATGAGCATGG	1850
	TATTAAAGCA	ACAATAAAGA	CAATTCATAC	TTCTGTCAGA	GATGGTTTGG	1900
25	TTTCCCTTGC	TCGTTCTTTA	GGCTTAGTAG	TCTCGGTAA	CGCAGAACCT	1950
	GCTAAGGTTG	ACATGAATGG	CACCAAACAT	AAAATTAGTT	ATGCTATTTA	2000
	TATGTCTGGT	GGAGATGTTT	TGCTTAACGT	TCTTTCGAAG	TGTGCCGGCT	2050
	CTAAAAAATT	CAGGCCTGCT	CCCGCCGCTG	CTTTTGCACG	TGAGTGCCGC	2100
	GGATTTTATT	TCGAGTTACA	AGAATTGAAG	GAAGACGATT	ATTATGGGAT	2150
30	TACTTTATCT	GATGATTCTG	ATCATCAGTT	TTTGCTTGCC	AACCAGGTTG	2200
	TCGTCCATAA	TTGCGGAGAA	AGAGGTAATG	AAATGGCAGA	AGTCTTGATG	2250
	GAATTCCCAG	AGTTATATAC	TGAAATGAGC	GGTACTAAAG	AACCAATTAT	2300
	GAAGCGTACT	ACTTTGGTCG	CTAATACATC	TAACATGCCG	GTTGCAGCCA	2350
	GAGAAGCTTC	TATTTACACT	GGTATCACTC	TTGCAGAATA	CTTCAGAGAT	2400
35	CAAGGTAAAA	ATGTTTCTAT	GATTGCAGAC	TCTTCTTCAA	GATGGGCTGA	2450
	AGCTTTGAGA	GAAATTTCTG	GTCGTTTGGG	TGAGATGCCT	GCTGATCAAG	2500
	GTTTCCCAGC	TTATTTGGGT	GCTAAGTTGG	CCTCCTTTTA	CGAAAGAGCC	2550
	GGTAAAGCTG	TTGCTTTAGG	TTCCCCAGAT	CGTACTGGTT	CCGTTTCCAT	2600
	CGTTGCTGCC	GTTTCGCCAG	CCGGTGGTGA	TTTCTCAGAT	CCTGTTACTA	2650
40	CTGCTACATT	GGGTATCACT	CAAGTCTTTT	GGGGTTTAGA	CAAGAAATTG	2700
	GCTCAAAGAA	AGCATTTCCC	ATCTATCAAC	ACATCTGTTT	CTTACTCCAA	2750
	ATACACTAAT	GTCTTGAACA	AGTTTTATGA	TTCCAATTAC	CCTGAATTTC	2800
	CTGTTTTAAG	AGATCGTATG	AAGGAAATTC	TATCAAACGC	TGAAGAATTA	2850
	GAACAAGTTG	TTCAATTAGT	TGGTAAATCG	GCCTTGTCTG	ATAGTGATAA	2900
45	GATTACTTTG	GATGTTGCCA	CTTTAATCAA	GGAAGATTTT	TTGCAACAAA	2950
	ATGGTTACTC	CACTTATGAT	GCTTTCTGTC	CAATTTGGAA	GACATTTGAT	3000
	ATGATGAGAG	CCTTCATCTC	GTATCATGAC	GAAGCTCAAA	AAGCTGTTGC	3050
	TAATGGTGCC	AACTGGTCAA	AACTAGCTGA	CTCTACTGGT	GACGTTAAGC	3100
	ATGCCGTTTC	TTCATCTAAA	TTTTTTGAAC	CAAGCAGGGG	TGAAAAGGAA	3150
50	GTCCATGGCG	AATTCGAAAA	ATTGTTGAGC	ACTATGCAAG	AAAGATTTGC	3200
	TGAATCTACC	GATTAA				3216

55 2) INFORMATION FOR SEQ ID NO: 691

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1860 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(B) STRAIN: 972 h-

(C) ACCESSION NUMBER: S47814

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691

	ATGGCGGGAG	GAATTGAACT	GGCCAAGAAG	GCTATCAGGA	GCCTCAAAAA	50
	TTACGACGAG	CATGAAAACC	GATATGGATC	TATTTTCAGC	GTTTCTGGTC	100
	CTGTCGTTGT	TGCAGCCAAT	ATGCTTGGAT	GTTTCGATGTA	CGAACTCGTT	150
15	CGCGTTGGTC	ATGAAGAACT	AGTTGGTGAA	GTAATTCGTA	TCCATCAAGA	200
	TAAATGTACT	ATTCAAGTAT	ACGAAGAGAC	GTCCGGTCTC	ACTGTTGGTG	250
	ATCCTGTCCA	ACGCACTGGA	AAGCCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAGCTGAGA	CTATTTATGA	TGGTATCCAA	CGTCCGTAA	AGCAAATTTT	350
	CGACAAATCT	CAAAGTATTT	ATATTCCTAG	AGGTATTAAT	ACAGAATCAC	400
20	TTAATCGTGA	GCATAAGTGG	GATTTCACAC	CAAATAAGGA	TTTACGCATT	450
	GGCGATCATG	TATCCGGTGG	TGATGTTTTC	GGTTCTGTAT	TTGAAAACCTC	500
	TCTTTTCAAT	GATCATAAAA	TTATGTTACC	CCCTAGAGCC	CGTGGTACCG	550
	TCACATATAT	TGCTGAAGCT	GGATCATAAC	ATGTTGATGA	AAAACCTTCTT	600
	GAAGTCGAGT	TTAATGGCAA	GAAACATTCT	TTTAGTATGT	TGCATACTTG	650
25	GCCTGTCCGT	GCTGCTCGTC	CAGTTGCGGA	CAACTTAACT	GCTAATCAAC	700
	CTTTATTGAC	TGGTCAACGT	GTTTTGGATG	CGTTATACCC	CTGTGTTCAA	750
	GGTGGCACTA	CTGCTATCCC	CGGTGCCTTT	GGTTGTGGTA	AAACAGTTAT	800
	TTCACAATCT	CTTTCTAAGT	ACTCTAATTC	TGATTTGATT	GTTTACGTCTG	850
	GTTGTGGTGA	ACGTGGAAAC	GAAATGGCAG	AAGTGTTAAT	GGATTTCCCA	900
30	GAACATAACAA	TTGATATTAA	TGGTAAACCA	GAGCCCATTA	TGAAGCGTAC	950
	TACATTGGTA	GCCAAACACTT	CTAACATGCC	TGTCGCTGCT	CGTGAAGCTT	1000
	CCATTTATAC	CGGTATTACA	CTTGCTGAAT	ATTATCGTGA	TCAAGGTAAG	1050
	AACGTTTCAA	TGATGGCTGA	TTCTACATCT	CGTTGGGCTG	AAGCTTTGCG	1100
	TGAAATTTCT	GGTCGTTTGG	CTGAGATGCC	TGCCGATTCT	GGTTATCCCG	1150
35	CTTATTTGGG	TGCCAAATTG	GCTTCTTTTT	ACGAACGTGC	TGGTCGTGCT	1200
	CGTTGCTTGG	GAAGTCCTGA	CCGTGAAGGA	ACAGTTTCAA	TTGTTGGAGC	1250
	TGTTTCTCCT	CCGGGTGGTG	ATTTTTCTGA	TCCTGTTACT	AGTGCAACCT	1300
	TGGGAATTGT	TCAAGTCTTC	TGGGGTTTGG	ACAAGAAATT	GGCCCAACGT	1350
	AAACACTTTC	CCTCAATCAA	CACCTCTCTT	TCCTATTCTA	AATACATCAA	1400
40	TGCTTTGCAA	CCTTGGTATG	AGGAAAGAGT	TCCAGGCTTT	AATACTCTTC	1450
	GTGATCAAAT	CAAACAGATC	ATTCAACAAG	AAGATTCCAT	GTTGGAAATT	1500
	ATTCAAGTTGG	TTGGTAAGTC	GGCTCTTTCT	GAAACGGATA	AAGTTACTTT	1550
	GGACATAGCC	GGTATTATTA	AGAATGACTT	CTTACAACAA	AACGGTTATT	1600
	CTGATTACGA	TCGCTGTTGC	CCTCTTTACA	AGACTTATCA	TATGATGCGA	1650
45	AACATGATTG	CTTACTACAC	AAAGGCTAAA	AGTGCCGTTG	AAACTGGTAG	1700
	CGTTCCTTGG	TCAAAGATTA	AAGAAAGTAC	TTCAGATATC	TTTTATGAGT	1750
	TAACCTCGAT	GAAATTTCGAA	AACCCTAATG	AAGGCGAGAA	GGAAATAGTC	1800
	GAACACTATG	AAACTCTGCA	CAAGAAGATT	GAGGACAAGT	TTCACACTCT	1850
	GACTGAGTAA					1860

50

2) INFORMATION FOR SEQ ID NO: 692

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1833 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Trypanosoma congolense*
 (B) STRAIN: IL3000
 (C) ACCESSION NUMBER: Z25814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692

10	ATGACGAGCG	ATAAAAACCC	TTACAAAACA	GAGCAGCGCA	TGGGGGCCGT	50
	GAAGGCCGTC	TCCGGGCCAG	TTGTCATTGC	TGAAAACATG	GGCGGTAGCG	100
	CTATGTATGA	GCTTGTGCAG	GTAGGTTCTT	TCCGGTTAGT	GGGCGAGATC	150
	ATTCGTCTAG	AGGGCGATAC	CGCCACTATT	CAGGTCTATG	AGGAAACAGG	200
	TGGCCTCACT	GTCGGAGACC	CGGTGTACTG	TACGGGTAAG	CCTCTTTTCG	250
15	TTGAGCTTGG	ACCTGGAATC	ATGTCTGAAA	TATTTGACGG	TATCCAGCGG	300
	CCTCTTGACA	CCATCTACCG	CATGGTGGAA	AACGTGTTTA	TCCCCAGGGG	350
	CGTTCAGGTG	AAGTCACTCA	ATGACCAGAA	ACAGTGGGAC	TTTAAGCCAT	400
	GCCTGAAGGT	TGGAGATCTT	GTGTCTGGTG	GTGATATCAT	TGGCTCAGTG	450
	GTGGAGAACT	CTCTCATGTA	CAATCACAGC	ATTATGATTC	CGCCCAATGT	500
20	GCGGGGCCGT	GTTACTTCCA	TTGTTCTTTC	AGGAAATTAC	ACCCTCCAAG	550
	ATGACATTAT	TGAATTGGAA	TATAATGGGA	CAGTGAAATC	ACTAAACTTT	600
	ATGCATCGCT	GGCCAGTACG	GACCCCGCGT	CCTGTGGCGT	CAAAAGAATC	650
	CGGCAATCAT	CCGCTTCTCA	CCGGACAGCG	TGTGCTCGAT	GCTCTCTTTC	700
	CATCCGTCCA	GGGTGGAACA	TGCGCCATCC	CTGGCGCGTT	TGGATGCGGA	750
25	AAGACGGTTA	TCAGTCAGGC	TCTTTCGAAG	TTCTCCAACA	GCGACGCTGT	800
	TATCTATGTC	GGCTGCGGCG	AGCGTGGGAA	TGAGATGGCA	GAGGTGCTCA	850
	TGGACTTCCC	CACACTCACC	ACCGTTATTG	ATGGTCGTGA	GGAGTCCATC	900
	ATGAAGCGTA	CCTGCCTGGT	GGCAAACACC	TCAAATATGC	CTGTGCTGCT	950
	TCGTGAGGCG	TCTATTTACA	CTGGCATCAC	TTTAGCTGAG	TATTATCGTG	1000
30	ATATGGGCAA	GCACATTGCT	ATGATGGCCG	ACTCTACCTC	TCGATGGGCT	1050
	GAGGCTCTCC	GTGAGATCTC	TGGGCGTCTC	GCTGAAATGC	CCGCTGATGG	1100
	TGGTTACCCT	GCGTACCTCA	GTGCGCGTCT	TGCTTCTTTC	TACGAGCGTG	1150
	CGGGGCGCGT	GACATGCATC	GGTGGGCCAA	AACGCGAGGG	CTCAGTAACC	1200
	ATCGTTGGTG	CCGTTTCTCC	TCCTGGAGGT	GACTTTTCTG	ACCCAGTGAC	1250
35	GTCCGCTACG	CTTGGTATTG	TGCAAGTCTT	TTGGGGTCTT	GAGAAGCGTC	1300
	TTGCGCAACG	TAAACACTTT	CCTTCTGTTA	ATTGGCTCAT	TTCTTATTCA	1350
	AAATACCTTA	ATGCTTTGGA	GCCCTTCTTC	AACACGCTTG	ACCCTGACTA	1400
	CATGCGCCTG	CGGTCAGTTG	CTGCGGAGAT	CCTTCAGCGT	GAGGAAGAGT	1450
	TGCAAGAAAT	TGTTCAACTT	GTCGGTAAGG	ACTCACTTTC	GGAGTCTGAC	1500
40	AAAATTATTC	TAGAAACGGC	TAAGGTTATT	CGTGAAGAGT	TTCTCCAGCA	1550
	GAATGCCTTT	ACGCCGTACG	ACAAGTATTG	CCCGCCGTAC	AAGACCTGCT	1600
	GGATGCTACG	TAACATTGTC	GCGTTCTACG	AGGAGAGCCA	GCGCGTTGTA	1650
	GCTGAGTCCG	CTGGGGAAC	TAAGATTACG	TGGAACATA	TTCGTGAAAT	1700
	GATTCCTCAT	ATTTACACGG	GTTTAACTGA	GATGAAGTTC	CGTGATCCTC	1750
45	AGGAGGGTGA	GGAGGCCAAC	GTAGAATTCT	ACAGAAAACA	AAATGAGGAA	1800
	ATTGTCAGCG	CATTCGCCTC	GCTGCTGCAA	TAA		1833

50 2) INFORMATION FOR SEQ ID NO: 693

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1758 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Thermus thermophilus*
(B) STRAIN: HB8
(C) ACCESSION NUMBER: D63799

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693

	ATGATCCAAG	GGGTGATCCA	GAAGATCGCG	GGCCCGGCGG	TGATCGCCAA	50
	GGGCATGCTC	GGGGCCCGCA	TGTACGACAT	CTGCAAGGTG	GGCGAAGAGG	100
	GCCTCGTGGG	CGAGATCATC	CGCCTGGACG	GGGACACGGC	CTTCGTCCAG	150
10	GTCTACGAGG	ACACCTCGGG	CCTAAAGGTG	GGGGAGCCCG	TGGTCTCCAC	200
	GGGCCTTCCC	TTGGCGGTGG	AGCTCGGCCC	CGGGATGCTG	AACGGCATCT	250
	ACGACGGCAT	CCAGCGCCCC	CTGGAGCGCA	TCCGGGAGAA	GACGGGGATC	300
	TACATCACCC	GGGGCGTGGT	GGTCCACGCC	CTGGACCGGG	AGAAGAAGTG	350
	GGCCTGGACG	CCCATGGTCA	AGCCCGGGGA	CGAGGTGCGG	GGGGGTATGG	400
15	TCCTGGGCAC	GGTGCCCGAG	TTCGGCTTCA	CCCACAAGAT	CCTGGTACCC	450
	CCGGACGTGC	GGGGCCGGGT	CAAGGAGGTG	AAGCCCGCCG	GGGAGTACAC	500
	CGTGGAGGAG	CCGGTGGTGG	TCCTCGAGGA	CGGCACCGAG	CTCAAGATGT	550
	ACCACACCTG	GCCCGTTTCG	CGGGCGAGGC	CCGTGCAAAG	GAAGCTTGAC	600
	CCCAACACCC	CCTTCCTCAC	GGGGATGCGC	ATCCTGGACG	TCCTCTTCCC	650
20	CGTGGCCATG	GGGGGCACCG	CCGCCATCCC	TGGGCCCTTC	GGCAGCGGCA	700
	AGACCGTGAC	CCAGCAGTCC	CTGGCCAAGT	GGTCCAACGC	CGACGTGGTG	750
	GTCTACGTGG	GCTGCGGGGA	GCGGGGGAAC	GAGATGACCG	ACGTGCTCGT	800
	GGAGTTCCCC	GAGCTCACCG	ACCCAAGAC	GGGTGGGCCC	TTGATGCACC	850
	GCACCGTCCT	CATCGCCAAC	ACCTCCAACA	TGCCCGTGGC	CGCCCGCGAG	900
25	GCCAGCATCT	ACGTGGGCGT	GACCATCGCC	GAGTACTTCC	GCGACCAGGG	950
	CTTCTCCGTG	GCCCTCATGG	CCGACTCCAC	GAGCCGCTGG	GCCGAGGCTT	1000
	TGCGCGAGAT	CTCTAGCCGC	CTCGAGGAGA	TGCCCGCCGA	GGAGGGCTAC	1050
	CCGCCCTACC	TCGCCGCCAG	GCTCGCCGCC	TTCTACGAGC	GGGCGGGCAA	1100
	GGTCATCACC	CTGGGCGGCG	AGGAGGGGGC	GGTGACCATC	GTGGGGGCGG	1150
30	TCTCCCCGCC	GGGCGGCGAC	ATGTCCGAGC	CCGTGACCCA	GTCCACCTTG	1200
	AGGATCGTGG	GGGCCTTCTG	GCGGCTTGAC	GCCTCCCTGG	CCTTCCGCCG	1250
	CCACTTCCCC	GCCATCAACT	GGAACGGCTC	CTACAGCCTC	TTCACCTCCG	1300
	CCCTTGACCC	CTGGTACCGG	GAGAACGTGG	CCGAGGACTA	CCCCGAGCTC	1350
	CGCGACGCCA	TCTCCGAGCT	TTTGCAGCGG	GAGGCGGGCC	TCCAGGAGAT	1400
35	CGTCCAGCTC	GTGGGGCCGG	ACGCCCTCCA	GGACGCCGAG	CGCCTCGTCA	1450
	TTGAGGTGGG	CCGGATCATC	CGCGAGGACT	TCCTGCAGCA	GAACGCCTAC	1500
	CACGAGGTGG	ACGCCTACTG	CTCCATGAAG	AAGGCCTACG	GGATCATGAA	1550
	GATGATCCTC	GCCTTCTACA	AGGAGGCGGA	GGCGGCCATC	AAGCGGGGGG	1600
	TTTCCATAGA	CGAGATCCTG	CAGCTCCCCG	TTCTGGAGCG	CATCGGCCGC	1650
40	GCCCGCTACG	TGAGCGAGGA	GGAGTTCCCC	GCCTACTTTG	AGGAGGCCAT	1700
	GAAGGAGATC	CAGGGGGCCT	TCAAGGCTGG	CCTAAAGGGG	GAGAGATGGA	1750
	CCTTCTGA					1758

45

2) INFORMATION FOR SEQ ID NO: 694

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694

CGGCGCIATC YTS GTT GTTG C

21

60

2) INFORMATION FOR SEQ ID NO: 695

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695

15 GTTTCACGTG ATGACGTACA 20

2) INFORMATION FOR SEQ ID NO: 696

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696

30 ATIGGICAYR TIGAYCAYGG IAARAC 26

2) INFORMATION FOR SEQ ID NO: 697

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697

45 CCIACIGTIC KICCRCCYTC RCG 23

50 2) INFORMATION FOR SEQ ID NO: 698

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1185 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: extracted from J01690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698

5
GTGTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTTA ACGTTGGTAC 50
TATCGGCCAC GTTGACCACG GTAAAACTAC TCTGACCGCT GCAATCACCA 100
CCGTACTGGC TAAAACCTAC GGCGGTGCTG CTCGTGCATT CGACCAGATC 150
GATAACGCGC CGGAAGAAAA AGCTCGTGGT ATCACCATCA ACACTTCTCA 200
10 CGTTGAATAC GACACCCCGA CCCGTCACTA CGCACACGTA GACTGCCCCG 250
GGCACGCCGA CTATGTTAAA AACATGATCA CCGGTGCTGC TCAGATGGAC 300
GGCGCGATCC TGGTAGTTGC TGC GACTGAC GGCCCGATGC CGCAGACTCG 350
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 400
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 450
15 GAAATGGAAG TTCGTGAAC TCTGTCTCAG TACGACTTCC CGGGCGACGA 500
CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 550
AGTGGGAAGC GAAAATCCTG GAACTGGCTG GCTTCCTGGA TTCTTATATT 600
CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 650
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC 700
20 GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG 750
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 800
CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 850
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG 900
CCGCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG 950
25 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 1000
GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG 1050
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 1100
CGCGATGGAC GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG 1150
TTGGCGCGGG CGTTGTTGCT AAAGTTCTGG GCTAA 1185
30

2) INFORMATION FOR SEQ ID NO: 699

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699

45 GTIACIGGYT CYTYRARRTT ICCICC 26

2) INFORMATION FOR SEQ ID NO: 700

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700

60

5 2) INFORMATION FOR SEQ ID NO: 701

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701

GTGTTACGA TCATCGATGC G

21

20

2) INFORMATION FOR SEQ ID NO: 702

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702

CTCTCGATAT CCGCGAAGCG

20

35

2) INFORMATION FOR SEQ ID NO: 703

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703

TATGGAAATT CGAAACATCT

20

50

2) INFORMATION FOR SEQ ID NO: 704

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

60

400

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704

5 AGTGCTCCAA TTAATGTTGG 20

2) INFORMATION FOR SEQ ID NO: 705

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705

20

GTACAGTTCC AATACCTGAA 20

25 2) INFORMATION FOR SEQ ID NO: 706

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706

TGAAATCTTC ACATCCAACA 20

40

2) INFORMATION FOR SEQ ID NO: 707

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707

TWACCATTTC AGTACCTTCT GGTA 25

55

2) INFORMATION FOR SEQ ID NO: 708

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 26 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708

TCRTCCATIC CIARIATIGC IATIAAT

26

2) INFORMATION FOR SEQ ID NO: 709

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*
- (C) ACCESSION NUMBER: extracted from AE001122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709

30	ATGAATGAAG	TTTTATTTGT	AAAGACTGCT	GGTAGGAATT	TAAAAGCAGA	50
	AGTAATTCGT	ATTAGGGGCA	ATGAAGTTGA	TGCACAGGTT	TTTGAATTGA	100
	CAAAAGGGAT	ATCTGTTGGA	GACCTAGTTG	AATTTACAGA	CAAACCTTTA	150
	ACAGTTGAAC	TCGGACCAGG	GCTTTTAACT	CAAGTATATG	ATGGGCTTCA	200
	AAATCCTTTG	CCTGAATTGG	CTATTCAATG	TGGATTTTTT	TTAGAAAGGG	250
	GAGTATATTT	AAGGCCCTTG	AATAAAGATA	AAAAGTGGAA	TTTTAAAAAA	300
35	ACCTCCAAAG	TTGGAGATAT	CGTTATTGCA	GGAGATTTTT	TAGGTTTTGT	350
	AATTGAGGGA	ACTGTTCAAC	ATCAAATAAT	GATTCCATTT	TATAAAAGGG	400
	ATTCTTATAA	AATTGTGGAG	ATTGTAAGTG	ATGGCGACTA	TTCGATTGAT	450
	GAGCAAATTG	CTGTAATTGA	AGATGATTCT	GGTATGAGGC	ATAATATTAC	500
	AATGTCTTTT	CATTGGCCTG	TTAAAGTTCC	TATTACTAAT	TATAAGGAAC	550
40	GCCTTATTCC	TAGTGAACCT	ATGTTGACTC	AAACTAGAAT	TATAGATACA	600
	TTTTTCCCAG	TTGCCAAAGG	TGGAACCTTT	TGCATTCCGG	GTCCTTTTGG	650
	AGCAGGAAAA	ACGGTTCTTC	AGCAGGTTAC	AAGTCGAAAT	GCTGATGTTG	700
	ATGTAGTGAT	TATTGCAGCT	TGTGGTGAGC	GAGCAGGAGA	AGTGGTAGAA	750
	ACTCTTAAAG	AATTTCCCGA	ATTAATGGAT	CCAAAAACCG	GCAAATCTTT	800
45	AATGGACAGG	ACTTGTATTA	TTTGTAATAC	ATCTTCAATG	CCAGTTGCAG	850
	CTAGAGAAGC	TTCTGTTTAT	ACTGCTATTA	CTATTGGTGA	GTATTACAGG	900
	CAAATGGGCC	TTGATATTCT	TCTTTTGGCA	GATTCAACTT	CAAGATGGGC	950
	TCAAGCAATG	AGAGAAATGT	CTGGACGCCT	TGAGGAAATT	CCTGGCGAGG	1000
	AGGCTTTTCC	GGCATATCTT	GAGTCTGTTA	TTGCTTCCTT	TTATGAAAGG	1050
50	GCAGGTATTG	TAGTTCCTAA	TAATGGGGAT	ATTGGATCTG	TAACAGTTGG	1100
	TGGCTCTGTA	AGTCCTGCTG	GTGGTAATTT	TGAAGAGCCA	GTTACTCAAG	1150
	CAACTTTAAA	AGTTGTAGGA	GCATTTACAG	GGCTTACAAG	AGAAAGGTCT	1200
	GATGCTAGGA	AATTTCCAGC	TATTAGTCCT	CTTGAATCTT	GGAGTAAATA	1250
	TAAAGGCGTT	ATTGATCAAA	AAAAGACTGA	ATATGCAAGA	TCTTTTTTGG	1300
55	TGAAAGGTAA	TGAAATTAAT	CAAATGATGA	AAGTTGTTGG	AGAAGAAGGC	1350
	ATAAGTAACG	ATGATTTTTT	AATTTATTTA	AAATCCGAGC	TACTTGATTC	1400
	GTGCTATTTG	CAGCAAAATT	CATTTGATTC	TATTGATGCT	GCTGTTAGTT	1450
	CAGAGCGTCA	AAATTATATG	TTTGATATAG	TTTATAACAT	TCTTAAAAC	1500
	AACTTTGAGT	TTTCTGATAA	ACTTCAAGCA	AGAGATTTTA	TAAATGAGTT	1550
60	AAGGCAAAAT	CTTTTAGACA	TGAATCTTTC	TTCTTTTAAG	GATCATAAGT	1600

TTAATAAATT GGAGCATGCT TTGGGTGAAT TGATAAATTT TAAAAAGGTA 1650
 ATTTAG 1656

5

2) INFORMATION FOR SEQ ID NO: 710

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*
 (B) STRAIN: Nichols
 (C) ACCESSION NUMBER: extracted from AE000520

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710

	GTGATCAAAG	ACGATGTGGT	TACAGGCCGT	GTAGTGAGGG	TGTCTGGTCC	50
	CATTGTGTAT	GGCGAGGGCC	TCTCTGCGTG	CAGCGTATAC	GATGTTGTCTG	100
25	ACGTAGGGGA	AGCATCGCTC	ATCGGAGAAA	TTATCCGGTT	GGATGAGAGC	150
	AAGGCGGTCG	TGCAAGTATA	CGAGGATGAC	ACAGGTATGC	GAGTCGGGGA	200
	GAAGGTGACA	AGCTTGCGTC	GACCACTCTC	AGTCCGCTTA	GGGCCTGGAT	250
	TAATCGGCAC	CATTTATGAC	GGTATTCAGC	GCCCACCTGA	GCGCCTCTTC	300
	CAAGAAGACG	GCGCCTTCTT	GCGTCCTGGT	GCGCGTTCAC	AACCGCTTGA	350
30	TGGCTCCGTA	CGCTGGGATT	TTCGTCCTCA	TTGTAACGAG	CGCGGTGAGG	400
	CCCTGTGCGC	GGGGATTCCG	ATTGCACCTG	GGTCAGTGTT	AGGGACCGTG	450
	CAGGAGACTC	CTTCTGTTGT	GCACACTATC	ATGGTTCCTC	CTGACATCCG	500
	GGGGAGCGTG	CTATCTTCGT	TCAAGGGCGC	AGGTGCTTAC	ACAATAGATG	550
	AAGAAATTGG	ACGCACTGAT	CTTGGTGAGC	CGCTTTTCT	ATCCCAGTAC	600
35	TGGCCAGTGC	GTCGTGCGCG	TCCTTTCAGC	AAAAAACTTG	CAGTGTGTGA	650
	GCCACTAGTT	ACTGGACAGC	GGGCGATTGA	TGTTTTCTTC	CCCCTATCAA	700
	AGGGAGGAAC	GGCGGCTATT	CCAGGGGGAT	TTGGAACCTG	GAAGACAATG	750
	ACGCAGCATG	CCGTTGCCAA	GTGGTGTGAT	GCAGATATTA	TCGTGTACAT	800
	CGGCTGCGGA	GAGCGGGGCA	ACGAGATGAC	AGACGTGCTC	TCTGAATTTC	850
40	CCAAACTCAT	CGATCCGCGC	ACAGGACGCT	CTCTTATGGA	GCGGACGATT	900
	TTGATCGCAA	ATACGTCCAA	TATGCCTGTG	TCCGCACGCG	AGGTGTCGCT	950
	GTATTCAGGG	ATTACCCTTG	CGGAATACTA	CCGTGATATG	GGTATGCATG	1000
	TGGCCATCAT	GGCTGATTCT	ACCAGCCGCT	GGGCGGAGGC	GCTGCGTGAA	1050
	TTGTCTGGGC	GCATGGAAGA	AATGCCTGCG	GAGGAGGGAT	TCCCTGCGTA	1100
45	CCTTCCGACG	CGTCTTGCA	AATTTTATGA	GCGCGCAGGA	CGCGTGGA	1150
	CCTGTGTGGC	GCGCGAGGGC	TCTGTGAGCA	TCATTGGTGC	TGTTTCTCCC	1200
	CTGGGTGGAG	ATTTCTCTGA	GCCGGTGACG	CAGCACACAA	AGCGCTTCAT	1250
	CCGTTGCTTT	TGGGCCTTGG	ATCGTGA <td>TGCACACGCG</td> <td>CGTCATTACC</td> <td>1300</td>	TGCACACGCG	CGTCATTACC	1300
	CTGCCATTGG	GTGGATAGAT	TCATACTCTG	AATATGCGCA	GGAAGTAAGT	1350
50	GCATGGTGG	GTAAGTATGA	CCCGCGCGCA	GGCGCGTTGC	GCGCCGCAGC	1400
	CTTGGAATTTG	CTGAGAAAGG	AACAGCGGTT	ACAGCAAATT	GTCAGGCTTG	1450
	TCGGTCCTGA	TGCGCTGCCT	GGAGAAGATC	GTCTGGTGCT	AATGGTGTGT	1500
	GAAATGATCA	AAGGTGGCTT	TCTGCAGCAG	AACGCTTTTG	ATCCGACGGA	1550
	TGTGTTCTCC	TGTCCTCGAAA	AGCAGGTGCA	GATCTTGCGT	ACCATAGTGG	1600
55	ATTTTCACGA	ACGTGCCGTG	GTGCTGCTGC	GTGCAGGTAT	TTGCTTTTCT	1650
	GCGCTGTCCC	AGCTTTCGTG	CCGGGAGCTC	ATCGTACGTA	TGAAAACACTAC	1700
	GTACGGGAAT	GAGGATGTAC	ACAAGATGCA	GAAAGTGTAC	GACACGATGT	1750
	GCACTGAGTT	TGACCAACTG	AGTGTGTGTG	CTGCCGCGCG	CACACAAGGG	1800
	GGGGAGAAAG	TCGAATGA				1818

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2) INFORMATION FOR SEQ ID NO: 711

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1779 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Chlamydia trachomatis*
 15 (B) STRAIN: MoPn

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711

20	CAGGGCTATG	TCGTAGAAGC	TTACGGAAAT	TTATTGCGGG	TGCATTTTGA	50
	TGGGCATGTG	CGTCAAGGAG	AAGTGGCCTA	TGTCAGCGTG	GATGATACTT	100
	GGTTGAAAGC	GGAAATTATA	GAAGTTGTGG	GAGATGAGGT	TAAAGTCCAA	150
	GTTTTTGAGG	AAACTCAAGG	AATTTCTCGA	GGCGCTTTGG	TAACCTTTTTC	200
	CGGGCATTTA	TTAGAAGCGG	AACTTGGGCC	CGGTCTATTG	CAAGGTATTT	250
	TTGACGGACT	TCAGAATCGC	TTAGAGGTAT	TGGCAGATAC	AAGCTTGTTT	300
25	TTGAAAAGAG	GGGAGTATGT	TAATGCCATT	TGTCGGGAAA	CTGTATGGGC	350
	TTATACGCAA	AAGGCTTCTG	TCGGGGATGT	TCTATCTCGG	GGAGATGTGC	400
	TTGGTACAGT	AAAGGAAGGG	CGGTTTGATC	ATAAAATCAT	GGTTCCTTTC	450
	TCTTGTTTTG	AGGAAGTGAC	TATCACTTGG	GTCATTTCTT	CAGGAGATTA	500
	CACTGTTGAT	ACCGTTATTG	CTAAAGGACG	TACTGCTTCA	GGAGCCGAGC	550
30	TTGAATTTAC	AATGGTTCAG	AAATGGCCCA	TTAAACAGGC	TTTTTTAGAA	600
	GGGGAAAAGG	TACCGTCTCA	TGAAATTATG	GATGTTGGGT	TACGAGTATT	650
	AGATACTCAG	ATCCCCGTCT	TAAAGGGAGG	AACTTTTTGT	ACTCCAGGGC	700
	CTTTTGGTGC	AGGAAAGACC	GTTTTACAGC	ACCATTTATC	TAAGTATGCA	750
	GCTGTAGATA	TCGTAGTTTT	GTGTGCTTGT	GGAGAGCGAG	CTGGAGAGGT	800
35	TGTAGAAATT	CTTCAGGAGT	TCCCGCATTT	GACAGATCCT	CATACGGGGC	850
	AGTCTTTGAT	GCATAGGACC	TGTATTATTT	GTAATACATC	TTCCATGCCT	900
	GTAGCAGCTA	GAGAGTCCTC	CATTTATTTG	GGTATTACTA	TAGCAGAATA	950
	TTACCGTCAA	ATGGGGTTGC	ATGTTTTGTT	ATTGGCTGAC	TCGACATCTA	1000
	GATGGGCTCA	AGCTTTAAGG	GAAATTTTCAG	GGCGATTAGA	AGAAATCCCT	1050
40	GGAGAAGAAG	CTTTCCCAGC	CTATTTGGCG	TCTCGAATAG	CAGCTTTTTA	1100
	TGAGCGAGGC	GGGGCTGTGA	AAATGAAAGA	TGGATCGGAA	GGCTCCTTGA	1150
	CTATCTGTGG	AGCGGTTTCT	CCCGCAGGAG	GAAATTTTGA	AGAGCCTGTT	1200
	ACACAAGCAA	CTTTATCTGT	TGTTGGGGCT	TTCTGTGGGC	TTTCTAAGGC	1250
	TAGAGCAGAT	GCTAGACGGT	ATCCTTCTAT	TGATCCGATG	ATTTTCATGGT	1300
45	CTAAGTACTT	GGATTCTGTG	GCGGAGATTT	TAGAGAAAAA	AGTTCCAGGA	1350
	TGGGGAGATT	CCGTAAAGAA	AGCTTCTCGT	TTCTTAGAAG	AAGGAGCAGA	1400
	AATTGGTAAG	CGAATAGAAG	TTGTTGGGGA	AGAAGGGATT	TCTATGGAAG	1450
	ATATAGAAAT	CTTTTTGAAA	TCAGAGTTGT	ATGATTTCTG	TTACTTACAG	1500
	CAAAACGCTT	TCGATGCAGA	GGACTGTTAT	TGTCCTTTTG	ATCGTCAAAT	1550
50	AGAGCTTTTT	TCTTTAATGA	GTCATATTTT	TAGCTCTAGA	TTCTGTTTTG	1600
	ATTGTCCAGA	TAATGCTCGG	AGTTTCTTTT	TAGAGCTTCA	AAGTAAAATT	1650
	AAAACGCTGA	ATGGTCAAAA	ATTCCTTTCT	GAAGACTATC	AGAAGGGGCT	1700
	AGAAGTGATC	TATAAACTAT	TAGAAAGCAA	AATGGTGCAG	ACGGCGTAGG	1750
	TATGCAAACA	ATATATACAA	GAATTACGG			1779

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2) INFORMATION FOR SEQ ID NO: 712

- 60 (i) SEQUENCE CHARACTERISTICS:

404

- (A) LENGTH: 965 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: V583

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712

	GTGCAAATTG	GAAAAATTGT	CAAAGTTTCA	GGTCCTTTGA	TTTtagCTGA	50
15	AAACATGTCA	GATGCTAGTA	TCCAAGACAT	TTGTCATGTA	GGAGATTTAG	100
	GCGTTATCGG	AGAGATTATT	GAAATGCGAG	GCGACGTCGC	TTCGATTCAA	150
	GTATATGAAG	AAACAACAGG	CATTGGACCA	GGAGAACCAG	TTATTTCAAC	200
	AGGAGAACCA	TTATCTGTTG	AATTAGCCCC	AGGTTTAATT	GCCGAAATGT	250
	TTGATGGTAT	TCAACGACCA	TTGGATACAT	TTCAAGAAGT	AACCCACAGT	300
20	AACTTTTTAG	GCCGTGGCGT	TAAAATTGAT	GCGTTAGATC	GTGAGAAAAA	350
	ATGGACGTTT	GAACCAACTG	TGGCAGTTGG	TGAAGAAGTG	TCGGCAGGTG	400
	ACATCGTCGG	TGTGGTTCAA	GAAACACCGA	TTATTCAACA	TAAAATTATG	450
	GTGCCTTTTCG	GCGTTTCAGG	AACGATTGCC	GAAATTAAAG	CAGGTGACTT	500
	TGCCATTGAT	GAAACAGTTT	ACTCAGTGGA	AACGGCTAAA	GGAACGGAAA	550
25	GTTTTAGCAT	GATGCAAAAA	TGGCCCGTTC	GGCGGGGACG	TCCCATTTTA	600
	GAAAAACTAA	GTCCCAAAGT	ACCGATGGTG	ACCGGACAAC	GCGTAATTGA	650
	TACCTTTTTC	CCAATTACGA	AAGGCGGAGC	GGCAGCAGTT	CCAGGACCAT	700
	TTGGCGCTGG	AAAAACAGTC	GTTCAGCACC	AAATTGCTAA	GTGGGCCGAT	750
	GTCGACTTAG	TCGTTTACGT	TGGTTGTGGG	GAACGCGGGA	ATGAAATGAC	800
30	AGATGTTTTA	AATGAATTTC	CAGAATTAAT	TGACCCAACA	ACTGGTGAGT	850
	CTTTGATGAA	TCGGACGATT	TTAATTGCCA	ATACGTCAA	TATGCCGGTA	900
	GCGGCACGGG	AAGCCTCGAT	TTATACAGGG	ATTACCATTG	CAGAATATTT	950
	CCGTGATATG	GGTTA				965

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2) INFORMATION FOR SEQ ID NO: 713

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1737 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanosarcina barkeri*
 (C) ACCESSION NUMBER: extracted from J04836

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713

	GTGGAAGTAA	AAGGTGAAAT	TTATCGTGTG	TCTGGGCCTG	TCGTCACCGC	50
	CATCGGCTTG	CAGGCAAAAA	TGTATGACCT	GGTCAAAGTC	GGTAATGAAG	100
55	GTTTAATGGG	TGAAGTCATT	CAGATATTAG	GGCCCAAGAC	CATCATCCAG	150
	GTATATGAAG	AGACCGCAGG	TATCAAGCCA	GGGGAACCCT	GTGTATCTAC	200
	AGGGTCGTCT	CTGTCCGTAG	AACTTGGTCC	GGGTCTTCTT	TCCAGTATTT	250
	ATGACGGGGT	TCAAAGGCCT	CTGCACGTCC	TGCTTGAAAA	AATGGGTAGC	300
	TTCATCCAGA	GAGGTGTCAG	CGCAGATGGG	CTTGATCATA	AGAAACTCTG	350
60	GGATTTCAAA	CCCATTGTCA	AGAAGGGCGA	TTCCGTAAAA	GGTGGAGACG	400

405

	TAATTGGTGT	TGTACAGGAA	ACCGTGAATA	TTGAACATAA	GATCATGGTG	450
	CCTCCTGATA	TCTCAGGTAC	AATTTCCGAC	ATAAAGAGCG	GAAACTTTAC	500
	GGTAGTAGAC	ACAATCTGTA	CTCTGACTGA	TGGGACCGAA	TTGCAGATGA	550
	TGCAGAGGTG	GCCTGTTCGA	AGACCCAGAC	CTGTGAAGGC	AAAACCTTACT	600
5	CCAACCAGGC	CTCTGGTTAC	AGGAATGAGA	ATCCTTGATG	GGCTTTTCCC	650
	TGTGGCAAAA	GGCGGAACAG	CTGCAATCCC	CGGACCTTTC	GGATCGGGAA	700
	AGACCGTAAC	TCAGCAGTCG	CTTGCAAAAT	GGAGTGATAC	CGAAATTGTG	750
	GTCTACATCG	GTTGTGGTGA	GCGTGGAAAC	GAAATGGCAG	ATGTTCTGAG	800
	CGAATTCCCT	GAATCGAAG	ATCCGCAGAC	CGGGCGCCCA	CTTATGGAGC	850
10	GTACTGTTCT	TATCGCTAAC	ACTTCAAACA	TGCCTGTGGC	CGCAAGAGAA	900
	GCATCTGTGT	ATACCGGAAT	CACCATTGCA	GAATACTACC	GTGACATGGG	950
	ATTAGATGTA	TCCCTTATGG	CAGACTCCAC	CTCAAGGTGG	GCAGAAGCCA	1000
	TGAGAGAAAT	CTCTTCCCGT	CTGGAAGAAA	TGCCTGGTGA	AGAAGGTTAC	1050
	CCAGCATACC	TGTCTGCAAG	ACTGGCCGAA	TTCTACGAGC	GTGCCGGGGT	1100
15	TGCGGAGAGT	CTTTGCGGCG	AAACAGGTTT	CATTACTGTT	ATTGGAGCAG	1150
	TATCTCCACC	TGGCGGTGAC	TTCTCAGAGC	CTGTTACACA	GAATACCCTG	1200
	CGTATCGTAA	AAGTGTTCCT	GGCTCTCGAT	GCCAAACTAT	CTCAGAGGCG	1250
	TCACTTCCCG	GCCATCAACT	GGCTGAACAG	TTACAGTCTG	TATAAGGACA	1300
	GTCTTAATGA	CTGGTTTGCA	GATAATGTGG	CTCCTGATTA	TGTGCCTTTG	1350
20	AGGGAAAGAG	CAATGGAAAT	GCTCCAGACA	GAATCTGAAC	TGCAGGAAAT	1400
	CGTGCAGCTT	GTAGGTTCCG	ATGCTCTGCC	AGACGACCAG	CAGCTTCTGC	1450
	TTGAAATCAC	CCGTATGCTT	AGGGAAATTT	TCCTGCAGCA	GAATGCATTG	1500
	CACCCAGTAG	ATGCATACAG	CCCGTTTCGAT	CAGCAGTACA	AGATCCTTAA	1550
	GGCAATCATG	AAATGGGGAG	ACGCTGCGAT	GGATGCCTTG	AAATCAGGTG	1600
25	TTCCCGTAAC	TGAAATTATC	AAGCTTGAAT	CCAAAAATGT	GCTTGCTAAG	1650
	GTCAAGTACG	AAGAGAAGTT	TGATGAGTCT	ATGAATGCTG	TCCTGGCACA	1700
	GATGGATAAA	GAGTTTGCAT	CCCTGAGAGG	TAGGTAA		1737

30

2) INFORMATION FOR SEQ ID NO: 714

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanosarcina jannaschii*
 (C) ACCESSION NUMBER: extracted from U67477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714

	ATGAAAAGAG	AGGTTGAGAA	TATGCCAGTT	GTTGGTAAGA	TTATTAAAAT	50
	CGCAGGGCCT	GTTGTAGTTG	CAGAGGGAAT	GAAAGGAGCT	CAGATGTATG	100
	AGGTCGTTAA	AGTAGGAGAA	GAGAAATTGA	CTGGAGAAAT	CATTCAGTTG	150
50	CACGATGATA	AAGCAGTTAT	TCAGGTTTAT	GAAGAAACAT	CTGGAATTAA	200
	ACCAGGAGAG	CCAGTTGTTG	GTAAGTGGAG	TCCATTGTCT	GTTGAATTAG	250
	GGCCAGGGAT	GTTAAGAGCT	ATGTATGATG	GTATTCAGAG	GCCTTTAACA	300
	GCAATTGAAG	AGAAAACAGG	TTCAATCTTT	ATCCCAAGAG	GAGTTGATGT	350
	CCCTGCATTA	CCAAGAGATA	TAAAATGGGA	ATTTAAACCA	GTGGTAAATG	400
55	AAGGAGATTA	TGTTGAAGAA	GGAGACATAA	TTGGAAGTGT	TGATGAAACT	450
	CCTTCAATAG	TTCATAAAAT	CTTAGTTCCA	ATTGGTGTGA	AAGGAAAAAT	500
	TGTTGAAATA	AAAGAGGGTA	AATTTACAGT	TGAAGAGACA	GTTGCAGTTG	550
	TAGAAACAGA	AAATGGAGAA	AGGAAAGAAA	TTACAATGAT	GCAAAAATGG	600
	CCAGTAAGAA	AACCAAGACC	ATATAAGAG	AACTACCTC	CAGAAATTCC	650
60	ATTAATTACA	GGGCAAAGAG	TTGAAGACAC	TTTCTTTACA	TTAGCAAAAG	700

	GAGGAACAGC	AGCAATTCCA	GGTCCATTCTG	GTTTCAGGAAA	AACCGTTACT	750
	CAGCATCAGT	TGGCAAAGTG	GTCTGACGCT	GATGTCGTTG	TTTATATCGG	800
	ATGTGGAGAA	AGAGGAAACG	AGATGACAGA	GGTTATTGAA	GAGTTCCCAC	850
	ACTTAGAAGA	TATTAGAACT	GGAAACAAAT	TAATGGATAG	AACTGTATTA	900
5	ATAGCCAACA	CATCAAACAT	GCCTGTCTGCT	GCAAGGGAAG	CATCTGTCTA	950
	TACAGGAATT	ACAATTGCAG	AGTACTTCAG	AGATATGGGT	TATGGAGTTT	1000
	TATTAACAGC	AGATTCAACA	TCAAGATGGG	CAGAGGCAAT	GAGAGAAATT	1050
	TCAGGTAGAT	TGGAAGAAAT	GCCAGGGGAA	GAAGGGTATC	CAGCATACTT	1100
	AGCTTCAAGA	TTGGCTCAGT	TCTATGAAAG	AGCTGGAAGA	GTTATAACCT	1150
10	TAGGGAAAGA	TAACAGACAA	GGATTTCGTTT	GTATCGTTTG	AGCTGTTTCA	1200
	CCACCAGGAG	GGGACTTCTC	AGAACCAGTT	ACATCAAACA	CACTAAGGAT	1250
	AGTTAAGGTA	TTCTGGGCGT	TAGATGCAAA	CTTGGCAAGA	AGAAGACACT	1300
	TCCCAGCTAT	CAACTGGTTG	CAGAGTTATT	CATTATACAT	TGATGATGTT	1350
	ACAGAGTGGT	GGAACACAAA	TACTGGTCCA	GATTGGAGAC	AATTAAGAGA	1400
15	TGAAGCAATG	AGCTTATTAC	AAAAAGAGGC	AGAGTTGCAA	GAGATTGTTC	1450
	AGTTAGTTGG	GCCTGATGCA	TTGCCAGATA	GGGAGAGAGT	TATTTTAGAA	1500
	GTTGCAAGAA	TGTTGAGGGA	GGATTTCTTA	CAGCAAGATG	CGTTTGATGA	1550
	GGTAGATACC	TACTGTCCTC	CAATGAAACA	GTAAGTAATG	TTAAAGATAA	1600
	TTATGACATT	CTACCAAGAA	GCATTGAAGG	CAGTTGAAAG	AGGAGTTGAA	1650
20	CCAGCTAAGA	TTTTAGGAGT	TTCAGTTAAG	CAAGATATTG	CAAGAATGAA	1700
	ATACATCCCA	CACGATGAGT	TTATAAATGT	TAAATCAAAA	GAAATAATGG	1750
	AGAAAATTAA	GAATGAATTA	GGTTCATTAA	ACTAA		1785

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2) INFORMATION FOR SEQ ID NO: 715

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1354 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

- (ii) MOLECULE TYPE: Genomic DNA

35

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*
- (B) STRAIN: W83

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715

40

	TGAGCGAGGT	GATCAAGGTG	ATCGGCAAAA	ATGCTTATGT	GCAGGTTTTTC	50
	GAAAGTACTC	GCGGTATGCA	CGTAGGAGAT	GAGGCAGAGT	TTACCGGCAG	100
	TATGCTTGAG	GTAACGCTCG	GCCCCGGTAT	GCTTTCGAAG	AACTACGACG	150
45	GTCTGCAACA	CGACTTGGAC	AAGATGGACG	GGATCTTCCT	CAAACGAGGC	200
	GATTATACTC	CCGCTCTCGA	TGACGACAAG	CTGTGGGACT	TCAAGCCTTT	250
	GGCCAATGTG	AACGACAATG	TGATCGCAGG	CTCATGGCTC	GGAGAGGTGA	300
	CGGAAAATTT	CCAACCGCAC	AAGATCATGG	TACCTTTCGT	TTTCGAAGGC	350
	AATTACAAGG	TGAAGAGTCT	GGCCAAAGCC	GGTTCGTACA	AAGTGAACGA	400
50	TGTGATCGCT	GTGGTAACGG	ATCAGGACGG	GAAAGACCAC	AATGTAACCA	450
	TGGTGACAGAA	ATGGCCGGTG	AAACGTGCTA	TCACTTGCTA	TCGCGAGAAG	500
	CCGCGTCCTT	TCAAACCTGCT	CGAAACGGGT	ATCCGTATCA	TCGACACTTT	550
	CAACCCCATC	GTAGAGGGTG	GTACGGGATT	TATCCCCGGT	CCTTTCGGTA	600
	CGGGAAAGAC	GGTGCTCCAG	CATGCTATCT	CGAAGCAGGC	GGAAGCCGAT	650
55	ATCGTGATCA	TTGCAGCCTG	TGGCGAGCGT	GCAAACGAGG	TTGTGGAGAT	700
	CTTTGCGGAA	TTCCCCCACC	TGAATGACCC	CCACACGGGA	CGTAAATTGA	750
	TGGAACGTAC	CATTATTATT	GCTAATACGT	CGAATATGCC	TGTGGCTTCG	800
	CGTGAGGCAT	CCGTATATAC	GGCCATGACG	ATAGCCGAGT	ACTATCGCTC	850
	CATGGGCCTT	CGCGTGCTGA	TGATGGCAGA	CTCCACTTCG	CGTTGGGCAC	900
60	AGGCTCTGCG	TGAGATGTCT	AACCGTCTGG	AAGAGCTTCC	CGGACCGGAT	950

	GCTTTCCCGA	TGGACTTGTC	AGCTATCGTA	GCCAACTTCT	ACGCTCGTGC	1000
	AGGATACGTT	TACCTGAACA	ACGGTTCGGC	CGGTTCGGTA	ACGTTCATCG	1050
	GTACGGTATC	TCCCGCCGGT	GGTAACCTCA	AAGAGCCTGT	GACGGAAAAC	1100
	ACCAAGAAAG	TGGCTCGCTG	CTTCTATGCT	TTGGAGCAGA	ATCGTGCCGA	1150
5	CCGCAAACGT	TATCCGGCTG	TAAACCCCAT	CGATAGTTAC	TCGAAGTACA	1200
	TCGAATATCC	CGAATTTCGAG	AGCTATATAT	CGAACCACAT	CAGTTTACTC	1250
	ATTATATTCA	ACAGAAGTTG	GCAGATATAT	GGATCAAATC	TTACAGCAGA	1300
	CTGGACTACT	AAGGTGAATG	AGCTGAAGAT	GCGCTTGCAT	CAGGGTAAAG	1350
	AAAT					1354
10						

2) INFORMATION FOR SEQ ID NO: 716

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1788 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 25 (B) STRAIN: Type 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716

	TTTGACTCAA	GGGAAGATTA	TAAAAGTATC	GGGACCTCTA	GTTATTGCAT	50
30	CAGGTATGCA	GGAGGCTAAT	ATTCAAGATA	TTTGCCGTGT	AGGTAAGCTA	100
	GGGTAAATCG	GTGAAATTAT	TGAAATGAGA	AGAGATCAGG	CATCTATCCA	150
	AGTCTATGAA	GAAACATCTG	GTCTTGGTCC	GGGAGAACCT	GTTGTTACAA	200
	CTGGAGAACC	TCTCTCGGTT	GAATTAGGGC	CAGGATTGAT	TTCTCAAATG	250
	TTTGATGGCA	TACAACGCCC	ATTAGATCGA	TTTAAATTGG	CTACTCATAA	300
35	TGATTTTCTA	GTTCGTGGGG	TAGAAGTTCC	AAGTTTGGAT	AGAGATATTA	350
	AGTGGCATT	TGATTCCACT	ATAGCAATTG	GTCAAAAAGT	GAGTACGGGT	400
	GATATTCTTG	GAACGTGCAA	GGAAACCGAG	GTAGTTAATC	ATAAAATTAT	450
	GGTTCCTTAT	GGAGTATCTG	GAGAAGTCGT	TTCTATTGCA	TCTGGCGATT	500
	TTACAATTGA	TGAAGTTGTA	TATGAAATAA	AAAAATTGGA	CGGTAGTTTC	550
40	TATAAAGGAA	CGCTTATGCA	AAAATGGCCT	GTCCGCAAGG	CGCGTCCTGT	600
	TTCTAAACGT	TTAATTCCAG	AAGAACCATT	AATCACAGGT	CAACGAGTTA	650
	TTGATGCATT	CTTTCCAGTA	ACCAAAGGGG	GAGCTGCAGC	AGTTCCTGGA	700
	CCGTTTGGAG	CAGGAAAGAC	AGTTGTACAA	CACCAAGTAG	CTAAATTTGC	750
	CAATGTTGAT	ATTGTTATTT	ATGTCGGTTG	TGGAGAACGT	GGAAATGAAA	800
45	TGACGGATGT	ACTGAATGAG	TTTCCTGAGT	TGATTGACCC	TAATACCGGA	850
	CAATCAATTA	TGCAACGGAC	AGTTCCTGATT	GCTAATACTT	CAAATATGCC	900
	TGTTGCTGCT	CGTGAGGCTT	CAATTTATAC	AGGAATTACC	ATGGCTGAGT	950
	ATTTTCGTGA	TATGGGCTAC	TCTGTCGCCA	TTATGGCTGA	TTCAACTTCA	1000
	CGTTGGGCAG	AAGCGCTACG	TGAAATGTCA	GGACGTCTAG	AAGAAATGCC	1050
50	TGGTGATGAG	GGTTATCCTG	CTTATCTGGG	AAGTCGTATC	GCTGAATATT	1100
	ATGAAAGAGC	AGGACGTTCT	CAGGTTCTAG	GGCTTCAGCA	ACGTGAAGGA	1150
	ACGATTACTG	CTATTGGAGC	TGTATCGCCA	CCTGGTGGAG	ATATTTTCAGA	1200
	ACCAGTTACT	CAAAACACTT	TACGGATTGT	GAAAGTTTTT	TGGGGGCTTG	1250
	ATGCTCCGTT	GGCACAGCGA	CGTCATTTTC	CTGCAATTAA	CTGGCTTACA	1300
55	TCTTATTCAC	TATATAAAGA	CAGTGTGGGC	ACTTATATAG	ATGGTAAAGA	1350
	GAAGACAGAT	TGGAATAGTA	AAATAACTCG	TGCGATGAAC	TACTTACAAC	1400
	GGGAATCTAG	TTTAGAGGAA	ATTGTTTCGTC	TTGTTGGAAT	TGATTCTCTG	1450
	TCTGATAATG	AACGACTAAC	GATGGAAATT	GCTAAACAAA	TTGAGAAGA	1500
	TTATTTGCAA	CAGAACGCTT	TTGATTCCGGT	AGATACATTC	ACTTCGTTTG	1550
60	CAAAACAAGA	AGCAATGCTA	AGTAATATTC	TCACTTTTGC	TGATCAGGCA	1600

AATCATGCTT	TAGAGTTGGG	TTCTTACTTT	ACAGAGATTA	TGGAAGGTAC	1650
CGTGGCAGTT	CGAGACCGTA	TGGCGAGAAG	TAAATATGTT	TCAGAAGATA	1700
GATTAGATGA	AATCAAAATT	ATATCAAATG	AGATTACACA	TCAAATTCAT	1750
TTGATATTAG	AAACAGGAGG	TCTATAAATG	AGTGTTAT		1788

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2) INFORMATION FOR SEQ ID NO: 717

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
 (B) STRAIN: GB8

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717

CGATCCTGGT	GTGCTCGGCC	GCTGACGGCC	CGATGCCGCA	AACGCGTGAG	50
CACATCCTGC	TGGCGCGTCA	GGTCGGTGTG	CCGTACATCA	TCGTGTTCTT	100
GAACAAGTGC	GACATGGTGG	ACGACGCGGA	GCTGCTCGAG	CTGGTCGAAA	150
TGGAAGTGCG	CGAACTGCTG	TCGAAGTACG	ACTTCCCAGG	CGACGACACG	200
CCGATCATCA	AGGGTTCGGC	GAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
GCTGGGCGAA	GTGGCGATCA	TGAACCTGGC	CGACGCGCTG	GACACGTACA	300
TCCCGACGCC	GGAGCGTGCG	GTCGACGGCG	CGTTCCTGAT	GCCGGTGGAA	350
GACGTGTTCT	CGATCTCGGG	CCGTGGTACG	GTGGTGACGG	GTCGTGTCTG	400
GCGCGGCGTG	ATCAAGGTTG	GCGAGGAAAT	CGAAATCGTC	GGTATCAAGG	450
CGACGGCGAA	GACGACCTGC	ACGGGCGTGG	AAATGTTCCG	CAAGCTGCTG	500
GACCAGGGTC	AGGCGGGCGA	CAACGTCGGT	ATCCTGCTGC	GCGGCACAAA	550
GCGTGAAGAC	GTGGAGCGCG	GCCAGGTTCT	GGCGAAGCCG	GGTTCGATCA	600
CGCCGCACAC	GCACTTCACG	GCAGAAGTGT	ACGTGCTGAG	CAAGGACGAA	650
GGCGGCCGCC	ACACGCCGTT	CTTCAACAAC	TACCGTCCGC	AGTTCTACTT	700
CCGTACGACG	GACGTGACGG	GCTCGATCGA	GCTGCCGAAG	GACAAGGAAA	750
TGGTGATGCC	GGGCGACAAC	GTGTCGATCA	CGGTGAAGCT	GATCGCGCCG	800
ATCGCGATGG	AAGAAGGTCT	GCG			823

45

2) INFORMATION FOR SEQ ID NO: 718

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia pseudomallei*
 (B) STRAIN: 1026B

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718

GCGATCCTGG	TGTGCTCGGC	CGCTGACGGC	CCGATGCCGC	AAACGCGTGA	50
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	GCACATCCTG	CTGGCGCGTC	AGGTCGGTGT	GCCGTACATC	AT>GTTCC	100
	TGAACAAGTG	CGACATGGTG	GACGACGCGG	AGCTGCTCGA	GCTGGTCGAA	150
	ATGGAAGTGC	GCGAACTGCT	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	200
	GCCGATCATC	AAGGGTTCGG	CGAAGCTGGC	GCTGGAAGGC	GACAAGGGCG	250
5	AGCTGGGCGA	AGTGGCGATC	ATGAACCTGG	CCGACGCGCT	GGACACGTAC	300
	ATCCCGACGC	CGGAGCGTGC	GGTCGATGGC	GCGTTCCTGA	TGCCGGTGGA	350
	AGACGTGTTC	TCGATCTCGG	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCTG	400
	AGCGCGGCGT	GATCAAGGTT	GGCGAGGAAA	TCGAAATCGT	CGGTATCAAG	450
	GCGACGGCGA	AGACGACCTG	CACGGGCGTG	GAAATGTTCC	GCAAGCTGCT	500
10	GGATCAGGGT	CAGGCGGGCG	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	550
	AGCGTGAAGA	CGTGGAGCGC	GGCCAGGTTC	TGGCGAAGCC	GGGTTCGATC	600
	ACGCCGCACA	CGCACTTCAC	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	650
	AGGCGGCCGC	CACACGCCGT	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	700
	TCCGTACGAC	GGACGTGACG	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	750
15	ATGGTGATGC	CGGGCGACAA	CGTGTCGATC	ACGGTGAAGC	TGATCGCGCC	800
	GATCGCGATG	GAAGAAGGTC	TGCG			824

20 2) INFORMATION FOR SEQ ID NO: 719

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium beijerincki* (deposited as
Clostridium butyricum)
 (B) STRAIN: ATCC 8260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719

	TGTATCAGCA	GCAGATGGTC	CAATGCCACA	AACAAGAGAA	CATATACTAC	50
	TAGGATCAAG	AGTTGGTATC	CAATATATCG	TAGTATTCTT	AAATAAAGCA	100
	GATATGGTAG	ACGATCCAGA	ATTATTAGAA	TTAGTAGAAA	TGGAAGTAAG	150
40	AGAATTATTA	AGCGAATATG	ACTTCCCAGG	AGACGATATT	CCAGTAATAA	200
	CAGGATCAGC	ATTAAAAGCA	TTAGAAAATC	CAACAGATGA	AGAAGCAATT	250
	AAGCCAATCA	TGGATTTAAT	GGAAGCAGTA	GATAGCTATA	TCCCAACTCC	300
	AGAAAGAGCA	ACAGATAAGC	CATTCTTAAT	GCCAATCGAA	GATGTATTCA	350
	CAATTACAGG	AAGAGGAACA	GTTGCAACAG	GAAGAGTTGA	AGCTGGAGTA	400
45	CTTCATGTAG	GAGATGAAGT	AGAAATCGTT	GGATTAACAG	AAGAAAAGAA	450
	GAAAGTTGTA	GTAAGTGGAA	TCGAAATGTT	CAGAAAGTTA	TTGGATGAAG	500
	CACAAGCTGG	AGATAACATC	GGAGCATTAT	TAAGAGGAGT	TCAAAGAACT	550
	GATATTGAAA	GAGGTCAAGT	TTTATCAAAA	CCAAATTCAG	TACACCCCTCA	600
	CACTAAATTT	GTAGGTCAAG	TATACGTACT	TAAAAAAGAA	GAAGGTGGAA	650
50	GACATACTCC	ATTCTTTGAT	GGATACAGAC	CACAATTCTA	TTTCAGAACA	700
	ACAGACGTTA	CAGGRTCAAT	CAAGTTACCA	GATGGAATGG	AAATGGTAAT	750
	GCCTGGAGAT	CACATTGATA	TGAATGTTGA	ATTAATCACT	CCAATCGCAA	800

55

2) INFORMATION FOR SEQ ID NO: 720

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium innocuum*
(B) STRAIN: ATCC 14501

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720

	GGTGCTATCC	TGGTTGTTGC	TGCATCTGAT	GGTCCTATGC	CTCAGACTCG	50
	TGAGCACATC	CTGCTTGCTC	GTCAGGTAGG	TGTTCCCTTAC	ATCGTTGTAT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAACTGAT	CGACCTTGTT	150
15	GAAATGGAAG	TACGTGAGCT	GTTAAGCGAG	TACGGATTCTG	ACGGAGATAA	200
	CGCTCCGGTT	ATCCGTGGTT	CTGCACTGAA	GGCTCTGGAA	GGTGACGACA	250
	AATACGTTGG	CGCTATCAAA	GAAGTATGAT	ATGCAGTTGA	TGAATTCATC	300
	CCAGATCCAA	CTCGTGAAAC	TGACAAACCA	TTCCTGATGT	CTGTAGAAGA	350
	CGTTATGACA	ATCACAGGAC	GTGGTACAGT	TGCTACAGGA	CGTGTGAGC	400
20	GTGGGGTAGT	AAAAGTGGGA	GAAGAAGTTG	AAATCGTTGG	TATCAAGGAT	450
	ACTCAGAAAA	CTGTTGTTAC	CGGACTGGAA	ATGTTCCGTA	AGCAGCTGGA	500
	CTTCGCAGAA	TCCGGAGACA	ACATCGGTGC	TCTGCTGCGT	GGTATCAACC	550
	GTGACCAGAT	TCAGCGTGGA	CAGGTTCTTG	CTAAACCAGG	ATCCGTACAT	600
	CCACACACAA	AGTTCAAGGC	TCAGGTTTAT	GTATTAACAA	AAGAAGAAGG	650
25	TGGACGTCAC	ACTCCATTCTG	TTTCTAATA	CCGTCCTCAG	TTCTACTTCC	700
	GTACAACTGA	CGTAACTGGT	GTTATTACAT	TACCGGAAGG	AACTGAAATG	750
	GTTATGCCTG	GTGACAACGT	TGAAATGAAC	GTTGAGCTGA	TTGCTCCAA	799

30

2) INFORMATION FOR SEQ ID NO: 721

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium novyi*
(B) STRAIN: ATCC 19402

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721

	TTGTATCAGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATCCTA	50
	TTAGCATCAA	GAGTAGGAGT	TAACCACATA	GTAGTATTCT	TAAACAAAGC	100
	AGACCAAGTA	GATGATCCAG	AATTACTAGA	ATTAGTAGAA	ATGGAAGTAA	150
50	GAGAATTATT	AAGCGAATAC	GGATTTGACG	GAGACGAATG	TCCAGTAGTA	200
	GTAGGATCAG	CATTAAAAGC	AATCGAAGAA	GGGGATGACC	AATGCATCCT	250
	AGACTTAATG	AAAGCTGTAG	ATGAATATAT	CCCAACTCCA	GAAAGAGCAA	300
	CAGATCAACC	ATTCTTAATG	CCTGTAGAAG	ATGTATTTAC	AATTACAGGA	350
	AGAGGAACAG	TTGCAACAGG	AAGAGTTGAA	AGAGGAGTAC	TACACGTAGG	400
55	AGATGAAGTA	CAAATCGTAG	GAATGAAAGA	AGAAATCGGA	AAGACAACAA	450
	TCACAGGAGT	AGAAATGTTC	AGAAAGATGT	TAGATGAAGC	AATGGCTGGA	500
	GATAACATCG	GAGCATTATT	AAGAGGAGTA	CAAAGAGACG	AAATCGAAAG	550
	AGGTCAAGTA	CTAGCAAAAC	CAGGTTTCTG	AACACCTCAC	AAAAAATTCG	600
	TAGGTCAAGT	TTACGTATTA	AAGAAAGAAG	AAGGTGGAAG	ACACACTCCA	650
60	TTCTTTAACG	GATACAGACC	ACAATTCTAC	TTCAGAACAA	CAGACGTAAC	700

AGGATCAATC GCTTTACCAG AAGGAGTAGA AATGGTAATG CCAGGAGACC 750
ATATAGACAT GAACGTAGAA TTAATCACAC CAGTAGCAA 789

5

2) INFORMATION FOR SEQ ID NO: 722

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 798 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
(B) STRAIN: ATCC 12464

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722

GTTCAGCAGC AGACGGTCCA ATGCCACAAA CAAGAGAACA TATACTACTA 50
GCATCAAGAG TTGGTGTTGA CTATATCGTA GTATTCTTAA ACAAGGCAGA 100
TATGGTAGAT GACGAAGAAT TATTAGAATT AGTAGAAATG GAAGTTAGAG 150
25 AATTATTATC AGAATACAAC TTCCCAGGAG ATGATATTCC AGTAATCAAG 200
GGATCAGCTT TAGTAGCATT AGAAAACCCA ACAGATGAAA AATCAATCGC 250
TCCAATCTTA GAATTAATGG AAGCAGTAGA TAGCTACATT CCAACACCAG 300
AAAGAGCAAC AGATAAGCCA TTCTTAATGC CAGTAGAAGA TGTATTCACA 350
ATAACTGGTA GAGGAACAGT TGCAACAGGA AGAGTTGAAA GAGGAGTTCT 400
30 TCATGTAGGA GACGAAGTAG AAATCGTTGG ATTATCAGAA GAAAGCAGAA 450
AAGTAGTAGT AACAGGAATA GAAATGTTCA GAAAGTTACT AGACGAAGCA 500
CAAGCTGGAG ATAATGTTGG AGTACTTTTA AGAGGTGTTC AAAGAACAGA 550
TATCGAAAGA GGTCAAGTAT TAGCAAAGAC TGGATCAGTT AAGCCACACA 600
GCAAGTTCGT AGGTCAAGTA TACGTACTTA AGAAAGAAGA AGGTGGAAGA 650
35 CATACTCCAT TCTTCGATGG ATACAGACCA CAATTCTACT TCAGAACAAC 700
AGACGTTACT GGATCAATCA AATTACCAGA CGGAATGGAA ATGGTTATGC 750
CAGGAGACCA CATTGATATG AACGTTGAAT TAATCACTCA AGTAGCAA 798

40

2) INFORMATION FOR SEQ ID NO: 723

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 799 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tertium*
(B) STRAIN: ATCC 14573

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723

GTTCAGCAGC AGATGGTCCA ATGCCTCAAA CAAGAGAACA CATACTACTA 50
GCTTCAAGAG TTGGTGTTGA CTACATAGTT GTTTTCTTAA ACAAGGCAGA 100
TATGGTAGAT GACGAAGAAT TATTAGAATT AGTTGAAATG GAAGTAAGAG 150
60 AATTATTATC AGAATACAAC TTCCCAGGAG ATGATATTCC AGTAATAAAG 200

	GGTTCAGCTT	TACAAGCATT	AGAAAACCCA	ACAGATGAAA	AAGCAATCGC	250
	TCCAATCCTT	GAGTTAATGG	AAGCTGTAGA	TAGCTACATT	CCAACTCCAG	300
	AAAGAGCAAC	AGATAAGCCA	TTCTTAATGC	CAGTAGAAGA	TGTATTCAAC	350
	ATCACTGGTA	GAGGAACAGT	TGCTACAGGA	AGAGTTGAAA	GAGGAGTTCT	400
5	TCACGTAGGA	GACGAAGTAG	AAATCGTTGG	ATTATCAGAA	GACAGCAGAA	450
	AAGTAGTAGT	AACAGGAATA	GAAATGTTCA	GAAAGTTACT	AGACGAAGCG	500
	CAAGCTGGAG	ACAACGTAGG	AGTTCTTTTA	AGAGGAGTTC	AAAGAACTGA	550
	CATCGAAAGA	GGTCAAGTTT	TAGCAAAAGT	TGGATCAGTT	AAGCCACACA	600
	AGAAATTTGT	AGGTCAAGTA	TACGTACTTA	AAAAAGAAGA	AGGTGGAAGA	650
10	CATACTCCAT	TCTTCGATGG	ATACAGACCA	CAATTCTACT	TCAGAACAAC	700
	AGAYGTTACT	GGTTCAATCA	AGTTACCAGA	TGGAATGGAA	ATGGTTATGC	750
	CAGGAGACCA	CATTGATATG	AACGTTGAAT	TAATCACTCA	AGTAGCTAT	799

15

2) INFORMATION FOR SEQ ID NO: 724

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 801 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium tetani*

(B) STRAIN: ATCC 19406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724

	TAGTAAGTGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATACTA	50
	TTAGCATCCA	GAGTTGGAGT	TGAGCACATA	GTAGTATTCT	TAAATAAAGC	100
	AGACCAAGTA	GATGACGCAG	AGTTAATCGA	ATTAGTAGAA	ATGGAAGTAA	150
35	GGGAATTAAT	GAACGAATAC	GGATTCCCAG	GAGATGACGC	ACCAGTAGTA	200
	GTAGGATCCG	CATTAAAAGC	ATTAGAAAAT	CCAGAAGATG	ATGCAGCAAC	250
	ACAATGCATA	ATGGACTTAA	TGGCAGCAGT	AGATGAATAT	ATACCAACAC	300
	CAGAAAGAGC	AACAGATAAG	CCATTCTTAA	TGCCAGTAGA	AGATATCTTC	350
	ACAATCACAG	GAAGAGGAAC	AGTTGCAACA	GGAAGAGTAG	AAAGAGGAAT	400
40	TCTAAAAGTA	GGAGACGAAA	TAGAAATCGT	AGGATTAAGT	GATGAAAGCA	450
	AGAAATCAGT	AATCACAGGA	ATAGAAATGT	TCAGAAAACT	ATTAGATGAA	500
	GCACAAGCAG	GAGATAACAT	CGGAGCATT	TTAAGAGGTG	TTCAAAGAGA	550
	TGAAATCCAA	AGAGGTCAAG	TATTAGCAGC	AACAGGATCA	GTAAAACCAC	600
	ATAAGAGTTT	TACAGGTCAA	GTATATGTAT	TAAAGAAAGA	AGAAGGAGGA	650
45	AGACACACTC	CATTCTTTAA	CGGATACAGA	CCACAATTCT	ACTTTAGAAC	700
	AACAGACGTA	ACAGGTTCAA	TCGCACTACC	AGAAGGAGTA	GAAATGGTAA	750
	TGCCAGGAGA	CCACATAGAC	ATGAAGGTAG	AATTAATAAC	AAGAGTAGCA	800
	A					801

50

2) INFORMATION FOR SEQ ID NO: 725

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 633 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

413

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus malodoratus*

(B) STRAIN: ATCC 43197

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725

	TATGCCTCAA	ACTCGTGAAC	ACATCTTGTT	ATCTCGTAAC	GTTGGTGTTT	50
	CTTACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGATGAAGAA	100
10	TTACTAGAAT	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATACGA	150
	CTTCCCAGGC	GACGACACTC	CAGTTATCGC	TGGTTCAGCT	TTGAAAGCTT	200
	TAGAAGGCGA	TGCTTCATAC	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCT	250
	GTTGATGAAT	ATATCCCAAC	ACCAGTTCGT	GATACTGACA	AACCATTTCAT	300
	GATGCCAGTC	GAAGATGTAT	TCTCAATCAC	TGGTCGTGGA	ACTGTTGCAA	350
15	CTGGTCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGCAAC	TGCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTGTTAGATT	ACGCTGAAGC	AGGCGATAAC	ATTGGTG CAT	500
	TGTTACGTGG	TGTTGCACGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	550
	AAACCAGCTT	CAATCACTCC	ACATACAAAA	TTCTCTGCAG	AAGTTTACGT	600
20	TTTAACTAAA	GAAGAAGGCG	GACGTCATAC	TCC		633

2) INFORMATION FOR SEQ ID NO: 726

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Enterococcus sulfureus*

(B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726

40	CACGTGAACA	CATCTTGTTA	TCTCGTAACG	TAGGTGTTCC	TTACATCGTT	50
	GTATTCTTAA	ACAAAATGGA	TATGGTTGAT	GACGAAGAAT	TATTAGAATT	100
	AGTAGAAATG	GAAGTTCGTG	ACTTATTATC	AGAATACGAT	TTCCCAGGCG	150
	ATGACACTCC	AGTTGTTGCA	GGTTCTGCTT	TGAAAGCTTT	AGAAGGCGAC	200
	GCTTCTTACG	AAGAAAAAAT	CATGGAATTA	ATGGCTGCAG	TTGACGAGTA	250
45	CATCCCAACT	CCAACCTCGT	ACACTGACAA	ACCATTCATG	ATGCCAGTTG	300
	AGGATGTATT	CTCAATCACT	GGACGTGGTA	CTGTTGCTAC	AGGTCGTGTT	350
	GAACGTGGAC	AAGTTCGCGT	TGGTGACGTT	GTAGATATCG	TTGGTATCGC	400
	TGACGAAACT	GCTCAAACAA	CTGTAACAGG	TGTTGAAATG	TTCCGTAAAT	450
	TATTAGACTA	CGCTGAAGCA	GGCGATAACA	TCGGTGCTTT	ATTACGTGGT	500
50	GTTGCTCGTG	AAGACATCCA	ACGTGGACAA	GTTTTAGCTA	AACCAGCTTC	550
	AATCACTCCA	CATACAAAAT	TCTCTGCTGA	AGTATACGTA	TTAAGCAAAG	600
	AAGAAGGTGG	ACGTCATACT	CCA			623

55

2) INFORMATION FOR SEQ ID NO: 727

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 bases

60

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus garvieae*
(B) STRAIN: ATCC 49156

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727

	CGGTCCTATG	CCTCAAACCTC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
	GCGTACCATA	CATCGTTGTT	TTCTTGAACA	AAATGGATAT	GGTTGATGAC	100
	GAAGAATTGC	TAGAATTAGT	TGAAATGGAA	GTTTCGTGACC	TATTGTCTGA	150
15	ATATGACTTC	CCAGGCGACG	ATGTTCTCTGT	AATCGCTGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGAGATCCT	TCATACGAAG	AAAAAATCAT	GGAATTGATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACTCCA	GAACGTGATA	CTGACAAACC	300
	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	400
20	GAAATCGTTG	GTATTGCTGA	CGAAACTGCT	AAAACAACTG	TAACAGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	600
	TTATGTTTTG	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA	TTCTTC	646

25

2) INFORMATION FOR SEQ ID NO: 728

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma pirum*
(B) STRAIN: ATCC 25960D

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728

	GAGCAATTTT	AGTTGTTTCT	GCAACTGATG	GTCCAATGCC	TCAAACCTCGT	50
	GAACATATCT	TATTAGCACG	CCAAGTTGGT	GTTCTTAAAA	TGGTTGTTTT	100
45	CTTAAACAAA	TGTGATGTTG	CTTCTGATCC	AGAAATGCAA	GAATTAGTTG	150
	CTGAAGAAGT	AAAAGACTTA	TTAAATCTT	ATGGTTTTGA	TGGTGACAAT	200
	ACTCCAATTA	TTCGTGGTTC	AGCATTAGAA	GCATTAAATG	GTAAACCTGA	250
	ATGAGAAGAA	AAAATTAAAG	AATTAATGAA	GGCAGTGGAT	GACACTATTC	300
	CTGATCCAGT	TCGTGATACT	GAAAAGCCAT	TCTTGTTACC	AATTGAAGAC	350
50	GTAATGACAA	TTACAGGTCG	TGGTACTGTT	GTTACAGGTC	GTGTAGAACG	400
	TGGTACTCTA	AAATTAAATG	ATGAAGTTGA	AATTGTTGGT	TTAGGTGAAA	450
	CATTTAAATC	TGTTGTAACA	GGTATTGAAA	TGTTCCGTAA	AGAATTAGAT	500
	GAAGCTCGTG	CTGGTGACAA	TGCTGGTATT	TTACTTCGTG	GTGTTGACCG	550
	TGGTCAAGTA	CAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCTATTACTC	600
55	CTCATACTAA	ATTTAAAGCT	GAAATTTATG	CTTTGAAAAA	AGAAGAAGGT	650
	GGTCGTCATA	CTGCTTTCTT	AAACGGTTAT	CGTCCTCAAT	TCTATTTTCAG	700
	AACAACCTGAT	GTTACAGGTT	CTATTAAATT	AAAAGATGGA	ACTGAAATGG	750
	TTATGCCTGG	TGACAATACT	GAAATCACTG	TAGAATTAAT	TTCACCAATT	800
	GCTTGTAATA	AGGAAGTAAG	TTT			823

60

2) INFORMATION FOR SEQ ID NO: 729

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycoplasma salivarium*
 15 (B) STRAIN: ATCC 23064
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729

	GGAGCAATCT	TAGTTGTTGC	TGCAACTGAT	GGTGCGATGC	CTCAAACCTCG	50
20	TGAACACGTT	TTACTTGCAA	AACAAGTTGG	TGTTCCCTAAA	ATCGTTGTTT	100
	TCTTAAACAA	AATCGATATG	TTCAAGCCAG	AAGAAAGAGC	CGAAATGGTT	150
	GAAATGGTTG	AAATGGACAT	TCGTGACTTA	TTAAACAAAT	ACGACTTTGA	200
	TGGTGACAAT	ACTCCTATTA	TTGCTGGTTC	AGCATTAAAA	GCATTACAAG	250
	GTGATCCAGA	ATATGAAAAG	AATATTCTAG	AACTTATGGA	TGCAGTAGAC	300
25	ACATACATTG	ATGAACCTAC	TCGTGATAAA	GATAAACCAT	TCTTAATGGC	350
	TGTAGAAGAC	GTATTTACAA	TTACTGGTCG	TGGAAC TGTT	GCTACTGGTA	400
	GAGTAGAACG	TGGTACATTA	CATCTAAATG	ATGAAGTTGA	AATCGTTGGT	450
	CTACGTCCAA	CAATTAAAAC	TGTTGTTACT	GGAATTGAAA	TGTTCCGTAA	500
	AAATTTAAAA	GAAGCTCAAG	CTGGAGATAA	TGCAGGACTT	TTACTACGTG	550
30	GAATTGATAG	AGATCAAGTA	GAACGTGGAC	AAGTTTTGGC	CAAACCAAAA	600
	AGTATTATTC	CTCACACAGA	ATTTGAAGCT	GCTGTGTATG	TTCTAAAAGC	650
	TGAAGAAGGT	GGACGTCACA	CTCCATTCTT	TGAACACTAT	AAACCACAAT	700
	TTTACTTTTCG	TACAACCGAC	GTTACTGGTG	GAATTAAATT	CAAACCTGGA	750
	CGTGAAATGG	TTATGCCTGG	CGAAAATGTT	GAATTTACAG	TTACTTTAAT	800
35	TGCTCCTATT	GCAGTTGAAG	AAGGAA			826

2) INFORMATION FOR SEQ ID NO: 730

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730

55	TGGTATGTTC	CGCAGCYGAY	GGYCCTATGC	CTCAAACCTCG	CGAACACATC	50
	CTGYTGGCTC	GCCAAGTAGG	YGTACCTTAC	ATCATCGTRT	TCATGAACAA	100
	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAAC TGTT	GAAATGGAAA	150
	TCCGYGACCT	GYTGTCMAGC	TACGACTTCC	CMGGCGACGA	CTGCCCAATC	200
	GTACAAGGTT	CTGCACTGAA	AGCTTTTGAA	GGYGAYGCTG	GTTACGAAGA	250
60	GAAAATCTTC	GAAYTGGCTG	CTGCTTTGGA	CAGCTACATC	CCAACCTCCTG	300

	AGCGTGCTGT	GGACAAACCK	TTCYTGYTGC	CTATCGAAGA	CGTRTTCTCT	350
	ATCTCTGGYC	GYGGTACMGT	AGTAACYGGY	CGTGTAGAGC	GCGGTRTCAT	400
	CCACGTTGGT	GACGAGATYG	AAATCGTAGG	TCTGAAAGAA	ACCCAAAAAA	450
	CCACTTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAA	500
5	GCWGGTGACA	ACGTAGGCGT	ATTGYTGCGT	GGTACCAARC	GTGAAGACGT	550
	AGAGCGTGGT	CAAGTATTGG	CYAAACCAGG	YACCATYACT	CCSCACACCA	600
	AATTCAAAGC	AGAAGTATAC	GTAAGTGGCA	AAGAAGAGGG	TGGTCGYCAC	650
	ACTCCATTCT	TCGCYAACTA	CCGYCCMCAA	TTCTACTTCC	GTACYACTGA	700
	CGTAACYGGT	GCAGTTACTT	TGGAAGAAGG	TGTAGAAATG	GTAATGCCAG	750
10	GTGAGAACGT	AACCATTACY	GTAGAACTGA	TTGCGCCTAT	CGCTAGGAAG	800
	AAGGTCTGCG					810

15 2) INFORMATION FOR SEQ ID NO: 731

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Enteritidis
 (B) STRAIN: ATCC 13076

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731

	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	GTGAGCACAT	50
	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	TTCCTGAACA	100
	AATGCGACAT	GTTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	TGAAATGGAA	150
35	GTTCGYGAAC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	ACACTCCGAT	200
	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	GAGTGGGAAG	250
	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	CCCGGAACCA	300
	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	ACGTATTCTC	350
	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	CGCGGTATCA	400
40	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	GAATCAGAAG	450
	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	ACGAAGGCCG	500
	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	CGTGAAGAAA	550
	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	GCCGCACACC	600
	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	GCGGCCGTCA	650
45	CACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	GGTAATGCCG	750
	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	TCGCAATGGA	800
	CGACGGTCTG	CGT				813

50

2) INFORMATION FOR SEQ ID NO: 732

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Gallinarum
5 (B) STRAIN: ATCC 9184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732

	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	GTGAGCACAT	50
10	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	TTCCTGAACA	100
	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACCTGGT	TGAAATGGAA	150
	GTTCGYGAAC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	ACACTCCGAT	200
	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	GAGTGGGAAG	250
	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	CCCGGAACCA	300
15	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	ACGTATTCTC	350
	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	CGCGGTATCA	400
	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	GA CTCAGAAG	450
	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	ACGAAGGCCG	500
	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	CGTGAAGAAA	550
20	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	GCCGCACACC	600
	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	GCGGCCGTCA	650
	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	GGTAATGCCG	750
	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	TCGCAATGGA	800
25	CGACGGTCTG	CG				812

2) INFORMATION FOR SEQ ID NO: 733

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi B
(B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733

45

	TGGTTGTTGC	TGCGACTGAC	GGYCCGATGC	CGCAGACCCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	GCTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAACCTGGT	GAAATGGAAG	150
	TTCGYGAACT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	200
50	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
	GAAAATCATC	GAACCTGGCTG	GCTTCCTGGA	TTCTTACATT	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	GCGGTATCAT	400
	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACTCAGAAGT	450
55	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCTC	650
	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
60	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750

GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCAATGGAC 800
 GACGGTCTGC GTTT 814

5

2) INFORMATION FOR SEQ ID NO: 734

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Virchow
 (B) STRAIN: ATCC 51955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734

GGCGCGATCC TGGTTGTTGC TGC GACTGAC GGCCCGATGC CGCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
 25 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
 GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA 200
 CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
 AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATT 300
 CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
 30 CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC 400
 GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG 450
 ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
 GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG 600
 35 CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG 650
 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 GTACTACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
 GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
 CGCAATGGAC GACGGTCTGC GTTTCGCA 828

40

2) INFORMATION FOR SEQ ID NO: 735

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia grimesii*
 (B) STRAIN: ATCC 14460

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735

GGCGCTATCC TGGTTGTTGC TGC GACTGAT GGCCCAATGC CACAGACCCG 50
 60 TGAGCACATC CTGCTGGGTC GTCAGGTTGG CGTTCCTTTC ATCATCGTAT 100

	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAC TGGTA	150,
	GAAATGGAAG	TTCGTGAACT	TCTGTCTGCT	TATGACTTCC	CTGGTGATGA	200
	CCTGCCAGTT	GTTTCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	TAAAATCATC	GA ACTGGCTG	GCTACCTGGA	TTCTTACATC	300
5	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGYC	GTGGTACYGT	AGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCGT	TAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
10	GTGAAGACAT	CGAACGTGGT	CAGGTACTGG	CTAAACCAGG	TTCAATCAAG	600
	CCACACACCA	AATTCGACTC	AGAAGTTTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAAC TGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTAACCCTGA	TTCACCCAAT	800
15	CGCGATGGAC	GACGGTCTGC	GTTTC			825

2) INFORMATION FOR SEQ ID NO: 736

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Clostridium difficile*
 (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736

35	TATTAGTTTG	TTCAGCAACA	GATGGACCAA	TGCCACAAAC	AAGAGAGCAT	50
	ATACTATTAT	CAAGACAAGT	TGGAGTACCA	TATATAGTAG	TATTCTTAAA	100
	CAAATGTGAC	ATGGTAGATG	ATGAAGAGTT	ATTAGAGTTA	GTAGAGATGG	150
	AAGTAAGAGA	TTTATTAACA	GAATATGATT	TCCCAGGAGA	TGACACTCCA	200
	ATAGTAAGAG	G TTCAGCATT	AATGGCATT	GAAGATCCAA	AGAGYGAGTG	250
40	GGGAGATAAG	ATAGTAGAAT	TATTCGAGCA	AATAGATGAG	TATATAACCAG	300
	CTCCAGAGAG	AGATACAGAT	AAACCATTCT	TAATGCCAGT	AGAGGACGTA	350
	TTCTCAATCA	CAGGAAGAGG	AACAGTTGCA	ACAGGAAGAG	TGGAAAGAGG	400
	AGTACTAAAA	GTACAAGACG	AAGTAGAKTT	AGTAGGATTA	ACAGAAGCAC	450
	CAAGAAAAGT	AGTAGTAACA	GGAGTAGAGA	TGTTTCAGAAA	ATTATTAGAC	500
45	CAAGCACAAG	CAGGGGATAA	TATAGGAGCA	TTATTAAGAG	GAGTACAAAG	550
	AAACGAGATA	GAAAGAGGAC	AAGTACTAGC	AAAGACTGGA	TCAGTAAAGG	600
	CACACACAAA	GTTTACAGCA	GAAGTATATG	TACTTAAAAA	AGAAGARGGT	650
	GGAAGACATA	CACCATTCTT	TGATGGATAT	AGACCACAAT	TCTATTTTCAG	700
	AACAACAGAC	GTAACAGGAG	CTTGTAAGTT	ACCAGAAGGA	ATAGAGATGG	750
50	TAATGCCTGG	AGATAACGTA	ACAATGGAAG	TAGACTTAAT	AAACTCAA	798

2) INFORMATION FOR SEQ ID NO: 737

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

420

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia pseudomallei*
(B) STRAIN: 1026B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737

10	GTCAACATGA	TGGAGCTCAT	CAACAACATC	GCGAAGGAGC	ACGGCGGTTA	50
	CTCCGTGTTC	GCGGGCGTGG	GCGAGCGTAC	CCGTGAAGGG	AACGACTTCT	100
	ACCACGAAAT	GAAGGACTCG	AACGTTCTCG	ACAAGGTCGC	GCTGGTGTAC	150
	GGCCAGATGA	ACGAGCCGCC	GGGCAACCGT	CTGCGCGTGG	CGCTGACGGG	200
	CCTCACGATG	GCCGAGCACT	TCCGTGACGA	AGGCCTCGAC	GTGCTGTTCT	250
15	TCGTCGACAA	CATCTACCGT	TTCACGCTGG	CCGGTACCGA	AGTGTCGGCG	300
	CTGCTCGGCC	GTATGCCGTC	GGCAGTGGGC	TATCAGCCGA	CGCTGGCTGA	350
	AGAAATGGGC	AAGCTGCAAG	AGCGCATCAC	GTCGACGAAG	AAGGGCTCGA	400
	TCACGTCGGT	T				411

20

2) INFORMATION FOR SEQ ID NO: 738

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium bifermentans*
(B) STRAIN: ATCC 638

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738

	TACAAGAGCT	TATTAACAAT	ATAGCTACTC	AACACGGTGG	TATATCAGTA	50
	TTCGCAGGTG	TTGGAGAGAG	AACAAGAGAA	GGTAACGACT	TATTCCATGA	100
40	GATGAGCGAT	ACAGGAGTTA	TAAATAAAAC	AGCTCTAGTA	TTCGGACAAA	150
	TGAATGAGCC	ACCTGGAGCA	AGAATGAGAG	TTGCTTTAAC	TGGTCTTACA	200
	ATGGCTGAAT	ACTTCAGAGA	TCAACAAGGG	CAAGACGTTT	TATTATTCTG	250
	AGATAATATA	TTCCGTTTCA	CTCAAGCAGG	ATCTGAGGTT	TCTGCACTTC	300
	TTGGACGTAC	TCCATCAGCA	GTTGGATAAC	AACCAACATT	AGCAACAGAG	350
45	ATGGGTAGAT	TACAAGAGAG	AATAACATCT	ACAAATAAAG	GGTC	394

2) INFORMATION FOR SEQ ID NO: 739

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium beijerincki* (deposited as
Clostridium butyricum)
 (B) STRAIN: ATCC 8260

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739

	TTAATAAACA	ACATAGCTAA	ACAACATGGT	GGTTTATCAG	TATTTACTGG	50
	AGTTGGTGAA	AGATCAAGAG	AAGGTAATGA	CTTATATCAT	GAAATGAGAG	100
	AGTCAGGAGT	TATTGATAAG	ACAGCATTAG	TATTTGGACA	AATGAATGAG	150
10	CCACCGGGTG	CCAGAATGAG	AGTTGCATTA	ACAGGTCTTA	CTATGGCAGA	200
	GTATTTTAGA	GATAAAGGTC	AAGATGTGTT	ACTATTCATA	GATAACATAT	250
	TCAGATATAC	TCAAGCAGGT	TCAGAGGTTT	CAGCATTACT	TGGAAGAACA	300
	CCTTCAGCGG	TTGGATATCA	GCCAACACTT	GCAACTGAAA	TGGGTGCACT	350
	TCAGGAAAGA	ATTACATCAA	CAGTTAATGG	TTCTATTACG	TCAG	394

15.

2) INFORMATION FOR SEQ ID NO: 740

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium difficile*
 (B) STRAIN: ATCC 9689

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740

	TTATAAACAA	TATTGCTAAG	CAACATGGTG	GTATTTCTGT	ATTTTCAGGA	50
35	GTAGGAGAAA	GAACAAGAGA	AGGTAACGAC	CTTTATGGCG	AAATGAGTGA	100
	GTCTGGAGTT	ATAAATAAAA	CAGCTCTAGT	ATTTGGTCAA	ATGAATGAAC	150
	CACCTGGAGC	GAGAATGAGA	GTTGCTTTAA	CTGGACTTAC	AATGGCAGAA	200
	CATTTTAGAG	ATGAGCAAGG	ACAAGACGTT	TTACTTTTCG	TTGATAATAT	250
	ATTCCGTTTC	ACACAAGCTG	G TTCAGAAGT	TTCAGCACTT	CTAGGACGTA	300
40	TGCCATCAGC	TGTTGGTTAT	CAGCCAACAT	TAGCTACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATAACATC	AACTAAGAAA	GGTTCAATAA	CAT	393

45 2) INFORMATION FOR SEQ ID NO: 741

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium ramosum*
 (B) STRAIN: ATCC 25582

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741

60

	TTGATTCAAG	AATTCATTAA	TAACATTGCT	ACAGAACATG	GTGGTTTATC	50
	AGTTTTTGCT	GGAGTTGGTG	AACGTAGCCG	TGAAGGTAAT	GATTTATATT	100
	ATGAAATGAA	GGAAAGTGGT	GTTTTATCTA	AAACAACACT	AGTATTTGGA	150
	CAGATGAATG	AACCCCCAGG	AGCTCGTTTA	AGAGTTGCTT	TAACGGGTCT	200
5	TACTATGGCA	GAAGAATTCC	GTGATGAACA	AGGTCAGGAT	GTCTTATTAT	250
	TCATCGATAA	TATTTTCCGT	TTTACTCAAG	CTGGATCTGA	AGTATCTGCC	300
	TTACTTGGAC	GGGTACCATC	ACAAGCTGGG	TATCAGCCAA	CTTTAGCAAC	350
	CGAAATGGGT	GCTTTACAAG	AACGGATTAC	ATCAACTAAA	AAAGGATC	398

10

2) INFORMATION FOR SEQ ID NO: 742

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 380 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium septicum*

(B) STRAIN: ATCC 12964

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742

	TAGCTAAGGA	ACACGGTGGA	CTTTCAGTAT	TCACAGGTGT	TGGAGAAAGA	50
	TCAAGAGAAG	GTAATGATTT	ATATTACGAA	ATGAAAGAAT	CAGGAGTTAT	100
30	AGACAAGACA	GCTCTAGTGT	TTGGACAAAT	GAATGAATCT	CCAGGAGCTA	150
	GAATGAGAGT	ATCTTTAACA	GGATTAAC TA	TGGCTGAATA	TTTCAGAGAT	200
	CAAGGTCAAG	ATGTGCTTTT	ATTCATAGAT	AACATATTTA	GATTTACTCA	250
	AGCTGGATCA	GAAGTATCGG	CTTTACTTGG	AAGAATACCA	TCAGCAGTTG	300
	GTTATCAACC	AACACTAGCA	ACTGAAATGG	GTGCACTTCA	AGAAAGAATT	350
35	ACTTCAACTA	AAAATGGATC	AATAACTTCA			380

40

2) INFORMATION FOR SEQ ID NO: 743

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50 (A) ORGANISM: *Clostridium tertium*

(B) STRAIN: ATCC 14573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743

55	TTAATAAATA	ATATAGCAAA	AGAGCATGGT	GGTCTTTCTG	TATTTACAGG	50
	AGTTGGAGAA	AGGTCAAGAG	AAGGTAACGA	CTTATATTAT	GAAATGAAAG	100
	AGTCAGGGGT	TATAGATAAG	ACAGCTTTAG	TATTTGGACA	AATGAATGAA	150
	TCACCAGGAG	CAAGAATGAG	AGTTTCATTA	ACTGGATTAA	CTATGGCTGA	200
	ATATTTTAGA	GATCAAGGTC	AAGACGTTCT	TTTATTTATA	GATAATATAT	250
60	TTAGATTTAC	TCAAGCGGGA	TCAGAAGTTT	CTGCGTTATT	AGGAAGAATT	300

CCTTCAGCAG TTGGATATCA ACCAACTCTT GCAACTGAAA TGGGAGCACT 350
TCAAGAAAGA ATAACATCAA CAAAGAATGG ATCAATCAC 389

5

2) INFORMATION FOR SEQ ID NO: 744

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Comamonas acidovorans*
(B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744

TTCCCCCGCA CGCATGCCCA AGGTGTTCGA TGCCCTGAAG CTCGACGGCT 50
CGGCCCTGAC GCTGGAAGTG CAGCAACTGC TGGGTGACGG CGTTGTGCGT 100
ACCATCGCCC TGGGTTCGTC CGACGGTCTG CGTCGCGGCC TGATGGTGTC 150
25 CAACACCGGC AACCCCATCA CCGTGCCCGT GGGCAAGGCG ACGCTGGGTC 200
GCATCATGGA CGTGCTGGGC AATCCCATCG ACGAACGTGG TCCCGTGGAT 250
CAGGCGCTGA CGGCTCCCAT CCACCGCAAG GCACCGGCTT ATGACGAGCT 300
GTCGCCTTCG CAGGAACTGC TGGAACCCGG CATCAAGGTG ATCGACCTGA 350
TCTCGCCCTT CGCCAAGGGC GGCAAGGTGG GTCTGTTCGG TGGCGCCGGT 400
30 GTGGGCAAGA CCGTGAACAT GATGGAATC ATCAACAACA TCGCCAAGGG 450
CCACGGTGGT CTGTCGGTGT TCGCCGGTGT GGGTGAACGT ACCCGCGAAG 500
GCAATGACTT CTATCACGAA ATGTCGGACG CCGGCGTGGT CAACCAGGAG 550
TCGCTGAACG ACTCCAAGGT GGCCATGGTC TACGGCCAGA TGAACGAACC 600
CCCGGGCAAC CGTCTGCGCG TGGCGCTGAC CGGCCTGACC ATGGCCGAAG 650
35 CCTTCCGTGA CGAAGGCAAG GACGTGCTGT TCTTCGTGGA CAACATCTAC 700
CGCTACACGC TGGCCGGTAC CGAAGTGTCC GCTCTGCTGG GTCGCATGCC 750
TTCCGCCGTG GGCTACCAGC CCACGCTGGC CGAGGAAATG GGCCGCCTGC 800
AAGAGCGCAT CACCTCGACC AAGGTCGGTT CGATCACTTC CAC 843

40

2) INFORMATION FOR SEQ ID NO: 745

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
55 (B) STRAIN: ATCC 13884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745

GCCGTACCAC GCGTGTACGA AGCCCTTGAG GTACAGAATG GTAATGAAGT 50
60 TCTGGTGCTG GAAGTTCAGC AGCAGCTGGG CGGCGGTATC GTACGTACCA 100

	TCGCCATGGG	TTCTTCTGAT	GGTCTGCGCC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTA	CTGGGTCAAC	CGGTTGACAT	GAAAGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CGTCCTATGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCC	AAGGGCGGTA	AAGTTGGTCT	GTTCCGGCGGT	GCGGGTGTAG	400
	GTA AAACTGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
	TATCCGCGCT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
15	CGGTTCTATC	ACCTCCGTA				819

2) INFORMATION FOR SEQ ID NO: 746

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Neisseria canis*
 (B) STRAIN: ATCC 14687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746

35	GCGATTCTAT	TCCGCGCGTA	TATGATGCTC	TTAAACTAGT	GGATAGAGAA	50
	CTGACGCTTG	AAGTACAACA	ACAGTTGGGT	GATGGTGTCG	TTCGTACTAT	100
	TGCGATGGGT	AGTTCCGACG	GCCTCAAACG	AGGTTTGGCG	GTAGTTAACA	150
	CCGGTGCTCC	AATTACAGTG	CCTGTGGGCA	AAGCAACATT	AGGCCGTATT	200
	ATGGACGTAT	TAGGTAATCC	GGTTGATGAA	GCTGGTCCGA	TTGGCTCCGA	250
40	GCAAACCCGA	GCAATCCACC	AACCTGCTCC	TAAGTTCGAC	GAGCTTTCTA	300
	GCGCCACAGA	GATTTTGGAA	ACAGGTATTA	AAGTAATTGA	TTTGCTTTGC	350
	CCGTTTGCCA	AAGGCGGTAA	AGTAGGTTTG	TTTGGTGGTG	CGGGAGTGGG	400
	CAAAACCGTA	AATATGATGG	AGTTGATTAA	CAACATCGCG	AAAGCACACA	450
	GCGGTTTGTC	TGTATTTGCC	GGTGTGGGTG	AACGGACGCG	TGAAGGTAAT	500
45	GACTTTTATC	ATGAGATGAA	AGATTCCAAT	GTATTAGATA	AAGTAGCCAT	550
	GGTTTACGGT	CAGATGAACG	AGCCTCCCGG	TAACCGTTTG	CGCGTTGCGC	600
	TA ACTGGCTT	GTCTATGGCC	GAATTCTTCC	GTGACGAGAA	AGATGAAAAC	650
	GGTAAAGGCC	GTGATGTATT	GTTCTTTGTA	GACAATATTT	ACCGCTATAC	700
	CCTAGCCGGT	ACAGAAGTAT	CTGCATTGCT	TGGCCGTATG	CCTTCGGCAG	750
50	TAGGTTATCA	GCCGACGTTG	GCAGAGGAAA	TGGGCCGCTT	GCAAGAGCGT	800
	ATTACYTCAM	CCCAAACAGG	CTCT			824

55 2) INFORMATION FOR SEQ ID NO: 747

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

425

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cinerea*

(B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747

10 CGCGACGCTA TCCCGCATGT TTACGATGCC CTGAAATTGG ACGAGAACGG 50
 TCTGACTCTG GAGGTTCAAC AGCTTCTGGG CGACGGCGTT GTCCGTACTA 100
 TTGCAATGGG TAGTTCAGAC GGCCTTAAAC GCGGTATGTC TGTAAGCAAT 150
 ACTGGTGCGC CAATCACTGT GCCGGTAGGT AAAGGTACAT TGGGTCGTAT 200
 15 TGTCGACGTA TTGGGTACGC CTGTTGATGA AGCAGGTCCG ATCGATACCG 250
 ACAAAGCCG TGCCATTAC CAACTGCTC CGAAATTCGA CGAGTTGTCT 300
 TCAGCTACCG AATTGTTGGA AACCGGTATT AAAGTGATCG ACTTGCTGTG 350
 TCCGTTTGCT AAAGGCGGTA AAGTAGGTCT GTTCGGTGGT GCCGGTGTGG 400
 GCAAACCGT GAACATGATG GAATTGATCA ACAACATCGC CAAAGCGCAC 450
 20 AGCGGTCTGT CCGTGTTTCGC AGGTGTGGGT GAGCGTACCC GTGAAGGTAA 500
 CGACTTCTAC CACGAGATGA AAGATTCCAA CGTATTGGAT AAAGTAGCCA 550
 TGGTGTATGG CCAAATGAAC GAACCTCCGG GCAACCGTCT GCGCGTTGCT 600
 TTGACCGGTT TGACTATGGC CGAATACTTC CGTGACGAAA AAGACGAAAA 650
 CGGTAAAGGC CGCGACGTAT TGTTCCTTCGT TGACAACATC TACCGTTACA 700
 25 CTTTGGCCGG TACTGAAGTA TCTGCACTGT TGGGCCGTAT GCCTTCTGCA 750
 GTGGGTACC AACCGACATT GGCTGAAGAA ATGGGTCGTT TGCAAGAGCG 800
 TATTACCTCT ACCCAAACCG GTTCCATTAC T 831

30

2) INFORMATION FOR SEQ ID NO: 748

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 862 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cuniculi*

(B) STRAIN: ATCC 14688

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748

CCGTGGCCAA GTACCACAAA TTTATGACGC ACTGAGTGTT GATGGCACCG 50
 AAACAACCTT GGAAGTTCAA CAGCAGTTGG GTGATGGCGT GGTGCGTACC 100
 ATTGCGATGG GTTCAACCGA AGGCTTGAAG CGTGGTTTGA CTGTATCTAA 150
 50 CTCTGGTGCA CCGATTTCTG TGCCAGTGGG TCAAGCGACT TTGGGTCGTA 200
 TTATGGATGT GTTGGGTCGT CCAATCGACG AGGCAGGTCC TGTAATGCT 250
 CAAGAAAAAT GGTCAATTCA CCGTGAAGCA CCAAGCTATG ATGAGCAATC 300
 AAACCTCACT GAGCTGCTAG AAACAGGCAT CAAAGTAATT GATTTGCTTT 350
 GCCCATTTGC TAAAGGTGGT AAAGTTGGCT TGTTCGGTGG TGCAGGTGTG 400
 55 GGTAACACCG TGAATATGAT GGAGCTGATT AATAATATCG CTCTGAAGCA 450
 TTCAGGTCTT TCTGTTTTTG CAGGTGTTGG TGAGCGTACT CGTGAGGGTA 500
 ACGATTTTAA TCACGAAATG CAAGAAGCAG GCGTTGTTAA TACCGAAGAC 550
 TTCACCAAGT CAAAAGTAGC GATGGTTTAT GGTCAGATGA ATGAGCCACC 600
 AGGAAACCGT TTGCGTGTG CATTGACAGG CTTGACGATG GCAGAATATT 650
 60 TCCGTGACGA AAAAGATGAA GCAACAGGCA AAGGGCGTGA TGTTCTATTG 700

TTCGTTGATA	ACATCTATCG	TTACACACTG	GCTGGTACGG	AAGTGTÇAGC	750'
ACTTCTAGGT	CGTATGCCAT	CAGCAGTAGG	TTATCAACCG	ACTCTGGCTG	800
AAGAAATGGG	TGCGTTGCAA	GAGCGTATTA	CCTCAACGCA	ATCGGGTTTCG	850
ATCACTTCGG	GG				862

5

2) INFORMATION FOR SEQ ID NO: 749

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 20 (B) STRAIN: ATCC 25295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749

GGA	ACT	CCCA	CGT	GAC	GCTA	TCC	CGC	ATGT	TTT	TGAT	GCA	TTAA	AATT	AG	50		
25	TTG	AAA	ATGA	CCT	AAC	TTA	GAAG	TTCA	AAC	AACT	TTT	GGG	GGAT	GGT	GTA	100	
	GTG	CGT	ACCA	TTG	CGAT	GGG	TAG	TTCA	GAT	GGAT	TAA	AGC	GTG	GTAT	GGC	150	
	TGT	GAATA	AAT	ACCG	GAG	CTC	CGAT	TACT	GT	TCCT	GTT	GGC	CGT	GAA	ACTT	200	
	TGG	GTC	GTAT	CAT	GGAT	GTA	TTG	GGT	AATC	CGGT	TGAT	GTA	GGC	AGG	TCCG	250	
	GTAA	ATGC	AT	CCA	ATA	CAC	G	TGCG	ATCC	AT	CAAG	AGG	CTC	CTA	AGTTT	GTA	300
30	TGAG	CTTT	CT	TCA	ACA	ACG	G	AATT	ATT	AGA	AACT	GGC	ATT	AAG	GTT	ATCG	350
	ACT	TGT	TATG	TCC	GTT	TGCC	AAAG	GTGG	TAA	AAG	TAGG	TCT	GTTT	GGT	GGT		400
	GCG	GGT	GTA	G	TAAA	ACCG	TAA	TAT	GATG	GAG	TAA	TTA	ACA	A	CATT	G	450
	CAAG	G	CACAT	AGC	G	TTT	GT	CTGT	GTT	TGC	AGG	CGT	GGG	T	GAAC	G	500
	GTGA	AGG	TAA	TG	ACT	TCT	AT	CAC	GAG	ATGA	AAG	ATT	CCAA	CGT	ATT	GGAC	550
35	AAAG	TGG	CAA	TGG	TTT	ACGG	TCAG	ATGA	AC	GAAC	CTCC	AG	GCA	ACC	GTCT		600
	GCG	CGT	TGCT	TTG	ACCG	GT	TG	ACT	ATGG	C	GAATA	ACTT	C	CGT	GAC	GAAA	650
	AAG	ACG	AAAA	CGG	TAA	AGGT	CGC	GAC	GTAT	TG	TTCT	TT	CGT	GG	ACA	ACATT	700
	TACC	GTT	TACA	CTT	TGG	CCGG	TAC	GGA	AGTA	TCC	G	CATT	G	TGG	G	TCGTAT	750
	GCCT	TCAG	CA	GTAG	GTT	TACC	AAC	CGAC	ATT	GGCT	GAA	GAA	ATGG	G	TCGT		800
40	TGCA	AGAG	CG	TATT	ACCT	CT	ACCC	AGAC	AG	GCT	CTAT	TAC	TTCC				844

2) INFORMATION FOR SEQ ID NO: 750

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria flavescens*
 55 (B) STRAIN: ATCC 13120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750

60	CGCGACGCTA	TTCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
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427

	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACCGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGCCGTAT	200
	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATAACG	250
5	ACAAGAGCCG	TGCCATTAC	CAAACCTGCTC	CGAAATTTCGA	TGAGTTGTCT	300
	TCAACTACCG	AATTGTTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
	AGCGGCCTGT	CCGTGTTTCGC	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
10	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	TCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGATGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGTCGTAT	GCCTTCTGCA	750
15	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAGGAGCG	800
	TATTACTTCT	ACGCAAACCG	GTTCCATTAC	TTCC		834

20 2) INFORMATION FOR SEQ ID NO: 751

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 bases
- (B) TYPE: Nucleic acid
- 25 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
- (B) STRAIN: ATCC 31426

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751

	CGCGACATGA	TTCCGCGCGT	TTACGACGCT	TTGAAATTAG	ACGAAAACGG	50
	TCTGACTTTG	GAAGTCCAAC	AGCTTTTGGG	TGATGGCGTA	GTCCGTACCA	100
	TCGCTATGGG	CAGCTCGGAC	GGTTTGAAAC	GCGGCATGAC	TGTGAGCAAT	150
	ACTGGTTCGC	CCATTACTGT	GCCGGTAGGT	AAAGGTACGT	TGGGACGCAT	200
40	TGTCGATGTA	TTGGGAACCTC	CTGTTGACGA	GGCAGGTCCA	ATTGATAACG	250
	ACAAGAGTCG	TGCCATCCAC	CAAGCCGCTC	CTAAGTTTGA	CGAACTGTCT	300
	TCCACAACCG	AATTGCTCGA	AACGGGCATT	AAAGTGATTG	ACTTGCTGTG	350
	TCCGTTTGCC	AAAGGCGGTA	AAGTAGGTCT	GTTCCGGCGGT	GCCGGTGTGG	400
	GTAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGCTTGT	CCGTGTTCTC	AGGCGTGGGT	GAGCGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	TGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGTGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCCAAACCG	GTTCCATTAC	TTCC		834

55

2) INFORMATION FOR SEQ ID NO: 752

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 825 bases
- 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*
(B) STRAIN: ATCC 27628

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752

	ACATGATTCC	GCGCGTTTAC	GACGCTTTGA	AATTAGACGA	AAACGGTCTG	50
	ACTTTGGAAG	TCCAACAGCT	TTTGGGTGAT	GGCGTAGTCC	GTACCATCGC	100
	TATGGGCAGC	TCGGACGGTT	TGAAACGCGG	CATGACTGTG	AGCAATACTG	150
15	GTTCGCCCCAT	TACTGTGCCG	GTAGGTAAAG	GTACGTTGGG	ACGCATTGTC	200
	GATGTATTGG	GAACGCCTGT	TGACGAGGCA	GGTCCAATTG	ATACCGACAA	250
	GAGTCGTGCC	ATCCACCAAG	CCGCTCCTAA	GTTTGACGAA	CTGTCTTCCA	300
	CAACCGAATT	GCTCGAAACG	GGCATTAAAG	TGATTGACTT	GCTGTGTCCG	350
	TTTGCCAAAG	GCGGTAAAGT	AGGTCTGTTC	GGCGGTGCCG	GTGTGGGTAA	400
20	AACCGTGAAC	ATGATGGAAT	TGATCAACAA	CATCGCCAAA	GCGCACAGCG	450
	GCTTGTCCGT	GTTCTCAGGC	GTAGGTGAGC	GTACCCGCGA	AGGTAACGAC	500
	TTCTACCACG	AGATGAAAGA	TTCCAACGTA	TTGGATAAAG	TAGCCATGGT	550
	GTATGGCCAA	ATGAACGAAC	CTCCAGGCAA	CCGTCTGCGC	GTTGCTTTGA	600
	CCGGTTTGAC	TATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	CGAAAACGGT	650
25	AAAGGTCGTG	ACGTATTGTT	CTTCGTTGAC	AACATCTACC	GTTACACTCT	700
	GGCCGGTACC	GAAGTATCCG	CACTGTTGGG	CCGTATGCCT	TCTGCAGTGG	750
	GTTACCAACC	GACATTGGCT	GAAGAAATGG	GTCGTTTGCA	AGAGCGTATT	800
	ACCTCTACCC	AAACCGGTTC	CATTA			825

30

2) INFORMATION FOR SEQ ID NO: 753

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria lactamica*
(B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753

	GATGCGATTG	CGCATGTTTA	CGATGCCCTG	AAATTGGACG	AGAACGGTCT	50
	GACCCTGGAA	GTCCAACAGC	TTTTGGGTGA	CGGCGTTGTC	CGTACTATTG	100
50	CAATGGGTAG	TTCAGACGGC	CTGAAACGCG	GCATGTCTGT	CAGCAATACC	150
	GGTGCGCCAA	TCACTGTGCC	GGTAGGTAAA	GGTACGTTGG	GCCGTATTGT	200
	CGACGTATTG	GGTACACCTG	TTGACGAAGC	AGGTCCGATC	GATACCGACA	250
	AGAGCCGCGC	CATCCACCAA	ACCGCCCCGA	AATTCGACGA	GTTGTCTTCA	300
	ACTACCGAAT	TGTTGGAAAC	CGGCATTAAA	GTGATCGATT	TGCTGTGTCC	350
55	GTTTGCTAAG	GCGGTAAAG	TAGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	400
	AAACCGTGAA	CATGATGGAA	TTGATCAACA	ACATCGCCAA	AGCGCACAGC	450
	GGTCTGTCCG	TGTTTGCAGG	CGTGGGCGAG	CGTACCCGCG	AAGGTAACGA	500
	CTTCTACCAC	GAGATGAAAG	ATTCCAACGT	ATTGGATAAA	GTAGCCATGG	550
	TGTATGGTCA	GATGAACGAA	CCTCCGGGCA	ACCGTCTGCG	CGTTGCTTTG	600
60	ACCGGTTTGA	CGATGGCCGA	ATACTTCCGC	GACGAAAAAG	ACGAAAACGG	650

CAAAGGCCGC	GACGTATTGT	TCTTCGTGGA	CAACATCTAC	CGTTACACCC	700
TGGCCGGTAC	CGAAGTATCC	GCACTGTTGG	GCCGTATGCC	TTCCGCAGTG	750
GGTTACCAAC	CGACATTGGC	TGAAGAAATG	GGTCGTTTGC	AAGAGCGTAT	800
TACCTCTACC	CAAACCGGTT	CCATTACTTC	C		831

5

2) INFORMATION FOR SEQ ID NO: 754

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: 2241C

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754

CCACGCGACA	TGATTCCGCG	CGTTTACGAC	GCTTTGAAAT	TAGACGAAAA	50
CGGTCTGACT	TTGGAAGTCC	AACAGCTTTT	GGGCGACGGC	GTAGTCCGTA	100
CCATTGCGAT	GGGCAGCTCG	GACGGTTTGA	AACGCGGCAT	GACTGTGAGC	150
AATACCGGTG	CGCCCATTA	TGTGCCGGTA	GGTAAAGGTA	CGTTGGGACG	200
CATTGTGAT	GTATTGGGAA	CGCCTGTTGA	CGAGGCAGGT	CCAATCGATA	250
CCGACAAGAG	CCGTGCCATC	CACCAAGCCG	CTCCTAAGTT	TGACGAACTG	300
TCTTCCACAA	CCGAATTGCT	CGAAACGGGC	ATTAAAGTGA	TTGACTTGCT	350
GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCCGG	GGTGCCGGTG	400
TGGGTAAAC	CGTGAACATG	ATGGAATTGA	TCAACAACAT	CGCCAAAGCG	450
CACAGCGGCT	TGTCCGTGTT	CGCAGGCGTG	GGTGAGCGTA	CCCGCGAAGG	500
TAACGACTTC	TACCACGAGA	TGAAAGATTC	CAACGTATTG	GATAAAGTGG	550
CAATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGCAACCG	TTTGCGCGTC	600
GCATTGACCG	GTTTGACCAT	GGCGGAATAC	TTCCGTGACG	AAAAAGACGA	650
AAACGGCAAA	GGCCGCGACG	TATTGTTCTT	CGTGGACAAC	ATCTACCGTT	700
ACACTCTAGC	TGGTACCGAA	GTATCCGCAT	TGTTGGGCCG	TATGCCGTCT	750
GCAGTGGGCT	ACCAACCGAC	ATTGGCAGAA	GAAATGGGTC	GTTTGCAGGA	800
GCGTATTACC	TCTACCCAAA	CCGGTTCTAT	TACTTC		836

45

2) INFORMATION FOR SEQ ID NO: 755

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria mucosa*
- (B) STRAIN: ATCC 19696

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755

CCGCGTGATG	CCATTCCGCG	TGTTTACGAC	GCCCTGAAAT	TGGATGCAAA	50
------------	------------	------------	------------	------------	----

	CGGCCTGACT	TTGGAAGTGC	AACAGCTTCT	GGGTGACGGC	GTAGTTCGTA	100
	CTATTGCAAT	GGGTAGTTCG	GATGGTTTGA	AACGCGGCAT	GACTGTAAGC	150
	AATACAGGTG	CGCCGATTAC	AGTACCGGTA	GGTAAAGGTA	CTTTGGGACG	200
	TATTGTGCGAT	GTATTGGGTA	CGCCTGTTGA	CGAAGCAGGT	CCGATTGATA	250
5	CCGACAAACA	CCGTGCCATC	CATCAGACAG	CTCCGAAATT	TGATGAACTG	300
	TCTGCGACTA	CTGAGCTGCT	GGAAACCGGC	ATTAAAGTGA	TTGACTTGCT	350
	GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCCGT	GGTGCCGGTG	400
	TAGGCAAAAC	CGTCAACATG	ATGGAATTAA	TTAACAACAT	CGCCAAAGCA	450
	CATAGCGGTT	TGTCCGTGTT	TGCAGGTGTG	GGTGAGCGTA	CCCGTGAAGG	500
10	TAATGACTTC	TACCACGAGA	TGAAAGATTC	CAACGTATTG	GACAAAGTGG	550
	CGATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGTAACCG	TCTGCGTGTA	600
	GCCTTGACCG	GTTTGACGAT	GGCCGAATAC	TTCCGTGATG	AAAAAGACGA	650
	AAGCGGCAAA	GGCCGTGACG	TATTGTTCTT	CGTGGACAAT	ATCTACCGTT	700
	ACACCCTGGC	CGGTACCGAA	GTATCCGCAT	TGTTGGGTCG	TATGCCTTCA	750
15	GCAGTAGGTT	ACCAACCGAC	ATTGGCTGAA	GAAATGGGTC	GTTTGCAAGA	800
	GCGTATTACC	TCTACCCAAA	CAGGCTCCAT	TACCTCC		837

20 2) INFORMATION FOR SEQ ID NO: 756

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756

35	CGCGACGCTA	TCCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACTGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGTCGTAT	200
40	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
	ACAAGAGCCG	TGCCATTAC	CAAACCTGCTC	CGAAATTCTGA	CGAGTTGTCT	300
	TCAACTACCG	AATTGCTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGTCTGT	CCGTGTTCGC	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCGG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCGG	TACCGAAGTA	TCTGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCCAAACTG	GTTCCATTAC	TTCC		834

55

2) INFORMATION FOR SEQ ID NO: 757

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria weaveri*
(B) STRAIN: ATCC 51223

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757

	CCCGTGATGC	TATTCCCATG	TATACGATGC	CCTGAAATTG	GTAGATAACG	50
	ATCTGACCCT	GGAAGTGCAA	CAACTTTTAG	GTGATGGTGT	GGTTCGTACC	100
	ATTGCAATGG	GTAGTTCAGA	CGGCCTAAAA	CGTGGTATGG	CTGTTAACAA	150
15	TACCGGCGCT	CCGATTACTG	TTCCGGTGGG	GAAAGCCACC	TTGGGACGTA	200
	TTATGGATGT	GTTGGGTAAT	CCGGTTGATG	AAGCAGGTCC	TGTTGTATCA	250
	GAAGAAACTC	GCGCTATTCA	TCAAGCTGCC	CCTAAATTTG	ACGAACTGTC	300
	TTCAGCAACT	GAGTTGTTGG	AAACAGGCAT	TAAAGTAATT	GACTTGCTGT	350
	GCCCGTTTGC	CAAAGGTGGT	AAAGTAGGTT	TGTTTGGTGG	TGCCGGCGTG	400
20	GGTAAAACCG	TAAATATGAT	GGAGTTGATC	AACAACATCG	CGAAGGCACA	450
	TAGTGGTTTG	TCTGTATTCG	CCGGTGTAGG	TGAGCGTACC	CGTGAAGGTA	500
	ACGACTTCTA	CCATGAAATG	AAAGACTCTA	ACGTATTGGA	TAAAGTAGCC	550
	ATGGTTTATG	GCCAGATGAA	TGAACCTCCG	GGTAACCGTT	TGCGCGTTGC	600
	TTTGACTGGT	TTGACTATGG	CCGAATATTT	CCGTGACGAG	AAAGATGAAA	650
25	ACGGCAAAGG	TCGTGACGTC	TTGTTCTTTG	TGGATAATAT	CTATCGCTAT	700
	ACTCTGGCCG	GTACTGAAGT	GTCTGCACTG	TTAGGTCGTA	TGCCGTCTGC	750
	AGTAGGTTAT	CAGCCTACAT	TGGCAGAAGA	AATGGGTCGC	TTGCAGGAGC	800
	GTATTACTTC	TACTCAAACA	GGTTCGATTA	CTT		833

30

2) INFORMATION FOR SEQ ID NO: 758

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria animalis*
(B) STRAIN: ATCC 19573

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758

	CGCGATGCCA	TTCCTCACGT	TTACGATGCC	CTGAAATTGG	ACGACACCGG	50
	TCTGACTTTG	GAAGTACAAC	AACTTCTGGG	CGACGGTGTG	GTACGTACCA	100
50	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GGGGTTTGTC	TGTGAGCAAT	150
	ACCGGTTCTC	CGATTGCCGT	TCCTGTCCGT	AAAGCGACTT	TGGGTCGTAT	200
	TATGGACGTA	TTGGGCAATC	CGGTTGATGA	AGCCGGTCCG	GTTGCTACCG	250
	AAGAGAAACG	TGCTATTAC	CAAGCCGCAC	CGAAGTTTGA	TGAATTGTCA	300
	TCAGCTACCG	AGTTGTTGGA	AACCGGTATT	AAAGTAATCG	ACTTGCTGTG	350
55	TCCGTTTGCA	AAAGGCGGTA	AAGTAGGTCT	GTTCCGGCGG	GCCGGTGTGG	400
	GCAAAACCGT	AAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCACAC	450
	AGCGGTCTGT	CTGTGTTTGC	CGGTGTAGGT	GAACGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTGTTGGAT	AAAGTAGCCA	550
	TGGTGTACGG	TCAGATGAAT	GAGCCGCCGG	GCAACCGCTT	GCGCGTGGCT	600
60	TTGACCGGCC	TGACTATGGC	CGAATACTTC	GTGACGAAAA	AGACGAAAAC	650

GGCAAAGGTC	GTGACGTATT	GTTCTTCGTG	GACAACATTT	ACCGCTACAC	700
ACTGGCCGGT	ACCGAAGTAT	CAGCATTGTT	GGGCCGTATG	CCGTCTGCAG	750
TAGGTTATCA	GCCGACATTG	GCAGAGGAAA	TGGGTCGCTT	GCAAGAGCGT	800
ATTACCTCTA	CCCAAACCGG	TTCGATTACC	TCT		833

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2) INFORMATION FOR SEQ ID NO: 759

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus penneri*
- (B) STRAIN: ATCC 33519

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759

AGCGTCCCTA	AAGTATACGA	CGCTCTTGAG	GTTATGAATG	GTAAAGAAAA	50
25 ACTGGTGCTG	GAAGTTCAGC	AACAGTTAGG	CGGTGGTATC	GTTTCGTTGTA	100
TCGCAATGGG	TACATCAGAC	GGTTTAAGCC	GTGGCTTAAA	AGTTGAAGAT	150
TTAGGCCACC	CAATTGAAGT	ACCAGTAGGT	AAAGCAACAC	TGGGACGTAT	200
CATGAACGTT	CTGGGTACAC	CTATTGATAT	GAAAGGTGAT	ATTGCAACTG	250
AAGAACGTTG	GTCTATTCAC	CGTGAAGCAC	CAACCTACGA	AGAGTTATCA	300
30 AACTCACAAG	AACTGCTTGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
TCCGTTTGCT	AAAGGTGGTA	AAGTAGGTCT	GTTTCGGTGGT	GCGGGTGTGG	400
GTAAAACAGT	TAACATGATG	GAATTGATCC	GTAATATCGC	GATCGAGCAC	450
TCAGGTTACT	CTGTATTTGC	TGGTGTGGT	GAGCGTACTC	GTGAGGGTAA	500
CGACTTCTAT	CATGAAATGA	CAGATTCTAA	CGTTCCTGAC	AAAGTATCGT	550
35 TAGTTTATGG	TCAGATGAAT	GAGCCACCAG	GAAACCGTCT	GCGTGTAGCA	600
CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGATGAAG	GCCGTGACGT	650
ACTGTTATTC	GTCGATAACA	TTTATCGTTA	CACCTTAGCC	GGTACAGAAG	700
TATCAGCACT	GTTAGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCAACA	750
TTGGCTGAAG	AGATGGGTGT	TCTGCAAGAA	CGTATCACTT	CAACCAAAAC	800
40 AGGTTCATC	ACCTCTGTA				819

2) INFORMATION FOR SEQ ID NO: 760

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Enteritidis
- (B) STRAIN: ATCC 13076

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CAGTGTTTGC	GGGCGTAGGG	GAACGTAATC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCGGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CGGTTCTATC	ACCTCCGTA				819

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2) INFORMATION FOR SEQ ID NO: 761

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Yersinia pestis*
- (B) STRAIN: KIM D27

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761

	ACCAAAAGTG	TACAACGCCC	TTGAGGTAGA	AGGTACAAC	GAAAAGTTAG	50
	TGCTGGAAGT	TCAGCAACAG	TTGGGCGGTG	GTGTTGTTCG	TTGTATCGCA	100
	ATGGGCTCTT	CCGATGGTCT	GAGCCGTGGG	TTGAAAGTAA	CCAACCTAGA	150
40	ACACCCGATC	GAAGTACCGG	TTGGTAAAGC	GACCCTTGGC	CGTATCATGA	200
	ACGTATTGGG	TGAACCAATC	GACATGAAAG	GTCCTATCGG	TGAAGAAGAG	250
	CGTTGGGCAA	TCCATCGCGA	AGCGCCTTCT	TATGAAGAGC	TTGCTAGCTC	300
	ACAAGATCTG	TTAGAAACCG	GTATCAAGGT	TATGGACCTG	ATTTGTCCGT	350
	TTGCTAAGGG	CGGTAAAGTC	GGTCTGTTCG	GTGGTGCGGG	TGTAGGTAAA	400
45	ACAGTAAACA	TGATGGAGCT	GATCCGTAAC	ATCGCGATCG	AGCACTCTGG	450
	GTATTCTGTA	TTTGCCGGTG	TAGGTGAGCG	TACCCGTGAG	GGTAATGACT	500
	TCTACCATGA	AATGACTGAC	TCCAACGTTT	TGGACAAAGT	ATCCTTGGTT	550
	TACGGCCAGA	TGAATGAGCC	ACCAGGTAAC	CGTCTACGCG	TTGCACTGAC	600
	CGGCCTGACC	ATGGCGGAGA	AATTCCGTGA	TGAAGGTCGT	GACGTACTGC	650
50	TGTTTATCGA	TAATATCTAT	CGTTATACCC	TAGCTGGTAC	GGAAGTATCC	700
	GCATTGCTGG	GTCGTATGCC	ATCAGCGGTA	GGTTATCAGC	CAACACTGGC	750
	TGAAGAGATG	GGTGTGTTGC	AGGAACGTAT	TACTTCCACT	AAGACGGGTT	800
	CAATCACCTC	TG				812

55

2) INFORMATION FOR SEQ ID NO: 762

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 408 bases

60

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
- (B) STRAIN: GB8

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762

	CGACGTGATC	GAGCCCTTCT	TCGTCGACGT	GATGCGCTCT	TGCAGCTTGC	50
	CCATTTCTTC	AGCCAGCGTC	GGCTGATAGC	CCACTGCCGA	CGGCATACGG	100
15	CCGAGCAGCG	CCGACACTTC	GGTACCGGCC	AGCGTGAAAC	GGTAGATGTT	150
	GTCGACGAAG	AACAGCACGT	CGAGGCCTTC	GTCACGGAAG	TGCTCGGCCA	200
	TCGTGAGGCC	CGTCAGCGCC	ACGCGCAGAC	GGTTGCCCCG	CGGCTCGTTC	250
	ATCTGGCCGT	ACACCAGCGC	GACCTTGTCG	AGAACGTTTC	AGTCCTTCAT	300
	TTCGTGGTAG	AAGTCGTTCC	CTTCACGGGT	ACGCTCGCCC	ACGCCCCGCG	350
20	ACACGGAGTA	ACCGCCGTGC	TCCTTCGCGA	TGTTGTTGAT	GAGCTCCATC	400
	ATGTTGAC					408

25 2) INFORMATION FOR SEQ ID NO: 763

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium sordellii*
- (B) STRAIN: ATCC 9714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763

40

	GAACTTATAA	ACAACATAGC	TACTCAACAT	GGTGGTATAT	CAGTATTTCG	50
	AGGTGTTGGA	GAGAGAACAA	GAGAAGGTAA	CGACCTTTAC	GGAGAAATGA	100
	GTGAGTCTGG	AGTTATAAAC	AAGACAGCTC	TAGTATTTCG	ACAAATGAAT	150
	GAGCCACCTG	GAGCAAGAAT	GAGAGTTGCT	TTAACTGGTC	TTACAATGGC	200
45	TGAATATTTT	AGAGATCAAG	AAGGACAAGA	CGTTTTATTA	TTCGTAGATA	250
	ATATATTCCG	TTTCACTCAA	GCAGGATCTG	AGGTTTCTGC	ACTTCTTGGA	300
	CGTACTCCAT	CAGCAGTTGG	ATACCAACCA	ACATTAGCTA	CAGAGATGGG	350
	TAGATTACAA	GAGAGAATAA	CATCTACAAA	TAAAGGGTCT	ATAACATCAG	400

50

2) INFORMATION FOR SEQ ID NO: 764

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 405 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

435

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium novyi*

(B) STRAIN: ATCC 19402

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764

	TTAATTCAAG	AATTAATCAA	CAATATAGCG	AAGGAACACG	GTGGATTATC	50
	TGTATTTACA	GGAGTTGGAG	AAAGAACAAG	AGAAGGTAAT	GACCTTTACT	100
10	ATGAAATGAA	AGAATCTGGT	GTTATAAATA	AAACAGCACT	AGTATTTGGT	150
	CAAATGAATG	AGCCACCTGG	AGCAAGAATG	AGAGTTGCTC	TTACAGGACT	200
	TACTATGGCA	GAATATTTCA	GGGATCAAGG	ACAAAACGTA	CTTTTATTCA	250
	TAGACAACAT	ATTTAGATTC	ACTCAAGCAG	G TTCAGAGGT	GTCAGCTTTA	300
	CTTGGAAGAA	TACCTAGTGC	CGTTGGATAC	CAACCAACAC	TAGCAACAGA	350
15	AATGGGTGCG	CTTCAAGAAA	GAATAACATC	TACAAAGCAT	GGTTCTATAA	400
	CATCA					405

20 2) INFORMATION FOR SEQ ID NO: 765

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 bases

(B) TYPE: Nucleic acid

25 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium botulinum*

(B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765

35

	AATTAATAAA	TAACATAGCT	AAAGAACATG	GTGGATTATC	AGTGTTTACT	50
	GGAGTTGGAG	AAAGATCTAG	AGAAGGTAAT	GATCTTTATC	ATGAAATGAG	100
	AGAATCAGGC	GTTATAGATA	AAACCGCATT	AGTATTTGGT	CAAATGAATG	150
	AGCCACCTGG	TGCTAGAATG	AGAGTTGCAT	TAACAGGGTT	AACTATGGCT	200
40	GAATATTTTA	GAGATAAAGG	TCAAGATGTA	TTACTATTTA	TAGATAATAT	250
	ATTTAGATTT	ACTCAAGCTG	GATCAGAAGT	TTCAGCATTA	CTTGGAAGAA	300
	TACCATCAGC	AGTTGGTTAC	CAACCAACTT	TAGCAACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATTACATC	AACTAAGAAT	GGTTCTATAA	CAT	393

45

2) INFORMATION FOR SEQ ID NO: 766

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 399 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium histolyticum*

(B) STRAIN: ATCC 19401

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766

	AGGAACTTAT	AAATAATATT	GCAAAACAAT	ATGGAGGTCT	ATCTGTATTT	50
	ACAGGTGTTG	GTGAAAGAAC	AAGAGAAGGT	AATGACCTAT	ATAATGAAAT	100
5	GAAAGATTCT	GGGGTTATAG	AGAAAAC TGC	ACTAGTATTT	GGACAGATGA	150
	ATGAACCACC	AGGAGCGAGA	ATGAGAGTAG	CATTGACAGG	ACTTACTATG	200
	GCAGAATATT	TTAGAGATCA	AGGGCAAGAT	G TACTTTTAT	TTATAGATAA	250
	TATATTTAGA	TTTACGCAGG	CTGGTTCTGA	AGTTTCTGCA	TTGTTAGGAA	300
	GAATTCCAAG	TGCAGTTGGA	TATCAACCAA	CCCTTGCAAC	TGAAATGGGT	350
10	GCATTACAAG	AAAGAATAAC	ATCCACAAAA	AATGGATCAA	TTACTTCAG	399

2) INFORMATION FOR SEQ ID NO: 767

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767

30	CATGATGGAA	CTGATCCGTA	ACATCGCCAT	CGAGCACAGC	GGTTATTCCG	50
	TGTTGCGCCG	TGTGGGTGAG	CGTACTCGTG	AGGGTAACGA	CTTCTACCAC	100
	GAGATGAAGG	ACTCCAACGT	TCTGGACAAA	GTGGCACTGG	TCTACGGTCA	150
	GATGAACGAG	CCGCCGGGTA	ACCGTCTGCG	CGTAGCACTG	ACTGGCCTGA	200
	CCATGGCCGA	GAAGTTCCGT	GACGAAGGTA	ACGACGTTCT	GTTGTTTCGTC	250
35	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	ACTGAAGTAT	CCGCACTGCT	300
	GGGCCGTATG	CCTTCGGCAG	TAGGTTACCA	GCCGACCCTG	GCTGAAGAGA	350
	TGGGCGTTCT	GCAAGAACGT	ATCACTTCGA	CCAAGGAAGG		390

40

2) INFORMATION FOR SEQ ID NO: 768

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Absidia corymbifera*
 (B) STRAIN: ATCC 46775

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768

	AGGTCTTGTT	CGTGGCAAAA	GGTCATTGAC	ACTGGTGCTC	CTATCACCAT	50
	TCCTGTTGGT	AACGAAGTCC	TTGGTCGTAT	CATTAACGTC	ATTGGTGAGC	100
	CCATTGATGA	GCGTGGTCCY	ATCAAGTCCA	AGGCCACTCG	TGCTATCCAC	150
60	GCTGATGCTC	CCGAGTTCGT	TGATCAATCC	CCCCTCCCG	AGATTCTCGA	200

	GACTGGTATC	AAGGTTGTCG	ATTTGCTTGC	TCCCTATGCT	CGTGGTGGTA	250
	AGATTGGTCT	TTTCGGTGGT	GCCGGTGTCTG	GCAAGACTGT	CTTGATTCAA	300
	GAATTGATCA	ACAACATTGC	CAAGGCTCAC	GGTGGTACT	CTATCTTCTG	350
	TGGTGTCGGT	GAACGTACTC	GTGAAGGCAA	CGATTTGTAC	CACGAAATGA	400
5	TTTCCACTGG	TGTCATCAAG	CTTGAAGGTG	AATCCAAGTG	TGCTCTTGTC	450
	TTTGGTCAAA	TGAACGAACC	CCCCGGAGCT	CGTGCCCGTG	TTGCCTTGAC	500
	TGGTTTGACC	ATTGCCGAAT	ACTTCCGTGA	TGAGGAAGGT	CAAGATGTGT	550
	TGCTCTTCAT	TGACAACATT	TTCCGTTTCA	CTCAAGCCGG	TTCTGAAGTG	600
	TCCGCTTTGC	TTGGTCGTAT	TCCCTCTGCT	GTCGGTTACC	AACCCACTCT	650
10	YTCCACTGAT	ATGGGTGGTA	TGCAAGAGCG	TATTACTACC	ACCAAGAACG	700
	GTTCCATTAC	CTCCGTGCAA	GCTGTCTACG	TCCCTGCTGA	CGATTTGACT	750
	GATCCTGCTC	CTGCTACTAC	TTTTGCTCAC	TTGGACGCCA	CCACTGTGTT	800
	GTCTCGTTCC	ATTGCTGAGT	TGGGTATCTA	CCCTGCTGTC	GATCCCCTTG	850
	ACTCCAAGTC	CCGTATCTTG	GATCCCCGTA	TCGTTGGTGA	TGAGCACTAC	900
15	TCTGTTGCCA	CTGGTGTCCA	ACAAATCCTT	CAAAACTACA	AGTCGCTTCA	950
	AGA					953

20 2) INFORMATION FOR SEQ ID NO: 769

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1343 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769

35	CGCGGTTCCA	AGGCCACCGA	CACCGGTGCC	CCCATCAAGA	TTCCCGTTGG	50
	TCACGGTACC	CTTGGTTCGT	TCATGAACGT	CACTGGTGAC	CCCATTGACG	100
	AGCGTGGTCC	CATCAAGGCC	ACCAAGTACG	CTCCCATCCA	CGCCGACCCC	150
	CCGGAGTTCA	CCGAGCAATC	CACCTCCGCT	GAGGTCCTCG	TTACCGGTAT	200
40	CAAGGTTGTC	GACCTGTTGG	CTCCTTACGC	TCGTGGTGGA	AAGATTGGTC	250
	TCTTCGGAGG	TGCTGGTGTC	GGAAAGACTG	TCTTCATTCA	GGAGCTGATT	300
	GTAAGGAGAC	ACACTGTCTA	CTGGCTGAGC	ATTAGCTAAC	GGCAGGCAGA	350
	ACAACATCGC	CAAGGCCAC	GGTGGTTTCT	CTGTCTTCAC	TGGTGTCGGT	400
	GAGCGTACCC	GTGAGGGTAA	CGATCTGTAC	CACGAGATGC	AGGAGACTTC	450
45	CGTCATTGAG	CTTGACGGTG	ACTCCAAGGT	CGCCCTCGTC	TTCGGTCAGA	500
	TGAACGAGCC	CCCGGGTGCC	CGTGCCCGTG	TCGCTCTTAC	TGGTCTTACT	550
	GTTGCTGAGT	AAGTCTTGAA	TTCACTGTGT	TGACAACGTC	GTGGCTAATG	600
	GGAAAAAAGA	TACTTCCGTG	ACGAAGAGGG	ACAGGATGTG	CTTCTCTTCA	650
	TCGACAGTAA	GTGCTTGATC	GAAGTGCCTG	TGAGACATAC	ACTGACTTCG	700
50	GCAATAGACA	TTTTCCGTTT	CACCCAGGCC	GGTTCCGAGG	TGTCCGCTCT	750
	TCTTGGTCGT	ATCCCCTCTG	CCGTCGGTTA	CCAGCCCACC	CTCGCCATTG	800
	ACATGGGTGT	CATGCAGGAG	CGTATTACCA	CCACCACCAA	GGGTTCCATC	850
	ACCTCCGTCC	AGGCCGTCTA	CGTGCCCGCT	GACGATTTGA	CTGACCCTGC	900
	CCCCGCCACC	ACCTTCGCC	ATTTGGACGC	CACCACTGTC	TTGTCCCGTG	950
55	GTATCTCCGA	GTTGGGTATC	TACCCCGCCG	TCGACCCTCT	TGACTCCAAG	1000
	TCCCGTATGT	TGGACCCCGG	TGTCATTGGT	CAGGACCACT	ACGACACCGC	1050
	CACCCGCGTT	CAGCAGATTC	TCCAGGAGTA	CAAGTCGCTC	CAGGATATCA	1100
	TTGCCATTCT	CGGTATGGAC	GAGTTGTCGG	AAGCTGACAA	GCTTACCGTC	1150
	GAGCGTGCCC	GTAAGATCCA	GCGTTTCTTG	AGCCAGCCTT	TCGCTGTGCG	1200
60	CCAGGTCTTC	ACTGGTATTG	AGGGCAAGCT	TGTCGACCTC	AAGGACACCA	1250

TCCGATCATT CAAGGCTATC TTGACTGGTG AGGGTGACGA CCTTCCCGAG 1300
GGTGAGTCTC GACTATCTCC GCATTCATAG CGTATAACTG ACA 1343

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2) INFORMATION FOR SEQ ID NO: 770

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
(B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770

TTCAGGAGTT GATTGTATGT TCACCTGCAA CATAAGACTT CCCATTCTCC 50
ACTCTTTTCT AACTCTTCAC AGAACAACAT TGCCAAGGCT CACGGTGGTT 100
ACTCTGTCTT CACTGGTGTC GGTGAGCGTA CCCGTGAGGG TAACGATCTG 150
25 TACCACGAAA TGCAGGAGAC TGGTGTCATT CAGCTCGAGG GTGAATCTAA 200
GGTCGCCCTT GTCTTCGGTC AGATGAACGA GCCCCCAGGT GCCCGTGCCC 250
GTGTCGCCCT TACCGGTCTG ACCATCGCCG AGTACTTCCG TGACGAGGAA 300
GGTCAGGATG TGCTGCTCTT CATTGACAAC ATTTTCCGTT TCACCCAGGC 350
CGGTTCTGAG GTGTCTGCCC TTCTTGGTCG TATCCCCTCC GCTGTCGGTT 400
30 ACCAGCCCAC TCTGGCCGTC GACATGGGTG GTATGCAGGA GCGTATTACC 450
ACCACCACCA AGGGTTCCAT TACCTCCGTC 480

35 2) INFORMATION FOR SEQ ID NO: 771

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mucor circinelloides*
(B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771

CTCGAACAAG AYAACCTTGCC YGCCATTTTG AACGCCCTTG AAGTCAAGGA 50
YCACTCTGGT GGACGTCTCG TYCTCGAAGT CTCTCAACAT TTGGGTGAGA 100
ACACTGTCCG TACTATTGCT ATGGATGGTA CTGAAGGTAA GTTATGTYCA 150
TCCCANNGGA TACAGTCARA CAGMAATGTC TAGTGGTTAT AGCAGYAGCA 200
55 GATGATTGAC CAATATGTTA GGTCTTGTC GGTGGTCAAA AGGTTGTTGA 250
CACTGGTGCT CCCATTACCA TCCCCGTTGG TAAGGAAGTC CTTGGTCGTA 300
TCATCAACGT TATTGGTGAA CCCATTGATG AACGTGGTCC CATTGACGCC 350
AAGACTCACC GTCCTATTCA CGCTGAAGCT CCCGAATTCG TTGATCAATC 400
CCCCACTCCC GAAATCCTCG AGACTGGTAT CAAGGTYGTC GATTTGTTGG 450
60 CTCCTTATGC TCGTGGTGGT AAGATTGGTC TCTTCGGTGG TGCTGGTGTC 500

GGTAAGACTG TCTTGATTCA AGAATTGATT AACAAACATYG CCAAGGCTCA 550
 CGGTGGTTAC TCTATCTTCT GTGGTGTCGG TGAACGTACT CGTGAGGGTA 600
 ACGATTTGTA CCATGAAATG ATTGAAACCG GTGTCATTCA ATTGGAAGGC 650
 GAGTCCAAGT GTGCTCTCGT CTTTGGTCAA ATGAACGAAC CCCCAGGTGC 700
 5 TCGTGCCCGT GTCGCTTTGA CTGGTTTGAC TATTGCTGAA TACTTCCGTG 750
 ATGATGAGGG TCAAGATGTC TTGCTTTTCA TTGATAACAT TTTTCAGATTC 800
 ACTCAAGCTG GTTCTGAGGT ATCTGCCCTT TTGGGTCGTA TTCCTTCCGC 850
 TGTCGGTTAC CAACCCACTC TTTCCACYGA TATGGGTGGT ATGCAAGAGC 900
 GTATTACTAC CACCAAGAAC GGTTCATTA CCTCCGTCCA AGCTGTCTAC 950
 10 GTCCCTGCTG ATGATTTGAC CGATCCTGCT CCTGCCACCA CTTTTGCTCA 1000
 CTTGGATGCC ACCACTGTCT TGTCTCGTTC CATCGCTGAA TTGGGTATCT 1050
 AYCCCGCTGT CGATCCTCTT GATTCCAAGT CTCGTATCCT CGATCCCCGT 1100
 ATTGTCGGTG ATGAGCACTA CAAGGTTGCC ACTGAAGTTC AACAAATCCT 1150
 CCAAAACTAC AAGTCTCTCC AAGA 1174
 15

2) INFORMATION FOR SEQ ID NO: 772

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
 30 (B) STRAIN: ATCC 24292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772

AGGAGCTTAT CAACAACATC GCCAAGGCTC ACGGTGGTTA CTCCGTCTTC 50
 35 ACTGGTGTCTG GTGAGCGTAC TCGTGAGGGT AACGATTTGT ACCACGAGAT 100
 GCAAGAGACT TCCGTCATTC AGCTTGACSG CGAGTCCAAG GTCGCTCTCG 150
 TGTTCCGGTCA GATGAACGAG CCCCCGGGTG CCCGTGCCCCG TGTTGCCCTG 200
 ACTGGTCTTA CCATCGCTGA GTACTTCCGT GATGCCGAGG GTCAGGATGG 250
 TAAGTTCTAT AACTCTTGTC GCAAAGGTTT CATTCTGGTC GCTAACTTGC 300
 40 TCAGTGCTCC TGTTCAATCGA CAACATTTTC CGTTTCACCC AGGCTGGTAT 350
 GGAGGTGTCT GCCCTCCTCG GTCGTATTCC TTCTGCCGTC GGTTACCAAC 400
 CTACTCTCGC CGTCGACATG GGTGGTATGC AAGAGCGTAT TACCACTACC 450
 AAGAAGGGAT CCATTAC 467

45

2) INFORMATION FOR SEQ ID NO: 773

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
 60 (B) STRAIN: ATCC 44331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773

	TTGCCAAGGC	CCACGGTGGT	TACTCTGTCT	TCACTGGTGT	CGGTGAGCGT	50
	ACCCGTGAGG	GTAACGATCT	GTACCACGAA	ATGCAGGAAA	CCTCCGTCAT	100
5	TCAGCTTGAT	GGCGAGTCCA	AGGTCGCGCT	TGTCTTCGGT	CAGATGAACG	150
	AGCCCCCTGG	TGCCCCGTGCT	CGTGTCGCTC	TTACTGGTCT	TACCGTTGCC	200
	GAGTACTTCC	GTGATGAGGA	GGGTCAGGAT	GGTAAGTTAT	ATCGTTTTTA	250
	TTATCTTCTT	TGCCACCACC	CCTCTACGAA	TCCATGCCTC	CGTTGGTGAA	300
	GGCATCGTTT	GTAGGGCGGG	TCGGAGTTTG	CGGCAATTTT	TGCCGTCGGC	350
10	TTGAAGCCGC	GGATGCCCGA	TGTTTGACGC	GTATCGATGC	TAACAACAAT	400
	GACAACAGTG	CTTCTCTTCA	TTGACAACAT	TTTCCGATTC	ACCCAGGCCG	450
	GTTCCGAGGT	GTCTGCCCTT	CTCGGTCGTA	TTCCCTCTGC	CGTCGGTTAC	500
	CAGCCCCTC	TTGCCGTAGA	CATGGGTGCC	ATGCAGGAAC	GTATTACCAC	550
	CACCAAGAAG	GGTTCGATTA	CCTCCGTC			578

2) INFORMATION FOR SEQ ID NO: 774

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rhizopus oryzae*
 (B) STRAIN: ATCC 56015

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774

	AACTTACCYG	CTATCTTGAA	CGCTCTCGAA	GTCCAAGATC	ACTCTGGTGG	50
35	ACGTCTTGTC	CTTGAAGTTC	GCTCAACACT	TGGGTGAAAA	TACTGTCCGT	100
	ACTATTGCTA	TGGATGGTAC	TGAAGGTAAG	CTATACTATA	ACCGTKTTAT	150
	CCGAGTATGA	TATTAAGTTG	AAAAAAGGTC	TCGTYCGTGG	TCAAAAGGTT	200
	ATTGACACTG	GTGCTCCCAT	TACCATTCTT	GYTGGTAAGG	AAGTTCTCGG	250
	TCGTATCATT	AACGTCATTG	GTGAACCCAT	CGATGAACGT	GGTCCTATCA	300
40	ACGCCAAGAG	CCAACGTCCC	ATTCACGCCG	AAGCTCCCGA	ATTCGTTGAC	350
	CAATCTCCTA	CTCCCGAAAT	TCTTGAAACT	GGTATCAAGG	TTGTCGACTT	400
	GTTGGCTCCT	TATGCTCGTG	GTGGTAAGAT	TGGTCTTTTC	GGTGGTGCTG	450
	GTGTCGGTAA	GACTGTGTTG	ATTCAAGAAT	TGATTAACAA	CATCGCCAAG	500
	GCTCACGGTG	GTTACTCTAT	TTTCTGTGGT	GTCGGTGAAC	GTACTCGTGA	550
45	AGGTAACGAT	CTTTACCACG	AAATGATTGA	AACTGGTGTG	ATCAAGCTCG	600
	ATGGTGACTC	CAAGTGTGCT	CTTGTCTTTG	GTCAAATGAA	CGAACCCCCA	650
	GGAGCTCGTG	CCCGTGTTGC	CTTGACTGGT	TTGACCATTG	CTGAATACTT	700
	CCGTGATGAT	GAAGGTCAAG	ATGTGTTGCT	TTTCATTGAT	AACATTTTCC	750
	GTTTCACCCA	AGCTGGTTCW	GAAGTATCTG	CCCTTTTGGG	TCGTATTCCC	800
50	TCCGCTGTCG	GTTACCAACC	CACTCTTTCT	ACTGATATGG	GTGGTATGCA	850
	AGAACGTATT	ACAACCACCA	AGAACGGTTC	CATTACATCC	GTCCAAGCTG	900
	TCTACGTCCC	TGCTGATGAT	TTGACCGATC	CTGCTCCCGC	CACCACTTTT	950
	GCTCACTTGG	ATGCCACCAC	TGTCTTGTCT	CGTTCCATTG	CCGAATTGGG	1000
	TATTTACCCT	GCCGTCGATC	CTCTTGAYTC	CAAGTCTCGT	ATCTTGATC	1050
55	CTCGTATCGT	TGGTGACGAA	CACTACAAGG	TCGCTACCGA	AGTTCAACAA	1100
	ATCCTTCAAA	ACTACAAGTC	TCT			1123

60 2) INFORMATION FOR SEQ ID NO: 775

441

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Scopulariopsis koningii*
 (B) STRAIN: ATCC 38745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775

15	ATTCAGGAGC TCATCAACAA CATTGCCAAG GCTCACGGTG GTTACTCTGT	50
	GTTCACTGGT GTCGGTGAGC GTACCCGTGA GGGTAACGAT CTGTACCACG	100
	AAATGCAGGA GACTTCGGTC ATTCAGCTCG AGGGCGAGTC CAAGGTCGCG	150
	CTTGTGTTTCG GTCAGATGAA CGAGCCCCC GGTGCCCGTG CCCGTGTTCG	200
20	CCTTACCGGT CTGACCGTTG CCGAGTACTT CCGTGACGAG GAGGGCCAGG	250
	ATGGTGAGTA ACCGACGAAG TCTGAGATCT TGTCGGGCAT TATTCTAACG	300
	ACAAC TAGTG CTTCTCTTCA TCGACAACAT TTTCCGCTTC ACCCAGGCCG	350
	GTTCCGAGGT GTCCGCGCTT CTCGGCCGTA TCCCCTCTGC CGTCGGTTAC	400
	CAGCCCACCC TGGCCGTCGA CATGGGAGGT ATGCAGGAGC GTATTACCAC	450
25	GACTCAGAAG GGCTCGATTA CCTCGGT	477

2) INFORMATION FOR SEQ ID NO: 776

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 610 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776

45	TCCGGAGTTG ATTGTAAGTC ATTTGAAACC CAGCCCCAAG AAACAGAAGC	50
	TAGGCGAAAA TTGGACAATT GAGCAATTTA GCCATTGGAG AAAAGAAATT	100
	TCGAGTATTA ATTGTTTTTA TAGAACAACA TTGCCAAGGC TCACGGTGGT	150
	TACTCTGTCT TCACTGGTGT CGGAGAGCGT ACCCGTGAAG GAAACGATCT	200
	CTACCATGAA ATGCAGGAGA CCCGTGTCAT TCAGCTTGAT GCGGAGTCCA	250
50	AGGTCGCCCT GGTCTTCGGC CAGATGAACG AGCCCCCAGG TGCCCCGTGCC	300
	CGTGTTGCTC TTA CTGGTTT GACCATTGCT GAGTACTTCC GTGATGAGGA	350
	AGGTCAAGAC GGTGAGTTTY TTATGGATAA AARATTTTTT TTTTTTTTTT	400
	TTTTTTMAAR AAATTCATGT TCTAACAAAG TATATCCTAG TGCTTCTCTT	450
	CATCGACAAC ATTTTCCGTT TCACTCAGGC TGGTTCCGAA GTGTCTGCCC	500
55	TGCTTGGTCG TATCCCATCT GCCGTCGGTT ACCAACCAC TCTTGCCGTC	550
	GACATGGGTG GTATGCAGGA ACGTATTACC ACCACCAAGA AGGGATCCAT	600
	TACCTCCGTC	610

60

2) INFORMATION FOR SEQ ID NO: 777

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 593 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAAGAAA CAGAAGCTAG 50
 GTGAAAATTG GACAATTGAA CAATTTAGCC CTTGGAGAAA AGAAATTTCG 100
 AGTATTAATT ATTTTATAG AACAACATTG CCAAGGCTCA CGGTGGTTAC 150
 20 TCTGTCTTCA CTGGTGTCGG AGAGCGTACC CGTGAAGGAA ACGATCTCTA 200
 CCATGAAATG CAGGAGACCC GTGTCATTCA GCTTGATGGC GAGTCCAAGG 250
 TCGCCCTGGT CTTCGGCCAG ATGAACGAGC CCCCAGGTGC CCGTGCCCGT 300
 GTTGCTCTTA CTGGTTTGAC CATTGCTGAG TACTTCCGTG ATGAGGAAGG 350
 TCAAGACGGT GAGTTTCTTA TGGATGAAAG ATTTTTTTTT TTCAAGAAAT 400
 25 TCATGTTCTA ACAAAGTGTA TTCTAGTGCT TCTCTTCATC GACAACATTT 450
 TCCGTTTCAC TCAGGCTGGT TCCGAAGTGT CTGCCCTGCT TGGTCGTATC 500
 CCATCTGCCG TCGGTTACCA ACCCACTCTT GCCGTCGACA TGGGTGGTAT 550
 GCAGGAACGT ATTACCACCA CCAAGAAGGG ATCCATTACC TCC 593

30

2) INFORMATION FOR SEQ ID NO: 778

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1141 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778

CCGTGGTCAA GAAGTTATTG ACACTGGTGC CCCAATTACC ATTCCTGTTG 50
 GTCGTGGTAC TCTTGGTAGA ATTATCAACG TCATTGGTGA ACCAATTGAC 100
 50 GAACGTGGCC CTATCAAGGC TTCTAAGTAT GCTCCTATCC ATACTGAACC 150
 ACCAACCTTT GCTGAACAAT CTACTTCTGC TGAAGTTCTT GAAACCGGTA 200
 TCAAGGTTGT CGATCTTCTT GCTCCTTACG CCCGTGGTGG TAAGATTGGT 250
 CTTTTCGGTG GTGCTGGTGT CGGTAAGACT GTCTTCATTC AAGAACTTAT 300
 TAACAACATT GCCAAGGCTC ACGGTGGTTT CTCTGTCTTC ACTGGTGTCG 350
 55 GTGAAAGAAC CCGTGAAGGT AACGATCTTT ACCGTGAAAT GAAGGAAACT 400
 GGTGTCATCA ACCTCGAAGG TGACTCCAAG GTCGCTCTCG TTTTCGGTCA 450
 AATGAACGAA CCTCCAGGTG CCCGTGCCCCG TGTCGCTTTG ACTGGTCTTA 500
 CCATTGCCGA ATACTTCCGT GATGAAGAAG GACAAGATGT CTTGCTTTTC 550
 GTTGACAACA TTTTCAGATT CACCCAAGCC GGTTCCTGAAG TCTCTGCTCT 600
 60 TTTGGGTCGT ATTCCATCTG CCGTCGGTTA CCAACCTACC CTTGCTACCG 650

	ATATGGGTGC	CCTCCAAGAA	CGTATTACCA	CCACCCAAAA	GGGTTCCGTC	700✓
	ACATCTGTCC	AAGCCGTCTA	TGTCCCAGCA	GACGATTGTA	CTGATCCTGC	750
	CCCAGCCACC	ACTTTCGCTC	ACTTGGACGC	CACCACTGTC	TTGTCTCGTT	800
	CCATTTCCGA	ATTGGGTATC	TACCCAGCTG	TCGATCCTCT	CGATTCCAAG	850
5	TCTCGTCTTT	TGGATCCTGA	AGTTATTGGA	CACGAACACT	ACGAAGTTGC	900
	CACTCAAGTT	CAACAAACCC	TCCAAGCTTA	CAAGTCTCTC	CAAGATATCA	950
	TTGCCATTTT	GGGTATGGAT	GAATTGTCTG	AAGCTGATAA	GCTTACTGTC	1000
	GAACGTGCCC	GTAAGATCCA	AAGATTCCTT	TCCCAACCAT	TCGCTGTTGC	1050
	CGAAGTTTTC	ACTGGTATCG	AAGGTCGTCT	CGTTCCATTG	AAGGAAACCG	1100
10	TCAGATCTTT	CAAGGAAATC	CTTGAAGGTA	AGTACGATCA	C	1141

2) INFORMATION FOR SEQ ID NO: 779

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Cladophialophora carrionii*
 (B) STRAIN: ATCC 22864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779

30	GCTGAAGGCC	GAACGTGAGC	GTGGTATCAC	CATCGATATC	GCGCTCTGGA	50
	AGTTCGAGAC	TCCAAGTAC	TTCGTCACCG	TCATCGATGC	CCCTGGTCAT	100
	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	CTGATTGTGC	150
	TATTCTCATC	ATTGCCGCTG	GTACTGGTGA	GTTTCGAGGCC	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CATGCTCTGC	TCGCCTACAC	CCTGGGCGTG	250
35	AAGCAGCTTA	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AATGGTCTGA	300
	GGATCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAAC TTC	ATCAAGAAGG	350
	TCGGATACAA	CCCCAAGTCC	GTTCCATTCT	TGCCCATCTC	CGGCTTCAAC	400
	GGTGACAACA	TGATCGACGT	CTCCACCAAT	GCCCCCTGGT	ACAAGGGCTG	450
	GGAAAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTTGAGG	500
40	CTATCGACTC	CATCGACCCT	CCTGCTCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCACTCC	AGGATGTCTA	CAAGATTTCT	GGTATCGGCA	CGGTGCCCGT	600
	CGGTCGTGTT	GAGACTGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTTG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAAAT	GCACCACGAA	700
	CAGCTCGCCG	AGGGCGTTCC	GGGTGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
45	CGTCTCCGTG	AAGGAGGTTC	GTCGTGGAAA	CGTTGCTGGT	GA CTCCAAGA	800
	ACGACCCCCC	CAAGGGTGCC	GACTCCTTCA	ACGCCAGGT	CATCGTCCTC	850
	AACCACCCTG	GTCAGGTCGG	TGCTGGCTAC	GCCCCGGTCT	TGGATTGCCA	900
	CACTGCCCAC	ATTGCCTGCA	AGTTCTCTGA	GCTCCTCGAG	AAGATCGATC	950
	GTCGTACCGG	CAAGTCCATG	GAAAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
50	GATGCTGCCA	TCGTGAAGAT	GGTTCCCAGC	AAGCCTATGT	GCGTTGAGGC	1050
	TTTACCCGAC	TACCCTCCTC	TTGGTCGTTT	CGCCGTCCGT	GAC	1093

55 2) INFORMATION FOR SEQ ID NO: 780

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cunninghamella bertholletiae*

(B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780

10 TACTTGTAAG TGGTCTCAAG ATCGTTACAA CGAAATTGTT AAGGAAGTTT 50
 CTCCTTCAT CAAGAAGATT GGTACAATC CTAAATCCGT TCCTTTCGT 100
 CCTATCTCTG GTTGGCACGG TGATAACATG TTGGAAGCTT CTACCAACAT 150
 GCCTTGGTAC AAGGGATGGA CCAAGGAAAC TAAAGCTGGT TCTTCCACTG 200
 15 GTAAGACTCT CTTAGAAGCC ATTGACAGCA TTGAACCTCC TACCCGTCCT 250
 TCTGACAAGC CTTTACGTCT TCCTTTACAA GATGTTTACA AGATTGGTGG 300
 TATTGGTACT GTCCCTGTTG GTCGTGTTGA AACTGGTGTC ATCAAGGCTG 350
 GTATGGTTGT TACYTTCGCT CCCGCTAACG TCACCACTGA AGTTAAGTCC 400
 GTTGAAATGC ATCACGAACA ATTAGAACAA GGTGTTCCCTG GTGACAACGT 450
 20 TGGTTTCAAC GTCAAGAACG TTTCCGTAA GGATATCCGT CGTGGTAACG 500
 TCTGTTCCGA CTCCAAGAAC GACCCCGCTA AGGAATCTGC TTCCTTCAAC 550
 GCTCAAGTTA TCGTCTTGAA CCACCCTGGT CAAATTGGTG CTGGTTATGC 600
 CCCAGTTCTT GACTGTCACA CTGCTCACAT TGCTTGTAAG TTCGCTGAAT 650
 TATTAGAAA GATCGATCGT CGTTCCGGTA AGAAACTCGA AGATGCTCCT 700
 25 AAATTCGTTA AATCTGGTGA CTCTGCTATC GTTAAGATGG TTCCTTCCAA 750
 GC 752

30 2) INFORMATION FOR SEQ ID NO: 781

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*

(B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781

45 CAAGTGGTCT GAGGACCGTT ACCAGGAAAT CATCAAGGAG ACCTCCAAC 50
 TCATCAAGAA GGTCGGCTAC AACCCCAAGC ACGTTCCCTT CGTCCCCATC 100
 TCCGGTTTCA ACGGAGACAA CATGATTGAG GCCTCCACCA ACTGCCCCCTG 150
 GTACAAGGGT TGGGAGAAGG AGACCAAGGC CAAGGCCACT GGTAAGACCC 200
 50 TCCTTGAGGC CATCGACGCC ATCGACCCTC CTGTCCGTCC TACCGACAAG 250
 CCCCTCCGCC TTCCCCTCCA GGATGTTTAC AAGATTGGTG GTATTGGCAC 300
 GGTCCCCGTC GGTCGTGTCG AGACCGGTAT CATCAAGCCC GGTATGGTCG 350
 TCACCTTCGC CCCCCTGGT GTCACCACCG AAGTCAAGTC CGTCGAGATG 400
 CACCACGAGC AGCTTACTGA GGTGTCCCC GGTGACAACG TCGGCTTCAA 450
 55 CGTCAAGAAC GTCTCCGTCA AGGAGATCCG TCGTGGAAC GTTGCCGGTG 500
 ACTCCAAGAA CGACCCCCC AAGGGTTGCG AGTCCTTCAA CGCCCAGGTC 550
 ATCGTCCTCA ACCACCCTGG TCAGGTCGGT GCCGGTTACG CCCCAGTCCT 600
 TGACTGCCAC ACTGCCACA TTGCCTGCAA GTTCTCCGAG CTCCTCGAGA 650
 AGATCGACCG CCGTACCGGA AAGTCTGTTG AGAACTCCCC CAAGTTCATC 700
 60 AAGTCCGGTG ACGCCGCCAT CGTCAAGA 728

2) INFORMATION FOR SEQ ID NO: 782

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Fonsecaea pedrosoi*
 (B) STRAIN: ATCC 18831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782

20	TGAAGTCCGA	CGGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTCGAGACTC	CCAAGTAAGG	CTCAACAGAC	ACAACAAGCA	AATGCATACT	100
	CGCTAACCTA	TTCACCCACC	ACAGGTACAA	CGTCACCGTC	ATTGACGCCC	150
	CCGGTCACCG	TGATTTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	200
	GACTGCGCCA	TTCTCATCAT	TGCCGCCGGT	ACTGGTGAGT	TCGAGGCCGG	250
25	TATCTCCAAG	GACGGTCAGA	CCCGTGAGCA	CGCTCTTCTC	GCCTACACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAG	350
	TGGTCTGAGG	CCCGTTACCA	GGAGATCATC	AAGGAGACCT	CCGGTTTCAT	400
	CAAGAAGGTC	GGCTTCAACC	CCAAGCACGT	TCCCTTCGTG	CCCATCTCCG	450
	GTTTCAACGG	TGACAACATG	ATCGACGTCT	CCACCAACTG	CCCCTGGTAC	500
30	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGCCATCG	ACCCCCCAC	TCGTCCCACC	GACAAGCCCC	600
	TCCGTCTTCC	CCTYCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGCACGGTT	650
	CCCGTCGGTC	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTCAC	700
	CTTCGCCCCC	GCTGGTGTCA	CCACTGAGGT	CAAGTCCGTC	GAGATGCACC	750
35	ACGAGCAGCT	TCCCGAGGGT	CTCCCCGGTG	ACAACGTCCG	CTTCAACGTC	800
	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGCAACGTCG	CCGGTGACTC	850
	CAAGAACGAC	CCCCCAAGG	GCTGCGACAG	CTTCAACGCC	CAGGTCATCG	900
	TCCTCAACCA	CCCCGGTCAG	GTCGGCGCCG	GCTACGCGCC	CGTCCTCGAC	950
	TGCCACACTG	CTCACATTGC	TTGCAAGTTC	TCTGAGCTCC	TCGAGAAGAT	1000
40	CGACCGCCGT	ACCGGCAAGT	CCATTGAGGC	CAGCCCCAAG	TTCATCAAGT	1050
	CTGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	TATGTGCGTT	1100
	GAGGCCTTCA	CCGACTACCC	CCCTCTTGGA	CGTTTCGCCG	TCCGT	1145

45

2) INFORMATION FOR SEQ ID NO: 783

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporum audouinii*
 (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783

446

	GCTCAAGGCT	GAGCGTGAGC	GTGGTATCAC	CATTGACATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	ATGGTCACCG	TCATCGGTAT	GCTTTATCTG	100
	TTTCCCATT	ATAGTTGCGA	CAAGTAACTA	ATAAAAAGTA	GATGCCCCCG	150
5	GACACCGTGA	CTTCATCAAG	AACATGATTA	CTGGTACCTC	CCAGGCCCGAC	200
	TGCGCTATT	TCATCATTGC	TGCCGGTACT	GGTGAGTTCC	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCT	TTCACCCTCG	300
	GTGTCAAGCA	GCTCATCGTT	GCCATCAACA	AGATGGACAC	CACCAACTGG	350
	TCTGAGTCCC	GTTTCGGTGA	AATCATCAAG	GAAGTCACCA	ACTTCATCAA	400
10	GAAGGTCGGC	TACGACCCCA	AGGGTGTCCC	ATTCGTCCCA	ATCTCTGGCT	450
	TCAACGGTGA	CAACATGATT	GAGCCCTCCA	CCAAGTCCCC	ATGGTACAAG	500
	GGATGGAACA	AGGAGACCAA	GGCCGGTGGC	AAATCCTCTG	GTAAGACCCT	550
	CCTTGAGGCC	ATCGATGCCA	TTGACATGCC	CACTCGTCCC	ACCGACAAGC	600
	CTCTCCGTCT	CCCACCTCCAG	GATGTCTACA	AGATCTCTGG	TATCGGAACA	650
15	GTACCAGTCG	GTCGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTTGT	700
	CACTTTTCGCC	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	750
	ACCACCAGCA	GCTCGTTTCAG	GGTGTTCCTG	GTGACAACGT	TGGCTTCAAC	800
	GTCAAGAACG	TCTCTGTCAA	GGAAGTCCGC	CGTGGTAACG	TTGCCGGTGA	850
	TTCCAAGAAC	GACCCACCAT	CTGGCTGCGC	CTCTTTCAAG	GCCCAGGTCA	900
20	TCGTCCTCAA	CCACCCCGGC	CAGATCGGTG	CTGGTTACGC	CCCAGTCCTC	950
	GACTGCCACA	CTGCCCACAT	TGCTTGCAAG	TTCTCTGAGC	TTCTTGAGAA	1000
	GATTGACCGC	CGTACTGGTA	AATCCGTCGA	AACCAGCCCT	AAGTTCGTCA	1050
	AGTCTGGTGA	TGCCGCTATT	GCCACCATGG	TTCCATCCAA	GCCCATGTGC	1100
	GTTGAGGCTT	TCACTGACTA	CCCACCACTT	GGTCGTTTCG	CCGTCCGTGA	1150
25	C					1151

2) INFORMATION FOR SEQ ID NO: 784

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mucor circinelloides*
 (B) STRAIN: ATCC 38592

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784

45	CCAAGTGGTC	TCAAGATCGT	TACAACGAAA	TTGTCAAGGA	AGTTTCCGGT	50
	TTTCATCAAGA	AGATCGGTTT	CAACCCCAAG	TCCGTTCCCTT	TCGTTCCCAT	100
	TTCTGGCTGG	CACGGTGATA	ACATGTTGGA	TGAATCCACC	AACATGCCCT	150
	GGTTCAAGGG	ATGGAACAAG	GAGACCAAGG	CCGGTTCCAA	GACTGGTAAG	200
	ACTCTCCTCG	AAGCCATCGA	TGCCATTGAG	CCCCCTGTCC	GTCCTTCTGA	250
50	CAAGCCTCTC	CGTCTTCCTC	TTCAAGATGT	CTACAAGATT	GGTGGTATTG	300
	GTACAGTTCC	CGTCGGTCGT	GTTGAAACTG	GTACTATCAA	GGCTGGTATG	350
	GTTGTCAACT	TCGCTCCCGC	TGCTGTCACC	ACTGAAGTTA	AGTCCGTTGA	400
	AATGCATCAC	GAAACCCTCT	CTGAAGGTCT	CCCCGGTGAC	AACGTTGGTT	450
	TCAACGTCAA	GAACGTCTCC	GTCAAGGATA	TCCGTCGTGG	TAACGTCTGT	500
55	TCCGACTCCA	AGAACGATCC	CGCTAAGGAA	TCTGCCTCTT	TCACTGCTCA	550
	AGTTATTATC	TTGAACCATC	CCGGTCAAAT	CTCTGCTGGT	TACGCACCAG	600
	TTCTCGATTG	TCACACTGCT	CACATCGCCT	GTAAGTTCTC	TGAACTCATT	650
	GAGAAGATTG	ATCGTCGTTT	CGGTAAGTAC	CTGCATCTGT	CAGAATTGAA	700
	GGTCCGCCGT	TATAGCAAAG	GCTGGGTTTA	AATGTTGGGG	TTTGTCTGAT	750
60	CTATAATGAT	GATTGCTCCT	TCAATTTTTG	ACATAATTTG	ATGATCTGAA	800

TTGTGTTGCT	AACGTCGCAT	TTGCTTCTTT	TGCTTCTTTT	GCATGTAAGT	850
AAGAAGATGG	AAGATGCTCC	CAAAGTAAGT	ATTACGATTG	ATGGACAATT	900
AAAATAGAAT	ACTAACAATT	ATTGTTTATA	GTTTCGTCAAG	TCTGGTGACT	950
CTGCTATCGT	CAAGATGGTT	CCCTCCAAG			979

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2) INFORMATION FOR SEQ ID NO: 785

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phialaphora verrucosa*
 (B) STRAIN: ATCC 38561

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785

GGACAAGCTG	AAGGCCGAAC	GTGAGCGTGG	TATCACCATC	GATATCGCGC	50
25 TCTGGAAGTT	CGAGACTCCC	AAATACTTCG	TCACCGTCAT	TGATGCCCCT	100
GGTCATCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	150
TTGTGCCATC	CTCATCATTG	CCGCCGGTAC	CGGTGAGTTC	GAAGCCGGTA	200
TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTCCTCGC	CTACACCCTA	250
GGTGTGAAGC	AGCTTATCGT	CGCCATCAAC	AAGATGGACA	CCGCCAAATG	300
30 GTCCGAGGAT	CGGTTCAACG	AAATCATCAA	GGAGACTTCC	AACTTCATCA	350
AGAAGGTCGG	ATACAACCCC	AAGTCCGTCC	CGTTCGTGCC	CATCTCCGGT	400
TTCAACGGTG	ACAACATGAT	CGACGTCTCC	TCCAACGCCC	CCTGGTACAA	450
GGGTTGGGAG	AAGGAGACCA	AGGCCGGCAA	GGCCACTGGC	AAGACCCTCC	500
TCGAGGCCAT	CGACGCGATT	GACCCTCCTA	CTCGTCCCAC	CGACAAGCCC	550
35 CTCCGTCTCC	CTCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGCACGGT	600
GCCCGTTGGT	CGTGTTGAGA	CCGGTACCAT	CAAAGCCGGT	ATGGTCGTCA	650
CCTTCGCTCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	700
CACGAACAGC	TCGCCGAAGG	TGTTCAGGT	GACAATGTCG	GCTTCAACGT	750
CAAGAACGTC	TCCGTCAAGG	AGGTTCTGTCG	TGGAAACGTT	GCCGGTGACT	800
40 CCAAGAATGA	CCCCCACAAG	GGTGCCGACT	CCTTCAACGC	TCAGGTCATC	850
GTCCTCAACC	ACCCTGGTCA	GGTCGGTGCC	GGCTACGCCC	CGGTCTTGGA	900
TTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTC	CTCGAGAAGA	950
TCGATCGTCG	TACCGGCAAG	TCCATGGAAA	ACAACCCCAA	GTTTATCAAG	1000
TCTGGTGATG	CTGCCATCGT	GAAGATGGTT	CCCAGCAAGC	CTATGTGCGT	1050
45 TGAGGCCTTC	ACCGACTATC	CTCCTCTTGG	TCGTTTCGCC	GTCCGTGAC	1099

2) INFORMATION FOR SEQ ID NO: 786

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saksenaea vasiformis*

60

(B) STRAIN: ATCC 60625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786

5	ACCACCAAGT	GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	50
	CGGYTTCATC	AAGAAGGTCG	GCTTCAACCC	CAAGCACGTT	CCCTTCGTGC	100
	CCATCTCCGG	TTTCAACGGT	GACAACATGA	TCGACGTCTC	CACCAACTGC	150
	CCCTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGGCCAAGG	CCACCGGCAA	200
	GACCMTCCTC	GAGGCCATTG	ACGCCATCGA	CCCCCCYAGY	CGTCCCACCG	250
10	ACAAGCCCCT	YCGTCTTCCC	CTMCAGGATG	TYTACAAGAT	TGGCGGTATT	300
	GGCACGGTTC	CCGTCGGTCG	TGTYGAGACC	GGTRCCATCA	AGGGTGGCAT	350
	GGTCGTCACC	TTCCCCCCCCG	CTGGTGTCAC	CACTGAGGTC	AAGTCCGTCG	400
	AGATGCACCA	CGAGCAGCTC	GCCGAGGGTS	TCCCCGGTGA	CAACGTCGGC	450
	TTCAACGTCA	AGAACGTCTC	CGTCAAGGAG	ATCCGTCGTG	GCAACGTTGC	500
15	CGGTGACTCC	AAGAACGACC	CCCCCAAGGG	CTGCGACAGC	TTCAACGCCC	550
	AGGTCATCGT	CCTCAACCAC	CCCGGTCAGG	TCGGCGCCGG	CTACGCGCCS	600
	GTCCTSGACT	GCCACACTGC	TCACATTGCC	TGCAAGTTCT	CTGAGCTCCT	650
	CGAGAAGATC	GACCGCCGTT	CCGGCAAGTC	CATCGAGTCC	GGCCCCAAGT	700
	TCATCAAGTC	TGGTGACGCC	GCCATCGTCA	AGATGGTTCC	CTCCAAGCCC	750
20						

2) INFORMATION FOR SEQ ID NO: 787

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1084 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Syncephalastrum racemosum*
 (B) STRAIN: ATCC 32330

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787

	GCTCAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCTCTCTGGA	50
40	AGTTCGAGAC	CCCCAAGTAC	CACGTCACCG	TCATTGATGC	CCCCGGCCAT	100
	CGTGATTTCA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CTGACTGCGG	150
	TATCCTCATC	ATTGCCGCCG	GTACTGGTGA	GTTTCGAGGCT	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CACGCTCTGC	TTGCCTTCAC	CCTCGGTGTC	250
	CGTCAGCTGA	TCGTCGCCAT	CAACAAGATG	GACTCGACCA	AGTACTCTGA	300
45	GGCCCGTTAC	AACGAAATCG	TCAAGGAGGT	CTCCACCTTC	ATCAAGAAGA	350
	TCGGTTTCAA	CCCCAAGTCC	GTTCCCTTCG	TCCCCATCTC	TGGCTGGAAC	400
	GGTGACAACA	TGTTGGAGGA	GTCCTCCAAC	ATGCCCTGGT	TCAAGGGCTG	450
	GAAGAAGGAG	ACCAAGGCTG	GCGAGAAGTC	CGGCAAGACC	CTCCTTGAGG	500
	CCATTGACAA	CATTGACCCC	CCGGTCCGTC	CCTCGGACAA	GCCCCTCCGT	550
50	CTTCCCCCTC	AGGATGTCTA	CAAGATCGGT	GGTATCGGCA	CAGTCCCCCGT	600
	CGGTGCTGTC	GAGACTGGTG	TCATCAAGGC	TGGTATGGTC	GTGACCTTCG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAGAT	GCACCACGAG	700
	CAGCTCGTCG	AGGGTGTCCC	CGGTGACAAC	GTCGGTTTCA	ACGTCAAGAA	750
	CGTTTCCGTC	AAGGATATCC	GCCGTGGTAA	CGTCTGCTCT	GACTCCAAGA	800
55	ACGACCCCGC	CAAGGAGTCT	GCCTCGTTCA	CCGCCAGGT	CATCGTCCTG	850
	AACCACCCCG	GTCAGATCGG	TGCCGGTTAC	GCCCCGGTTC	TTGACTGCCA	900
	CACCGCTCAC	ATTGCCTGCA	AGTTCGCTGA	GCTCCTCGAG	AAGATCGACC	950
	GTCGTTCCGG	YAAGAAGCTC	GAAGAGTCCC	CCAAGTTCGT	CAAGTCGGGT	1000
	GACTCCGCCA	TCGTCAAGAT	GGTTCCTTCC	AAGCCCATGT	GCGTTGAGGC	1050
60	CTACACTGAG	TACCCCCCTC	TTGGCCGTTT	CGCC		1084

2) INFORMATION FOR SEQ ID NO: 788

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1155 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788

20	GCTCAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	AATGTCACCG	TCATTGGTAT	GTTTTTCTTT	100
	ACCTTTCCCC	TCCATCGTCT	TGCTGTGCCA	TAACTAACGA	GAGTAGACGC	150
	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	200
	CTGACTGTGC	TATTCTCATC	ATTGCTGCCG	GTACTGGTGA	GTTCGAGGCT	250
25	GGTATCTCCA	AGGATGGCCA	GACCCGTGAG	CACGCTCTGC	TCGCCTTCAC	300
	CCTTGGTGTC	AAGCAGCTCA	TCGTTGCCAT	CAACAAGATG	GACACCACCA	350
	ACTGGTCCGA	GGACCGTTTC	AAGGAAATCA	TCAAGGAAGT	CACCAACTTC	400
	ATCAAGAAGG	TTGGCTACGA	CCCCAAGGGT	GTTCCATTCG	TTCCAATCTC	450
	TGGTTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCAGCAAC	TGCCCATGGT	500
30	ACAAGGGATG	GAACAAGGAG	ACCAAGGCCG	GTGGTGCCAA	GACTGGCAAG	550
	ACCCTYCTCG	AGGCCATCGA	TGCCATCGAC	ATGCCAACC	GTCCTACCGA	600
	CAAGCCCCTY	CGTCTCCCAC	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	650
	GAACTGTACC	AGTCGGTCGT	GTTGAGACCG	GTATCATCAA	GCCTGGTATG	700
	GTCGTCACCT	TCGCCCCTGC	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	750
35	AATGCACCAC	CAGCAGCTTC	AGCAGGGTGT	CCCCGGTGAC	AACGTCGGCT	800
	TCAACGTCAA	GAACGTTTCC	GTCAAGGAAG	TCCGCCGTGG	TAACGTTGCC	850
	GGTGACTCCA	AGAACGACCC	ACCATCCGGC	TGTGCCTCCT	TCAACGCCCA	900
	GGTCATCGTC	CTCAACCACC	CCGGCCAGAT	CGGTGCTGGT	TACGCCCCAG	950
	TCCTCGACTG	CCACACTGCT	CACATTGCTT	GCAAGTTCGC	TGAGCTCCTC	1000
40	GAGAAGATTG	ACCGCCGTAC	CGGTAAATCC	GTCGAAGCCA	ACCCAAGTT	1050
	CGTCAAGTCT	GGTGATGCCG	CTATCGCCAA	GATGGTTCCC	TCCAAGCCCA	1100
	TGTGCGTTGA	GGCTTTCACT	GACTACCCCC	CACTTGGTCG	TTTCGCCGTC	1150
	CGTGA					1155

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2) INFORMATION FOR SEQ ID NO: 789

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1138 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 55 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789

	TCAAGGCCGA	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTCGAGACCC	CCAAGTACAA	TGTCACCGTC	ATTGGTATGT	TTCTCTTTAC	100
5	CTTTCCCCTC	CATCGTCTTG	CTGTGCCATA	ACTAACGAGA	GTAGACGCCC	150
	CCGGTCACCG	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	200
	GACTGTGCTA	TTCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	250
	TATCTCCAAG	GATGGCCAGA	CCCGTGAGCA	CGCTCTGCTC	GCCTTCACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAC	350
10	TGGTCCGAGG	ACCGTTTCAA	GGAAATCATC	AAGGAAGTCA	CCAACTTCAT	400
	CAAGAAGGTT	GGCTACGACC	CCAAGGGTGT	TCCATTTCGTT	CCAATCTCTG	450
	GTTTCAACGG	TGACAACATG	ATTGAGGCCT	CCACCAACTG	CCCATGGTAC	500
	AAGGGATGGA	ACAAGGAGAC	CAAGGCCGGT	GGTGCCAAGA	CTGGCAAGAC	550
	CCTCCTCGAG	GCCATCGATG	CCATCGACAT	GCCAACCCGT	CCTACCGACA	600
15	AGCCCCCTCCG	TCTCCCCTC	CAGGATGTCT	ACAAGATCTC	TGGTATCGGA	650
	ACTGTACCAG	TCGGTCGTGT	TGAGACCGGT	ATCATCAAGC	CCGGTATGGT	700
	CGTCACCTTC	GCCCCTGCCA	ACGTCACCAC	TGAAGTCAAG	TCCGTCGAAA	750
	TGCACCACCA	GCAGCTTCAG	CAGGGTGTCC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCAAGA	ACGTTTCCGT	CAAGGAAGTC	CGCCGTGGTA	ACGTTGCCGG	850
20	TGACTCCAAG	AACGACCCAC	CATCCGGCTG	TGCCTCCTTC	AACGCCCAGG	900
	TCATCGTCCT	CAACCACCCC	GGCCAGATCG	GTGCTGGTTA	CGCCCCAGTC	950
	CTCGACTGCC	ACACTGCTCA	CATTGCTTGC	AAGTTCGCTG	AGCTCCTCGA	1000
	GAAGATTGAC	CGCCGTACCG	GTAAATCCGT	CGAAGCCAAC	CCCAAGTTCG	1050
	TCAAGTCTGG	TGATGCCGCT	ATCGCCAAGA	TGGTTCCATC	CAAGCCTATG	1100
25	TGCGTTGAGG	CTTTCACCTGA	CTACCCCCCA	CTTGGTTCG		1138

2) INFORMATION FOR SEQ ID NO: 790

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790

45	CACCACCAAG	TGGTCTGAGG	AGCGTTACCA	GGAAATCATC	AAGGAGACCT	50
	CCAACTTCAT	CAAGAAGGTC	GGCTACAACC	CCAAGCACGT	TCCCTTCGTC	100
	CCCATCTCTG	GTTTCAACGG	AGACAACATG	ATTGAGGCTT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACTGGTA	200
	AGACCCTTCT	CGAGGCCATC	GACGCCATCG	ACCCCCCTGT	CCGTCCTACC	250
50	GACAAGCCCC	TCCGCCTTCC	CCTCCAGGAT	GTGTACAAGA	TTGGTGGTAT	300
	TGGCACGGTT	CCCGTCGGTC	GTGTCGAGAC	CGGTATCATC	AAGCCCGGTA	350
	TGGTCGTCAC	CTTCGCCCCC	GCTGGTGTCA	CCACTGAAGT	CAAGTCCGTC	400
	GAGATGCACC	ACGAGCAGCT	TGCCGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
	CTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGTAACGTTG	500
55	CCGGTGACTC	CAAGAACGAC	CCCCCAAGG	GTTGCGAGTC	CTTCAACGCC	550
	CAGGTCATCG	TCCTCAACCA	CCCGGTCAG	GTCGGTGCCG	GTTACGCACC	600
	AGTCCTTGAC	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGCTCC	650
	TCGAGAAGAT	TGACCGCCGT	ACCGGAAAGT	CTGTTGAGAA	CTCCCCCAAG	700
	TTCATCAAGT	CCGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAG	748

60

2) INFORMATION FOR SEQ ID NO: 791

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 958 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Aspergillus fumigatus*
 15 (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791

	CGCTATTGTC	GTTGTTGCTG	CCTCCGACGG	TCAGATGTAG	GTGGAACATC	50
20	TTGGGAAATA	CGTCGTAAAA	CACGGCGCTT	ACGTTTTTCGC	GAATAGGCCC	100
	CAGACTCGTG	AGCATTGCT	GCTCGCCCGC	CAGGTTGGTG	TCCAGAAGAT	150
	CGTTGTCTTC	GTCAACAAAA	TCGATGCTAT	TGATGATCCG	GAGATGCTGG	200
	AACTGGTCGA	ACTCGAGATG	CGTGAGCTGC	TGAACAGCTA	CGGTTTCGAG	250
	GGTGAAGAGA	CTCCGATCAT	TTTCGGTTCC	GCTCTCTGTG	CTCTCGAAGG	300
25	ACGCCGTGAC	GACATCGGTA	AAGACAGAAT	TGAGCAGCTT	ATGAACGCTG	350
	TCGACACCTG	GATCCCCACT	CCTCAGCGTG	ACCTCGACAA	ACCTTTCTTG	400
	ATGTCTGTCTG	AGGAAGTGTT	CTCTATCGCC	GGCCGTGGTA	CCGTGGCTTC	450
	TGGTCGTGTC	GAGCGTGGTA	TCTTGAAGAA	GGACTCTGAG	GTTGAGATTG	500
	TTGGAGGCTC	CTTCGAACCC	AAGAAGACCA	AAGTCACCGA	CATTGAAACC	550
30	TTCAAGAAGA	GCTGTGATGA	ATCGCGTGCT	GGTGACAAC	CTGGTCTCCT	600
	CCTGCGTGGT	ATCCGACGTG	AAGACGTCAA	GCGTGGTATG	GTCATTGCTG	650
	TTCCCGGCAG	CACCAAAGCT	CACGACAAGT	TCCTCGTCTC	CATGTACGTC	700
	CTGACCGAGG	CGGAGGGTGG	TCGTCGTACT	GGCTTCGGTG	CCAACCTACG	750
	TCCCAAGTC	TTCATCCGTA	CTGCAGGTAA	GTTCCCGCAC	ACCGTGTCCA	800
35	GATCTTCCGA	GAGATTAGCG	ATATATGCTA	ATGATTCATC	AGACGAGGCT	850
	GCTGACCTCA	GCTTCCCTGA	CGGCGACCAA	TCTCGCAGAG	TTATGCCTGG	900
	TGACAACGTC	GAGATGATCC	TGAAGACCCA	CCACCCTGTT	GCTGCTGAGG	950
	CTGGTCAA					958

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2) INFORMATION FOR SEQ ID NO: 792

- (i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792

	CGTTGTGCA	GCTTCTGACG	GTCAAATGTA	ATTGAATGCC	CGCCCAGACG	50
	GATGAAAGGA	TTTGACGTTT	CTAACATCAT	TCTAGGCCTC	AGACCAGAGA	100
60	ACATTTGCTC	CTTGCCCGCC	AGGTCGGTGT	CCAGAAGCTG	GTCGTTTTTCG	150

	TTAACAAGGT	CGATGCCGTT	GAGGACCCAG	AGATGTTGGA	GCTTGTCGAA	200
	CTTGAAATGC	GTGAACTCCT	CAGCCACTAC	GGTTTCGAGG	GTGAGGAGAC	250
	CCCCATCATT	TTTGGCTCTG	CTCTCTGTGC	CCTCGAGTCC	CGTCGACCTG	300
	AGCTTGGTGT	CGAGAAGATT	GACGAGCTAT	TGAACGCCGT	CGACACCTGG	350
5	ATCCCCACCC	CCGAGCGCGC	CACTGATAAG	CCTTTCCTCA	TGTCCATTGA	400
	GGAAGTGTTT	TCTATCTCTG	GTCGTGGTAC	CGTCGTCTCC	GGTCGTGTTG	450
	AGCGTGGTAT	CCTCAAGAAG	GATTCCGACG	TCGAAATTGT	TGGTGGCTCT	500
	ACCACCCCTA	TCAAGACCAA	GGTCACAGAT	ATCGAAACCT	TCAAGAAGTC	550
	CTGCGATGAA	TCTCGAGCTG	GTGACAACCT	TGGTCTCCTT	CTCCGAGGTA	600
10	TCAAGCGTGA	GGACTTGAAG	CGTGGAATGG	TTGTTGCTGC	CCCCGGATCC	650
	ACCAAGGCTC	ACACCGACTT	CATGGTCTCC	CTCTACGTCC	TGACTGAGGC	700
	TGAGGGTGGT	CGTTCCAACG	GCTTCACCCA	CAAGTACCGC	CCCCAAATGT	750
	TCATCCGTAC	TGCTGGTATG	TAACCCAAGT	TTCCGCTATT	TACTAAGTAG	800
	ATCATTGCTA	ACTTGTATTT	CCTTCCGTAG	ACGAAGCCGC	ATCTTTCAGC	850
15	TGGCCTGGAG	AAGACCAAGA	CAAGAAGGCT	ATGCCTGGTG	ACAACGTCGA	900
	GATGATTTGC	AAGACCCTCC	ACCCCATTCG	TGCCGA		936

20 2) INFORMATION FOR SEQ ID NO: 793

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - 25 (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793

TTATTGTTGC TGCTGGTACT

20

35

2) INFORMATION FOR SEQ ID NO: 794

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - 40 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794

50

GACGACAAGT CGGTGAACTT

20

55 2) INFORMATION FOR SEQ ID NO: 795

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - 60 (C) STRANDEDNESS: Single

453

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795

10 ACTTGCACGC GATGTGGCAG 20

2) INFORMATION FOR SEQ ID NO: 796

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796

25 GGTCCAATGC CWCAAACWAG A 21

30 2) INFORMATION FOR SEQ ID NO: 797

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797

CATTAAGAAT GGYTTATCTG TSKCTCT 27

45 2) INFORMATION FOR SEQ ID NO: 798

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798

60

5 2) INFORMATION FOR SEQ ID NO: 799

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799

20 ACCTGTGAAT ACAAGCAATC T 21

25 2) INFORMATION FOR SEQ ID NO: 800

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: single
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:
35 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800

40 GATGAAATCT TCAACGAAGT TGAT 24

2) INFORMATION FOR SEQ ID NO: 801

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Cryptosporidium parvum*

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801

60 ACAACACCGA GAAGATCCCA 20

2) INFORMATION FOR SEQ ID NO: 802

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA
10

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802
15 TTGCCATTTC TGGTTTCGTT 20

20 2) INFORMATION FOR SEQ ID NO: 803

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
25 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:
30 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803
35 ACTTCAGTGG TAACACCAGC 20

40 2) INFORMATION FOR SEQ ID NO: 804

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:
50 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804
55 CCTGGGACGG CCTCTGGCAT 20

2) INFORMATION FOR SEQ ID NO: 805

(i) SEQUENCE CHARACTERISTICS:
60 456

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805

CTCTTGTTCCA TCTTAGCAGT

20

15

2) INFORMATION FOR SEQ ID NO: 806

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 806

AGCATCACCA GACTTGATAA G

21

35

2) INFORMATION FOR SEQ ID NO: 807

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

50

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807

AAAGTGGCTT CAAAGGTTGC

20

55

2) INFORMATION FOR SEQ ID NO: 808

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

457

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808

GCITTAIWRG CATTAGAARA YCCA

24

10

2) INFORMATION FOR SEQ ID NO: 809

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809

TCTTCCTGTW GCAACTGTTC CTCT

24

25

2) INFORMATION FOR SEQ ID NO: 810

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810

AGAGMWACAG ATAARSCATT CTTA

24

40

2) INFORMATION FOR SEQ ID NO: 811

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811

TRAARTAGAA TTGTGGTCTR TATCC

25

55

2) INFORMATION FOR SEQ ID NO: 812

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 26 bases

458

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812

10 GTIACIGGIT CYTYRARRTT ICCICC 26

2) INFORMATION FOR SEQ ID NO: 813

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813

25 AATCYGTYGA AATGCAYCAC GA 22

2) INFORMATION FOR SEQ ID NO: 814

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814

40 GCIGGCACGT ACACIGCCTG 20

45 2) INFORMATION FOR SEQ ID NO: 815

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815

TGGTGATYT CKACRGACTT 20

60

2) INFORMATION FOR SEQ ID NO: 816

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816

GCTACGACGA GATCAAGGGC

20

15

2) INFORMATION FOR SEQ ID NO: 817

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817

TGGAAGAAGG CCGAGGAGTT

20

30

2) INFORMATION FOR SEQ ID NO: 818

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818

45 AGCCGGGCTG GATCTTCTTC

20

50

2) INFORMATION FOR SEQ ID NO: 819

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819

60

460

5 2) INFORMATION FOR SEQ ID NO: 820

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820

20 GAAGGAGGTG TCTGCTTACA C

21

25 2) INFORMATION FOR SEQ ID NO: 821

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821

40 GGCGCAAACG TCACCACATC A

21

45 2) INFORMATION FOR SEQ ID NO: 822

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 55 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822

60 CGGCGGATGT CCTTAACAGA A

21

2) INFORMATION FOR SEQ ID NO: 823

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823

15 GAGCGGTATG AYGAGATTGT 20

2) INFORMATION FOR SEQ ID NO: 824

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824

30 GGCTTCTGCG GCACCATGCG 20

2) INFORMATION FOR SEQ ID NO: 825

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825

45 ATGAGCARCG SAACCATCGT TCAGTG 26

50 2) INFORMATION FOR SEQ ID NO: 826

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826

TCGATCGTGC CGACCATGTA GAACGC

26

5

2) INFORMATION FOR SEQ ID NO: 827

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 446 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium novyi*
(B) STRAIN: ATCC 19402

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827

	CACCAACTTG	CTAAATGGGG	AGATGCCCAG	ATTGTTGTAT	ATATAGGCTG	50
	TGGAGAACGT	GGAAATGAAA	TGACAGATGT	TCTTAATGAG	TTTCCAGAAC	100
	TTAAAGATCC	TAAGACTGGC	AAATCAATAA	TGGAAAGAAC	AGTTTTAATA	150
25	GCAAATACTT	CTAATATGCC	AGTTGCAGCC	CGTGAAGCTT	GTATATATAC	200
	AGGAATCACA	ATAGCAGAAT	ATTTTAGAGA	TATGGGATAT	TCAGTAGCAC	250
	TTATGGCGGA	TTCCACTTCA	CGTTGGGCAG	AGGCATTAAG	AGAAATGTCT	300
	GGAAGACTTG	AAGAAATGCC	TGGTGATGAA	GGTTACCCAG	CTTATTTAGG	350
	ATCAAGACTT	GCTGATTTCT	ATGAAAGAGC	TGGAAAAGTT	GTGTGTTTAG	400
30	GAGACGATGA	AAGAGAAGGT	GCCATTACTG	CAATAGGTGC	TGTATC	446

35 2) INFORMATION FOR SEQ ID NO: 828

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 445 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Clostridium difficile*
(B) STRAIN: 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828

50	CAGCATCAGC	TTGCTAAATG	GGCAGATGCA	GATATAGTTG	TATATATAGG	50
	CTGTGGCGAG	CGTGGAATG	AAATGACAGA	TGTTCTTCTT	GAATTTCTG	100
	AATTAAAAGA	CCCAAGAACA	GGCGAGTCAC	TTATGCAAAG	AACTGTGCTT	150
	ATAGCAAATA	CATCAGATAT	GCCGGTTGCT	GCACGTGAAG	CTTCTATATA	200
	CACTGGTATT	ACAATAGCTG	AATATTTTAG	AGATATGGGA	TATAGTGTTG	250
55	CACTTATGGC	AGACTCTACA	TCAAGATGGG	CTGAGGCTCT	TAGAGAGATG	300
	AGTGGTCGTT	TAGAGGAGAT	GCCTGGTGAA	GAAGGTTATC	CTGCATACTT	350
	AGGTTACAGT	CTTGCTCAAT	TCTATGAGAG	AGCAGGAAAG	GTAAATTGTC	400
	TAGGTATGGA	TGAAAGAGAA	GGAACACTTA	CAGCAATTGG	TGCAG	445

60

2) INFORMATION FOR SEQ ID NO: 829

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 445 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Clostridium septicum*
(B) STRAIN: ATCC 12464
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829

	ATGCTATAGC	TAAATGGGGA	GACAGCGAAA	TAGTTGTTTA	CGTTGGATGT	50
	GGAGAACGTG	GTAACGAAAT	GACAGACGTT	CTTAACGAAT	TCCCAGAACT	100
20	TATTGACCCA	AAAAC TGGGG	AAAGTTTAAT	GAAGAGAACA	GTA CTTATAG	150
	CTAATACTTC	AAACATGCCA	GTTGCTGCTA	GAGAAGCTTG	CATATACACA	200
	GGTATTACAA	TAGCTGAATA	CTTCAGAGAT	ATGGGATACT	CAGTATCTAT	250
	AATGGCTGAT	TCAACTTCAA	GATGGGCAGA	AGCATTAAGA	GAAATGTCAG	300
	GTAGACTTGA	AGAAATGCCA	GGTGATGAAG	GATATCCAGC	GTA CTTAGGA	350
25	TCAAGACTTG	CTGATTATTA	CGAAAGAGCA	GGTAAGGTTG	TTTGTCTAGG	400
	TAAAGATGGT	AGAGAAGGTG	CTGTAACAGC	AATTGGAGCT	GTATC	445

30 2) INFORMATION FOR SEQ ID NO: 830

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 444 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 40 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Clostridium botulinum*
(B) STRAIN: 20:3.1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830

45	TCAAATTGCT	AAATGGGGAG	ATGCAGAAAT	CGTTGTTTAC	GTTGGATGCG	50
	GAGAACGTGG	TAACGAAATG	ACAGACGTTG	TTAATGAGTT	CCCAGAACTT	100
	ATTGACCCTA	AGACTGGCGA	AAGCTTAATG	AAGAGAACAG	TTCTTATAGC	150
	TAATACTTCA	AACATGCCAG	TTGCAGCGAG	AGAAGCTTCA	ATATATACAG	200
50	GTATCACAAT	AGCTGAATAT	TTCAGAGATA	TGGGATATGC	AGTATCAATA	250
	ATGGCTGACT	CAACTTCAAG	ATGGGCTGAG	GCATTAAGAG	AAATGTCTGG	300
	TAGACTTGAA	GAAATGCCTG	GTGATGAAGG	ATATCCAGCT	TACCTTGGAT	350
	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAGGTTGA	ATGTTTAGGT	400
55	AATGATGGAA	GAATTGGTTC	TATAACAGCA	ATCGGTGCGG	TATC	444

2) INFORMATION FOR SEQ ID NO: 831

- (i) SEQUENCE CHARACTERISTICS:
- 60 (A) LENGTH: 456 bases

464

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: ATCC 13124

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 831

	TAGTTCAGCA	CCAAGTTGCT	AAATGGGGAG	ATACTGAGAT	AGTTGTTTAC	50
	GTTGGATGTG	GAGAACGTGG	TAACGAGATG	ACAGACGTTC	TTAACGAATT	100
15	CCCAGAACTT	AAAGACCCTA	AAACTGGGGA	AAGCTTAATG	AAGAGAACAG	150
	TTCTTATTGC	TAATACATCT	AACATGCCAG	TTGCTGCCAG	AGAAGCATCA	200
	ATATATACTG	GTATAACAAT	AGCAGAGTAT	TTCAGAGATA	TGGGATACTC	250
	AGTATCAATC	ATGGCTGACT	CAACTTCACG	TTGGGCAGAG	GCTTTAAGAG	300
	AAATGTCAGG	AAGACTTGAA	GAAATGCCAG	GAGACGAAGG	TTACCCAGCA	350
20	TACTTAGGAT	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAAGTTGT	400
	AGCTTTAGGT	AAAGATGGAA	GAGAAGGAGC	TGTTACAGCT	ATCGGAGCAG	450
	TATCCC					456

25 2) INFORMATION FOR SEQ ID NO: 832

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tetani*
- (B) STRAIN: ATCC 19406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832

40

	CCAAGTTGCA	AAATGGGCTG	ATGCTCAAAT	AGTTGTGTAC	ATAGGATGTG	50
	GAGAACGTGG	AAATGAAATG	ACAGACGTTT	TAAATGAGTT	CCCAGAATTA	100
	AAGGATCCTA	AAACCGGGGA	ATCTTTAATG	AAAAGAACTG	TGTTAATAGC	150
	AAATACATCT	AATATGCCTG	TTGCAGCTAG	AGAAGCATCT	ATATATACTG	200
45	GTATAACAAT	AGGGGAATAT	TTTAGAGATA	TGGGATATTC	AATAGCACTA	250
	ATGGCAGATT	CGACTTCTAG	ATGGGCAGAG	GCTCTAAGAG	AAATGTCTGG	300
	AAGACTAGAG	GAGATGCCAG	GTGAAGAAGG	TTATCCAGCT	TATTTAGGAT	350
	CTAGATTAGC	AGAGTTCTAT	GAAAGAGCAG	GTAATGTTAT	ATGTTTAGGT	400
	CAGGATGGAA	GAGAAGGAGC	ATTAACAGCT	ATAGGAGCAG	TTTC	444

50

2) INFORMATION FOR SEQ ID NO: 833

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus pyogenes*
(C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833

10	TGAACCAAGG	AAAAATAATA	ACCGTTTCGG	GACCTCTTGT	TGTGGCTTCT	50
	GGGATGCAAG	AAGCTAATAT	TCAAGATATT	TGTCGTGTGG	GACATCTTGG	100
	CTTAGTCGGA	GAAATTATTG	AAATGCGTCG	CGATCAAGCG	TCTATTCAGG	150
	TTTATGAGGA	AACATCAGGG	ATCGGTCCAG	GAGAACCAGT	AGTGACTACT	200
	GGTTGTCCTT	TGTCGGTCGA	GTTAGGCCCG	GGCCTGATTT	CAGAAATGTT	250
	TGACGGTATT	CAGCGACCGC	TTGATCGTTT	TCAAAAAGCA	ACGGACAGCG	300
15	ACTTTTTTAAT	CCGTGGTGTG	GCTATCCCAA	GTCTTGATCG	AAAGGCTAAG	350
	TGGGCATTTA	TTCCCAAGCT	AAGTGTTGGT	CAAGAAGTAG	TTGCAGGTGA	400
	TATTTTAGGA	ACTGTGCAAG	AAACAGCTGT	CATTGAGCAC	CGTATCATGG	450
	TTCCTTATAA	AGTTTCAGGG	ACCTTGGTGG	CTATTCATGC	AGGGGACTTC	500
	ACAGTAACAG	ATACAGTTTA	TGAAATTAAG	CAGGAAGACG	GTTCCATTTA	550
20	CCAAGGTAGC	CTCATGCAGA	CTTGGCCAGT	TCGTCAAAGT	CGCCCTGTTG	600
	CTCAAAAGCT	TATCCCAGTC	GAACCTTTGG	TTACAGGTCA	ACGGGTTATT	650
	GACACCTTTT	TCCCTGTTAC	AAAAGGTGGT	GCCGCTGCCG	TTCTTGACC	700
	ATTTGGGGCA	GGAAAAACAG	TTGTGCAGCA	TCAAATAGCT	AAATTTGCCA	750
	ACGTTGATAT	TGTTATTTAT	GTCGGTTGTG	GGGAACGCGG	CAACGAGATG	800
25	ACCGACGTTT	TGAATGAGTT	TCCAGAGTTA	ATTGACCCAA	ATACAGGCCA	850
	GTCCATTATG	GAGCGCACGG	TGTTAATTGC	AAACACCTCT	AATATGCCAG	900
	TAGCAGCGCG	TGAAGCGTCG	ATTTACACAG	GTATTACCAT	TGCCGAATAT	950
	TTCCGTGATA	TGGGCTATTC	TGTGGCTATC	ATGGCAGACT	CGACATCACG	1000
	TTGGGCAGAA	GCTCTGCGCG	AGATGTCAGG	ACGCCTACAA	GAAATGCCTG	1050
30	GTGATGAAGG	CTACCCGGCT	TACTTAGGGA	GTCGTATTGC	CGAATATTAT	1100
	GAACGGGCTG	GTCGTGTTCT	GACCTTGGGA	AGTCAAGAAC	GTGAGGGAAC	1150
	CATTACAGCC	ATCGGCGCGG	TTTCTCCTCC	TGGAGGGGAT	ATTTCAGAGC	1200
	CTGTCACTCA	AAACACCCTT	CGGATTGTCA	AAGTTTTCTG	GGGGCTCGAC	1250
	GCGCCTCTTG	CGCAACGGCG	TCACTTCCCA	GCGATTAACT	GGCTGACGTC	1300
35	TTATTCATTG	TATCAAGATG	ATGTAGGAAG	CTATATTGAC	CGTAAACAGC	1350
	AATCTAATTG	GTCCAACAAG	GTAACCTCGT	CCATGGCTAT	TTTGCAGCGT	1400
	GAAGCCAGTC	TAGAAGAAAT	TGTACGCTTG	GTGGGGCTTG	ATTCACTGTC	1450
	TGAACAAGAT	CGTTTGACCA	TGGCTGTTGC	CCGGCAAATT	CGGGAGGATT	1500
	ATCTCCAGCA	AAATGCCTTT	GATTCGGTGG	ATACCTTTAC	TTCCTTTCCG	1550
40	AAACAAGAGG	CCATGCTAAC	CAATATTTTG	ACCTTTAATG	AGGAAGCCAG	1600
	CAAAGCCCTT	TCTTTGGGAG	CTTATTTTAA	TGAGATTATG	GAAGGCACTG	1650
	CTCAGGTACG	CGATCGCATC	GCACGCAGCA	AATTTATCCC	AGAAGAAAAC	1700
	TTAGAGCAGA	TTAAAGGGCT	TACTCAGAAG	GTTACCAAAG	AGATTCACCA	1750
	CGTTTTAGCA	AAGGGAGGAA	TTTAGATGAG	CGTTCT		1786

45

2) INFORMATION FOR SEQ ID NO: 834

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Babesia bovis*
(B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834

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5  TATCTCACGT AAGTTTTTGC GCGGCGGTTA TATATCACTC CAGGCCCTGG      50
   CTAAGTACGC TAATACTGAC GTTACTGTCT ATGTGGGATG TGGAGAGCGT      100
   GGAAACGAGA TTGCGGAGGT GCTTAAGGAG TTCCCTGAGC TGAAGACCAA      150
   GGTTGATGGC AAGGAAGTGA GCATTATGAA ACGCACTTGC TTGGTGGCCA      200
   AACTTCAAA  CATGCCAGTG GCCGCCAGGG AGGCTAGTAT CTACACTGGC      250
   ATTACCCTAT GTGAATACTT CAGGGATATG GGATACAACG CCTGTGTGAT      300
10  GGCGGATTCC ACCAGTCGTT GGGCTGAGGC TTTGCGTGAG ATATCAGGTC      350
   GTTTAGCTGA GATGCCTGCT GATTCAGGTT ATCCCGCCTA CCTTGCTTCT      400
   AGGCTTTCGG CGTTCTATGA GCGTGCTGGT ACAGCTGAGT GTATTGGAAC      450
   ACCACTTCGT GAAGGTTTCAG TTACCATTGT TGGTGCTGTA TCTCCACCA      499

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15

2) INFORMATION FOR SEQ ID NO: 835

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20  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 464 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

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25  (ii) MOLECULE TYPE: Genomic DNA

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     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Cryptosporidium parvum

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835

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   TTTCTCAAGC TTTGAGTAAA TATAGTAACT CTGATGTTAT TATTTACATT      50
   GGTGTGGAG  AAAGAGGAAA TGAAATGGCA GAAGTTCTTA CAGAATTCCC      100
   TGAGCTTTAT ACTATGGTTG ATGGAAAGAA GGAGTCAATT ATGCAAAGAA      150
35  CTTGTTTAGT AGCTAATACA TCAAATATGC CTGTCGCTGC TAGAGAAGCT      200
   TCCATCTACA CTGGTATTAC ACTTTCTGAA TACTTTAGAG ATATGGGATG      250
   TAATGTTTCT ATGATGGCAG ATTCAACTTC TCGTTGGGCT GAAGCTCTTA      300
   GAGAAATTTT TGGTAGATTA GCTGAAATGC CTGCAGATTC GGGTTACCCA      350
   GCATATTTAG GCGCCAGACT TGCTTCATTC TATGAAAGAT CAGGAAGAGT      400
40  TAAATGTATG GGTTCGCCAG ATAGAGAAGG TACAGTAACA ATTGTTGGTG      450
   CAGTTTCTCC ACCT                                     464

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45 2) INFORMATION FOR SEQ ID NO: 836

3)

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     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 446 bases
          (B) TYPE: Nucleic acid
50  (C) STRANDEDNESS: Double
          (D) TOPOLOGY: Linear

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     (ii) MOLECULE TYPE: Genomic DNA

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55  (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Leishmania infantum
          (B) STRAIN: MOU

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60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836

GCCCTCTCCA AGTACTCCAA CTCCGATTGC GTCATCTATG TCSSGCTGCGG 50
 CGAGCGCGGT AATGAGATGG CCGAGGTGCT CATGGAGTTC CCGACCCCTGA 100
 CGACCGTGAT CGATGGCCGC GAGGAGTCGA TCATGAAGCG CACCTGCCTC 150
 GTGGCGAACA CCTCGAACAT GCCAGTCGCA GCCCGTGAGG CCTCTATTTA 200
 5 CACCGGCATC ACCCTGGCCG AGTACTACCG TGATATGGGC AAGCATATCG 250
 CCATGATGGC TGACTCGACG TCTCGCTGGG CCGAGGCGCT TCGTGAGATT 300
 TCGGGTCGTC TGGCGGAGAT GCCGGCGGAT GGTGGCTACC CCGCCTACCT 350
 CAGCGCTCGT CTCGCCTCCT TCTACGAGCG CGCCGGCCTC GTCACCTGCA 400
 TCGGCGGGCC GAAGCGCCAG GGCTCCGTCA CGATCGTCGG TGCCGT 446
 10

2) INFORMATION FOR SEQ ID NO: 837

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 25 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837

TTAGTCAGGC CCTCTCCAAG TACTCCAACCT CCGACTGCGT CATCTATGTC 50
 30 GGCTGCGGCG AGCGCGGTAA TGAGATGGCT GAGGTGCTCA TGGATTTCCTC 100
 AACTCTGACG ACCGTGATCG ATGGTCGCGA GGAGTCCATC ATGAAGCGCA 150
 CCTGCCTCGT GGCAAACACT TCGAACATGC CAGTCGCAGC CCGCGAGGCC 200
 TCTATTTACA CCGGCATCAC CCTGGCCGAG TACTACCGTG ATATGGGCAA 250
 GCATATTGCC ATGATGGCCG ACTCGACATC TCGCTGGGCC GAGGCGCTTC 300
 35 GTGAGATTTC CGGTCGTCTG GCGGAGATGC CAGCCGATGG TGGCTACCCT 350
 GCCTACCTCA GCGCTCGTCT CGCCTCCTTC TACGAGCGCG CCGGCCTCGT 400
 CACCTGCATC GGCGGGCCGA AGCGCCAGGG CTCCGTCACG ATCGTCGGTG 450
 CTGTGT 456

40

2) INFORMATION FOR SEQ ID NO: 838

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 55 (B) STRAIN: MOU-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838

AGGCCCTCTC CAAGTACTCC AACTCCGACT GCGTCATCTA CGTCGGCTGC 50
 GGCGAGCGCG GTAATGAGAT GGCCGAGGTG CTCATGGAGT TCCCGACCCT 100
 60 GACGACTGTG ATTGATGGCC GTGAGGAGTC GATCATGAAG CGGACCTGCC 150

468

	TCGTGGCCAA	CACCTCCAAC	ATGCCAGTCG	CAGCCCGTGA	AGCCTCTATT	200
	TAACTGGTA	TCACCCTGGC	CGAATACTAC	CGTGATATGG	GCAAGCATAT	250
	CGCCATGATG	GCTGACTCGA	CGTCTCGCTG	GGCGGAGGCG	CTTCGTGAGA	300
	TTTCGGGTCG	CCTGGCGGAG	ATGCCGGCTG	ATGGTGGGTA	CCCCGCCTAC	350
5	CTTAGTGCTC	GTCTTGCCTC	CTTCTACGAG	CGTGCCGGCC	TCGTACACCTG	400
	CATCGGTGGG	CCGAAGCGCC	AGGGCTCCGT	CACGATCGTC	GGTGCCGTGT	450

10 2) INFORMATION FOR SEQ ID NO: 839

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 bases

(B) TYPE: Nucleic acid

15. (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma brucei*

(B) STRAIN: EATRO 795

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839

	GCACTCTCGA	AGTACTCGAA	CAGTGACGCT	GTTATTTACG	TGGGTTGTGG	50
	TGAGCGTGCG	AATGAGATGG	CGGAGGTGCT	CATGGACTTT	CCCACCCTCA	100
	CCACCATTAT	TGATGGACGT	GAGGAGTCTA	TCATGAAGCG	CACATGCCTG	150
	GTGGCAAATA	CTTCCAATAT	GCCTGTTGCT	GCTCGTGAGG	CATCTATTTA	200
30	CACTGGTATC	ACCTTAGCTG	AGTATTATCG	GGATATGGGA	AAACACATCG	250
	CCATGATGGC	CGATTCAACC	TCCCGCTGGG	CTGAGGCTTT	GCGTGAGATT	300
	TCCGGTCGTC	TTGCTGAAAT	GCCTGCAGAT	GGAGGTTATC	CCGCGTACCT	350
	CAGCGCCCGT	TTGGCCTCCT	TCTACGAGCG	TGCTGGCCGT	GTGACATGCA	400
	TCGGTGGGCC	GAAGCGTGAA	GGGTCTGTAA	CAATTGT		437

35

2) INFORMATION FOR SEQ ID NO: 840

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1052 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*

50 (B) STRAIN: MM3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840

	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
55	TTGAGTCGC	CCAAGTCTGT	GTTCACGATC	ATCGACGCCC	CCGGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GACGCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTCG	300
60	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350

	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GACGTGTACA	AGATCGGCGG	550
5	TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCG	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCCG	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
	TGTGCGGCAA	CTCGAAGAAC	GACCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
10	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTC	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
15	CC					1052

2) INFORMATION FOR SEQ ID NO: 841

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: CGL-1

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841

35	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
	TTCGAGTCGC	CCAAGTCTGT	GTTACAGATC	ATCGACGCCC	CCGGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GATGCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
40	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTTG	300
	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350
	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
45	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GATGTGTACA	AGATCGGCGG	550
	TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCG	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCCG	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
50	TGTGCGGCAA	CTCGAAGAAC	GATCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTT	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
55	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
	CCGTGCGTGA	C				1061

60 2) INFORMATION FOR SEQ ID NO: 842

470

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842

15 GCTGAAGGCT GAGCGCGAGC GCGGCATCAC GATCGACATC GCGCTCTGGA 50
 AGTTCGAGTC GCCCAAGTCT GTGTTCACGA TCATCGACGC CCCCGGCCAC 100
 CGCGACTTCA TCAAGAACAT GATCACGGGC ACGTCTCAGG CGGACGCCGC 150
 CGTCCTTGTC ATTGCGTCAT CGCAGGGTGA GTTTGAGGCG GGCATCTCGA 200
 20 AGGACGGCCA GACACGCGAG CACGCGCTGC TCGCCTTCAC GCTCGGCGTG 250
 AAGCAGATGG TTGTGTGCTG CAACAAGATG GACGACAAGT CGGTGAACTT 300
 CGCCCAGGAG CGCTACGATG AGATTGTGAA GGAGGTGTCG GCGTACCTGA 350
 AGAAGGTTGG GTACAACGTG GAGAAGGTGC GCTTCATCCC CATCTCCGGC 400
 TGGCAGGGCG ACAACATGAT TGACAAGTCG GAAAATATGC CGTGGTACAA 450
 25 GGGCCCCACG CTGCTGGAGG CACTCGACAT GCTGGAGCCC CCGGTGCGCC 500
 CCAGCGACAA GCCGCTGCGC CTGCCGCTGC AGGACGTGTA CAAGATCGGC 550
 GGTATCGGCA CCGTGCCGGT CGGTCGCGTG GAGACGGGCA CGATGAAGCC 600
 CGGCGACGTG GTGACGTTTG CGCCCGCCAA CGTGACGACG GAGGTGAAGT 650
 CGATTGAGAT GCACCACGAG CAGCTGGCCG AGGCCACGCC CGGCGACAAC 700
 30 GTCGGCTTCA ACGTGAAGAA CGTGTCCGTG AAGGACATCC GCCGTGGCAA 750
 CGTGTGCGGC AACTCGAAGA ACGACCCCCC AAAGGAGGCG GCCGACTTCA 800
 CGGCGCAGGT GATCATCCTG AACCACCCCG GCCAGATCGG CAACGGCTAT 850
 GCGCCGGTGC TCGACTGCCA CACCTGCCAC ATCGCGTGCA AGTTCGCCGA 900
 GATCGAGTCC AAGATCGACC GCCGCTCCGG CAAGGAGCTT GAGAAGAACC 950
 35 CCAAGTCGAT CAAGTCCGGT GACGCCGCCA TGGTGCGCAT GGTGCCGCAG 1000
 AAGCCCATGT GCGTGGAGGT GTTCAACGAC TACGCTCCTC TTGGCCGCTT 1050
 TGCCGTGCGT GA 1062

40

2) INFORMATION FOR SEQ ID NO: 843

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843

60 TACATTGACA GCTGCATTGA CCAAGGTCTG TTCGATGGGT GGTCATGGCG 50
 AGTACACTCC TTATGAAGCA ATTGACCGTG CTCCTGAGGA GCGTAAACGT 100
 GGTATTACTA TAAATTTCGAC ACATGTTGAA TATGAGACTA AGAACCGTCA 150
 TTACGGTCAC GTGGACTGTC CAGGTCACTC TGATTATGTG AAGAACATGA 200

	TATCTGGCGC	TGCTCAGATG	GATGGTGCCA	TATTGGTTGT	TTCTTGTGTT	250
	GACGGTCCCA	TGCCTCAGAC	TAAGGAGCAC	GTGTTGCTTG	CTAAGCAGAT	300
	TGGTGTACCT	CGTTTAGTTG	TGTTTTTGAA	CAAGCTTGAC	ATGTTAGAGG	350
	ACTCTGAGCT	ATTGGAGTTG	GTGGAGTTAG	AGGTTCTGTA	GTTATTGAGT	400
5	GAGTTTGGTT	ACGACGGTGA	CAACACGCCT	ATCGTTCGTG	GCAGTGCTAT	450
	AAAGGCATTG	AACAGTAGTT	CCGAGGCTGA	CATTAAGCCA	ATTCAGGATT	500
	TATTGGATGC	GTGTGATGCC	TTTTTACTGA	CTCCAGAACG	TAAGGATGAC	550
	ATGCCGCTCT	TGGTTGCTAT	TGACGATGTT	CTTGCCATTC	CTGGCAAGGG	600
	TACTGTTGTA	ACCGGTAGGA	TAGAGCAGGG	CAAGATTCTG	TGTGGTGACC	650
10	CTATTGAGGT	TTGCGCCGGT	CCGAAGTCCG	GCAAGAAGAC	TGTGTGTGTT	700
	GGTCTTRARA	TGTTCCGCAA	GAGTCTCAGT	RAGGGTATTG	CTGGTGACCA	750
	GATTGGTGTT	TTGCTCAAGG	GTGTGAAGCG	CGACRAGGTA	GAGCGCGGGT	800
	TTGTATTGAT	TCAACCCGGA	AGTTACAAAT	GTCACGGTGA	ATTTGATGCT	850
	GACTTGTACG	TGTTGACTAC	GRAGGAAGGT	GGGCGCAAGC	ATCCGTTTGT	900
15	GTCTAACTAC	CGTCCTCAGG	CGTTTATACG	TACTGGAGAC	GTTTGCTGCT	950
	CAGTTCATTT	GGATRAGGGT	GTTGAGATGG	CAGCTCCTGG	TGACAACGTG	1000
	CGTTGCAAGA	TCAAGTTACT	TTATCCCATG	CCTGTCCATG	AAGGTTTACG	1050
	ATTTGCG					1057

20

2) INFORMATION FOR SEQ ID NO: 844

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 943 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCACCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
40	TTCATCAACA	AAGTGGATAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGCGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAGGAGA	200
	CACCAATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AGTGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATCGAGCACG	350
45	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGCGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCGGC	550
	ACCGGCGACA	CAACCAAGTCT	GTCCAAGGAC	AACGTGGAAC	GCGGCATGGT	600
50	AATGGCGGCG	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACCGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCC	GAGGCGGAGA	AGCACCGGGA	GGAGCTGAAC	AAGAAATTCG	800
	GCCGCGGCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
55	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTCGCGTAC	CCGATGCCCA	TTGAAAAGGG	CCTGAAGTTC	ACC	943

60 2) INFORMATION FOR SEQ ID NO: 845

472

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845

15

CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
GCGAGCATCT	CTTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
CATGGAGGTG	CGTGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAAGAGA	200
20 CGCCCATCGT	GCGCGGCTCG	GCCCTCAAAG	CCGTCGAGGG	CGACGCGAAG	250
TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AATGGATCCC	300
CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATTGAGCACG	350
TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
25 CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
CGCTGAGTGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCGGC	550
ACCGGCGACA	CGATCAGTCT	CTCCAAGGAC	AACGTTGAAC	GCGGCATGGT	600
AATGGCGGCA	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGCCCC	700
30 CACTACCGCC	CGCAGCTCTT	CTTCCATTGT	GCTGACGTGA	CGGCGGACAT	750
GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTCG	800
GCCGCGGCC	CGAGGAGGAC	AAGCAGAAGG	AGGCGGAGAT	GAAAGAGTTC	850
GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAC	AACCGCGAGC	TGATCCTGAC	900
GCTGGCGTAC	CCGATGCCCA	TTGACAAGGG	TCTGAAGTT		939

35

2) INFORMATION FOR SEQ ID NO: 846

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 945 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania donovani*
 50 (B) STRAIN: ATCC 50212
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846

55

CATTGTGGTG	GCGGCCACCG	ACGGCGTCAT	GCCGCAGACA	CGCGAGCACC	50
TCCTGATCTG	CTCGCAGATC	GGGCTTCCGG	CGCTCGTAGG	GTTTCATCAAC	100
AAGGTGGACA	TGACGGACGA	GGACACGTGC	GACCTGGTGG	ACATGGAGCT	150
GCGCGAGCAG	CTGGAGAAAT	ACAAGTTTCC	GGCGGAGGAG	ACGCCAATCG	200
TGCGCGGCTC	AGCCCTCAAA	GCCGTCGAGG	GCGATGCGAA	GTACGAGGAG	250
AACATTCTCG	AACTGGTGCG	GAAGTGTGAC	GAGTGGATCC	CTGACCCGCC	300
60 GCGCAACACA	GACAAGCCTT	TCCTTATGGC	CATCGAGCAC	GTTTACGAGA	350

	TCGGCAAGGA	CAAGAAGAGC	GTTGTCGTGA	CCGGCCGCGT	CGATCAGGGC	400
	ATTCTGAAGC	TCAACACAGA	CGCCGAGCTG	GCCGGCTTCA	GCTCCAAGAA	450
	GTCGACGGTG	AGGGTGACGG	GCATCGAGAT	GTACCACAAG	ACGCTGAGCG	500
	AGTGCATGCC	TGGTGACTCC	GTCGGCGTCA	GCATTGTCGG	GACCGGCGAC	550
5	ACGACCAGTC	TATCCAAGGG	CAACGTGGAA	CGCGGCATGG	TGATGGCGGC	600
	GACGGGTAGC	ACGAACCTGT	ACAACAAGGT	GAAGGCGCAG	GTGTACGTGC	650
	TGACGAAGGA	TGAGGGCGGC	CGCCACACTG	GCTTTAGTCC	TCACTACCGC	700
	CCGCAGCTCT	TCTTCCATTG	TGCTGACGTG	ACGGCGGACA	TGAGCTTCCC	750
	GGAGGCGGAG	AAGCACCGCG	AAGAGCTCAA	CAAGAAATTC	GGCCGCGGCC	800
10	CCGAGGAGGA	CAAGAAGAAA	GAGGCAGCGA	TGAAGGAGTT	CGAGAGCAAG	850
	CTCGTCTGCA	TGCCGGGCGA	TAACCGCGAG	CTGATCCTGA	CGCTGGCGTA	900
	CCCGATGCCC	ATTGAAAAGG	GTCTGAAGTT	CACCATCCGT	GAGGG	945

15

2) INFORMATION FOR SEQ ID NO: 847

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 939 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania infantum*
(B) STRAIN: MOU

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847

	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	GCACCTCCTG	ATCTGCTCGC	AGATCGGGCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAGGT	GGACATGACG	GACGAGGACA	CGTGCGACCT	GGTGGACATG	150
35	GAGCTGCGCG	AGCAGCTGGA	GAAATACAAG	TTTCCGGCGG	AGGAGACGCC	200
	AATCGTGCGC	GGCTCAGCCC	TCAAAGCCGT	CGAGGGCGAT	GCGAAGTACG	250
	AGGAGAACAT	TCTCGAACTG	GTGCGGAAGT	GTGACGAGTG	GATCCCTGAC	300
	CCGCCGCGCA	ACACAGACAA	GCCTTTCCTT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTTGT	CGTGACCGGC	CGCGTCGATC	400
40	AGGGCGTTCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCGG	CTTCAGCTCC	450
	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATC	GAGATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCTGGTG	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTATCC	AAGGGCAACG	TGGAACGCGG	CATGGTGATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
45	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTT	AGTCCTCACT	700
	ACCGCCCGCA	GCTCTTCTTC	CATTGTGCTG	ACGTGACGGC	GGACATGAGC	750
	TTCCCGGAGG	CGGAGAAGCA	CCGCGAAGAG	CTCAACAAGA	AATTCCGGCCG	800
	CGGCCCCGAG	GAGGACAAGA	AGAAAGAGGC	AGCGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
50	GCGTACCCGA	TGCCCATTTGA	AAAGGGTCTG	AAGTTCACC		939

55

2) INFORMATION FOR SEQ ID NO: 848

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 933 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leishmania enriettii*
(B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848

10	CACCGACGGC	GTCATGCCGC	AGACACGGGA	GCACCTGCTC	ATCTGCTCGC	50
	AGATCGGGCT	GCCGGCGCTT	GTAGGGTTCA	TCAATAAAGT	TGACATGACG	100
	GACGAGGATA	CGTGCGACCT	CGTGGACATG	GAGGTGCGGG	AACAGCTGGA	150
	GAAGTACAAG	TTTCCGGCCG	AGGAGACGCC	CATCGTACGT	GGCTCGGCCC	200
	TCAAGGCCCT	CGAGGGGGAT	GCGCAATACG	AGGGGAGTAT	TCTCGAGCTG	250
15	GTGCGAAAGT	GCGACGAGTG	GATCCCCGAC	CCGCCGCGCA	ACACCGAAAA	300
	GCCTTTCTC	ATGGCTATCG	AGCACGTTTA	CGAGCTCGGC	AAAGACAAGA	350
	AGAGCGTCAT	CGTTACCGGC	CGCGTCGATC	AAGGTGTGCT	GAAGCTCAAC	400
	ACAGACGCCG	AGCTGGCCGG	CTTCAGCGCC	AAGAAGGCGA	CAGTCAAAGT	450
	GACGGGCATC	GAGATGTATC	ACAAGACACT	CAATGAGTGC	ATGCCCCGGC	500
20	ACTCTGTCGG	TGTCAGCATC	GTCGGTACCG	GTGACACGAC	CAGCTTATCC	550
	AAGGATAATG	TTGAGCGCGG	TATGGTAATG	GCGGCAACGG	GTAGCACGAA	600
	CCTGTACAAC	AAGCTGAAGG	CGCAGGTTTA	CGTGCTGACA	AAGGAGGAGG	650
	GTGGCCGCCA	CACCGGGTTC	AGCCCCCACT	ACCGCCCGCA	GCTCTTCTTC	700
	CACTGCGCTG	ACGTGACCGC	AGACATGAGC	TTCCCGGAGG	CGGAGAAGTA	750
25	CCGCGAGGAG	CTCAACAAGA	AGTTCGGCCG	TGGCCCTGAG	GAGGACAAGA	800
	AGAAAGAGGC	GGAGATGAAG	GAGTTCGAAA	GCAAACCTTG	CTGCATGCCA	850
	GGCGATAACC	GCGAGCTGAT	CCTAACTCTG	GCGTACCCGA	TGCCCATCGA	900
	CAAGGGCCTG	AAGTTCACCA	TCCGTGAGGG	CGG		933

30

2) INFORMATION FOR SEQ ID NO: 849

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 943 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania gerbilli*
(B) STRAIN: ATCC 50121

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCACCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
50	TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGCGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAGGAGA	200
	CACCAATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AGTGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATCGAGCACG	350
55	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACGGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATTGAGATG	TACCACAAGA	500
	CGCTGAGCGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTGCGC	550
	ACCGGCGACA	CGACCACTCT	GTCCAAGGAC	AACGTGGAAC	GCGGCATGGT	600
60	AATGGCGGCG	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650

	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTCG	800
	GCCGCGGCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
5	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGAAAAGGG	TCTGAAGTTC	ACC	943

10 2) INFORMATION FOR SEQ ID NO: 850

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850

25	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	ACACCTCCTG	ATCTGCTCGC	AAATTGGCCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAAGT	GGACATGACG	GACGAGGACA	CGTGTGACCT	GGTGGACATG	150
	GAGGTGCGCG	AGCAGCTGGA	GAAATACAAG	TTTCCGGCGG	AGGAGACACC	200
30	AATCGTGCGC	GGCTCGGCCC	TCAAGGCCGT	CGAGGGCGAC	GCGAAGTACG	250
	AGGAGAACAT	CCTCGAACTG	GTGCGGAAGT	GCGACGAGTG	GATCCCCGAC	300
	CCGCCGCGCA	ACACAGACAA	GCCTTTCTT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTCAT	CGTGACCGGC	CGCGTCGATC	400
	AGGGCGTGCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCGG	CTTCAGCGCC	450
35	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATT	GAAATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCCCGGT	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTGTCC	AAGGACAACG	TGGAGCGCGG	CATGGTAATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTC	AGCCCCCACT	700
40	ACCGCCCGCA	GCTCTTCTTC	CATTGCGCTG	ACGTGACAGC	GGACATGAGC	750
	TTCCCGGAGG	CGGAGAAGCA	CCGCGAGGAG	CTCAACAAGA	AATTCGGCCG	800
	CGGCCCCGAG	GAGGACAAGA	AGAAAGAGGC	GGAGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
	GCGTACCCGA	TGCCCCATT				918

45

2) INFORMATION FOR SEQ ID NO: 851

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 60 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
5	GCGAGCATCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
	TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGTGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAAGAGA	200
	CGCCCATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AATGGATCCC	300
10	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATTGAGCACG	350
	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGTCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGTGA	GTGCATGCCC	GGTGA CTCCG	TCGGCGTCAG	CATTGTCGGC	550
15	ACCGGCGACA	CGATCAGTCT	CTCCAAGGAC	AACGTTGAAC	GCGGCATGGT	600
	AATGGCGGCA	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGT	GCTGACGTGA	CGGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTCG	800
20	GCCGCGGCC	CGAGGAGGAC	AAGCAGAAGG	AGGCGGAGAT	GAAAGAGTTC	850
	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAC	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGAGAAGGG	TCTGAAGTT		939

25

2) INFORMATION FOR SEQ ID NO: 852

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tarentolae*

(B) STRAIN: MOU-2

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852

	TCATTGTGGT	GGCCGCCACC	GACGGCGTCA	TGCCGCAAAC	ACGGGAGCAC	50
	CTTTTGATCT	GCTCGCAGAT	CGGGCTGCCG	GCGCTCGTAG	GGTTCATCAA	100
	CAAAGTGGAC	ATGACAGACG	AAGACACGTG	CGACCTGGTA	GACCTGGAGG	150
45	TGCGTGAGCA	GCTGGAGAAG	TACAAGTTTC	CGGCAGAGGA	AACACCAATC	200
	GTGCGTGGCT	CGGCCCTCAA	GGCCGTTGAG	GGCGATGCAA	AGTACGAGGA	250
	GAACATCCTC	GAAGTGGTGC	GGAAGTGCGA	CGAGTGGATC	CCAGACCCGC	300
	CACGCAATAC	GGACAAGCCT	TTCCTTATGG	CCATTGAACA	CGTGTACGAG	350
	ATCGGCAAGG	ATAGGAAAAG	CGTCATCGTA	ACCGGCCGCG	TCGATCAAGG	400
50	TGTGCTGAAG	CTGAACACAG	ACGCCGAGCT	GGCCGGCTTC	AGCGCCAAGA	450
	AGTCGACGGT	GAAAGTGACG	GGCATTGAGA	TGTACCACAA	GACACTGACA	500
	GAGTGCATGC	CCGGCGACTC	TGTCGGCGTC	AGCATTGTGG	GCACTGGYGA	550
	CACGACCAGC	CTCTCTAAGG	ACAATGTTGA	GCGTGGCATG	GTACTGGCCG	600
	CTACGGGTAG	CACGAACCTG	TACAACAAAG	TAAAGGCGCA	GGTGTATGTA	650
55	CTCACGAAGG	ATGAGGGCGG	CCGCCACACC	GGCTTCAGCC	CCCCTACCG	700
	TCCGCAGCTC	TTCTTCCACT	GCGCTGACGT	AACGGCGGAC	ATGAGCTTCC	750
	CGGAGGCGGA	GAAGCACCGC	GAGGAACTCA	ATAAGAAATT	CGGCCGCGGC	800
	CCCGAGGAGG	ACAAGAAAAA	GGAGGCGGAG	ATGAAGGAGT	TCGAGAGCAA	850
	GCTGGTCTGC	ATGCCAGGCG	ATAACCGCGA	GCTGATCCTG	ACATTGGCGT	900
60	ACCCGATGCC	TA				912

2) INFORMATION FOR SEQ ID NO: 853

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: MM3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 853

20	ATTCTTGTGG TGGCAGCTAA CGACGGATGC ATGCCGCAGA CGCGTGAGCA	50
	CCTGCTTATT TGTTTCGAGA TTGGCCTTCC TGCTCTTGTA TGCTTTATCA	100
	ATAAGTGTGA CATGATGCAA GGGCAGGAGG AAATGATTGA ACTTGTGAA	150
	ATGGAGGTAC GTGAACCTTT GGAGAAGTAC AAGTTCCTG CGGAGGAGAC	200
	GCCATTTGTG CGGGGTCTG CGGTGAAGGC ATTGGAGGGT GATGCTGAAA	250
25	ATGAAGGAAA GATTTTGGAG CTTGTAAAAA AATGTGATGA ATGGATTCCC	300
	GACCCACCGC GTGCCATTGA AAAACCGTTC CTTATGGCCA TTGAGCACGT	350
	TTTTGAGGTT GGAAAGGATA AGAAGGCCGT TGTGTGAGC GGGCGTGTGG	400
	ACCAGGGGCA GTTGAAGGTC GGCGCAGATG CAGAACTTTC CGGGTTTAGC	450
	GCAAAGAAGC TGACGGTGAA GGTGTGCTAGC ATCGAAATGT ACCATAAAAT	500
30	TCTGGAGGAT TGCATGCCTG GTGACTCTGT TGGCGCGAAG ATCGTTGGCA	550
	GCGGTGAAAC AGTGAACCTG TCGAAGGAAA ATGTGGAACG CGGCATGGTA	600
	CTCTCCGCAC CAGGTGCAAC GACACTGTTC AACAAAGGTCC GCGCGCAGGT	650
	GTACGTGTTG ACAAAGGAAG AAGGCGGTCG TCACACAGCC TTTAGTCCTC	700
	ACTATCGTCC GCAGCTTTTC TTCCACTGTG CTGATGTCAC GGCAGATATT	750
35	AACTTCCCGG AAAGCGAGAA GCTTGCAGGG GAGCTGAACA AAAAGTATGG	800
	CCGTGATGCG GCGGAACAGA AGAAGAAGGA GGCAGAACTG AAAGAGTTTG	850
	AAAAGACGCT TGTCTGCATG CCTGGTGATA ACCGCGAACT CCTGCTCACC	900
	CTTGCCCTATC CAATGCCAAT GGAAAAGGGA CTCAAG	936

40

2) INFORMATION FOR SEQ ID NO: 854

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854

	CGGCATTCTT GTGGTGGCAG CTAACGACGG ATGCATGCCG CAGACGCGTG	50
	AGCACCTGCT TATTTGTTTCG CAGATTGGCC TTCCTGCTCT TGTATGCTTT	100
60	ATCAATAAGT GTGACATGAT GCAAGGGCAG GAGGAAATGA TTGAGCTTGT	150

	TGAAATGGAG	GTACGTGAAC	TTTTGGAGAA	GTACAAGTTC	CCTGCGGAGG	200
	AGACGCCATT	TGTGCGGGGG	TCTGCGGTGA	AGGCATTGGA	GGGTGATGCT	250
	GAAAATGAAG	GAAAGATTTT	GGAGCTTGTA	AAAAAATGTG	ATGAATGGAT	300
	TCCCGACCCA	CCGCGTGCCA	TTGAAAAACC	GTTCTTATG	GCCATTGAGC	350
5	ACGTTTTTGA	GGTTGGAAAG	GATAAGAAGG	CCGTTGTTGT	GAGCGGGCGT	400
	GTGGACCAGG	GGCAGTTGAA	GGTCGGCGCA	GATGCAGAAC	TTTCCGGGTT	450
	TAGTGCAAAG	AAGCTGACGG	TGAAGGTTGC	TAGCATCGAA	ATGTACCATA	500
	AAATTCTGGA	GGATTGCATG	CCTGGTGAAT	CTATTGGCGC	GAAGATCGTT	550
	GGCAGCGGTG	AAACAGTGAA	CCTGTCGAAG	GAAAATGTGG	AACGCGGCAT	600
10	GGTACTCTCC	GCACCAGGTG	CAACGACACT	GTTCAACAGG	GTCCGCGCGC	650
	AGGTGTACGT	GTTGACAAAG	GAAGAAGGCG	GTCGTCACAC	AGCCTTTAGT	700
	CCTCACTATC	GTCCGCAGCT	TTTCTTCCAC	TGTGCTGATG	TCACGGCGGA	750
	TATTAAC TTC	CCGGAAAGCG	AGAAGCTTGC	AGGGGAGCTG	AACAAAAAGT	800
	ATGGCCGTGA	CGCGGCGGAA	CAGAAGAAGA	AGGAGGCAGA	ACTGAAAGAG	850
15	TTTGAAAAGA	CGCTTGTCTG	CATGCCTGGT	GATAACCGCG	AACTCCTGCT	900
	CACCCTTGCC	TATCCAATGC	CAATGGAAAA	GGGA		934

20 2) INFORMATION FOR SEQ ID NO: 855

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 937 bases
- (B) TYPE: Nucleic acid
- 25 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
- (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 855

35	TGGCGGCATT	CTTGTGGTGG	CAGCTAACGA	CGGATGCATG	CCGCAGACGC	50
	GTGAGCACCT	GCTTATTTGT	TCGCAGATTG	GCCTTCCTGC	TCTTGTATGC	100
	TTTATCAATA	AGTGTGACAT	GATGCAAGGG	CAGGAGGAAA	TGATTGAACT	150
	TGTTGAAATG	GAGGTACGTG	AACTTTTGGA	GAAGTACAAG	TTCCCTGCGG	200
40	AGGAGACGCC	ATTTGTGCGG	GGGTCTGCGG	TGAAGGCATT	GGAGGGTGAT	250
	GCTGAAAATG	AAGGAAAGAT	TTTGGAGCTT	GTAAAAAAAT	GTGATGAATG	300
	GATTCCCGAC	CCACCGCGTG	CCATTGAAAA	ACCGTTCCTT	ATGGCCATTG	350
	AGCACGTTTT	TGAGGTTGGA	AAGGATAAGA	AGGCCGTTGT	TGTGAGCGGG	400
	CGTGTGGACC	AGGGGCAGTT	GAAGGTCCGC	GCAGATGCAG	AACTTTCCGG	450
45	GTTTAGCGCA	AAGAAGCTGA	CGGTGAAGGT	TGCTAGCATC	GAAATGTACC	500
	ATAAAATTCT	GGAGGATTGC	ATGCCTGGTG	ACTCTGTTGG	CGCGAAGATC	550
	GTTGGCAGCG	GTGAAACAGT	GAACCTGTCT	AAGGAAAATG	TGGAACGCGG	600
	CATGGTACTC	TCCGCACCAG	GTGCAACGAC	ACTGTTCAAC	AAGGTCCGCG	650
	CGCAGGTGTA	CGTGTTGACA	AAGGAAGAAG	GCGGTCGTCA	CACAGCCTTT	700
50	AGTCCTCACT	ATCGTCCGCA	GCTTTTCTTC	CACTGTGCTG	ATGTCACGGC	750
	AGATATTAAC	TTCCCGGAAA	GCGAGAAGCT	TGCAGGGGAG	CTGAACAAAA	800
	AGTATGGCCG	TGATGCGGCG	GAACAGAAGA	AGAAGGAGGC	AGAACTGAAA	850
	GAGTTTGAAA	AGACGCTTGT	CTGCATGCCT	GGTGATAACC	GCGAACTCCT	900
55	GCTCACCTT	GCCTATCCAA	TGCCAATGGA	AAAGGGA		937

2) INFORMATION FOR SEQ ID NO: 856

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bigemina*
 (B) STRAIN: Suarez-2

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856

15	CTTATTATGG	AGCTGATCAA	CAACGTCGCG	AAGAAGCACG	GTGGTTTCTC	50
	CGTGTTTCGCC	GGCGTCGGCG	AGCGCACCAG	GGAGGGCAAC	GAGCTGTACC	100
	ACGAGATGAT	GGAGACCGGC	GTCATCAAGC	GCCGCCAGCT	GGATGACGGC	150
	ACGTTCGACT	TCTCCGGCTC	CAAGGCCGCG	CTGGTGTACG	GCCAGATGAA	200
	CGAGCCGCCA	GGTGCCAGGG	CGCGTGTTGC	CCTCACTGGC	CTGACGGTGG	250
	CCGAGTACTT	CCGTGATGAG	GACGGCCAGG	ACGTGCTGCT	CTTCATCGAC	300
20	AACATCTACC	GTTTCACCCA	GGCTGGTTCT	GAGGTGAGTG	CCCTTTTGGG	350
	GCGCATCCCG	TCCGCCGTCG	GTTACCAGCC	GACCCTCGCC	ACCGACCTTG	400
	GCGCGCTGCA	GGAGCGTATC	ACGACGACCA	ACAAGGGCTC	CATCACCTCC	450
	GTGCAGGCCG	TCTACGTGCC	GGCCGACGAT	ATCACCGACC	CGGCGCCTGC	500
	GACCACCTTC	ACCCATCTGG	ACGCGACCAC	TGTGCTCTCC	CGTTCCATCG	550
25	CCGAGCTGGG	TATCTACCCC	GCCGTCGACC	CGCTCGACTC	CACCTCGCGT	600
	ATGCTGTCCG	CGAACATCGT	CGGCGAGGAG	CAGTACAACG	TGGCGCGTGG	650
	CGTGCAGAAA	ATACTGCAGG	ACTACAAATC	GCTGCAGGAT	ATCATCGCCA	700
	TCCTGGGTAT	GGACGAGCTG	TCTGAGCAGG	ACAAGTTCGT	CGTCGCGCGT	750
	GCGCGCAAGG	TTCAGCGTTT	CCTATCCCAG	CCCTTCCAGG	TGGCTGAGGT	800
30	ATTCACCGGC	AAGCCCGGAC	GTTTCGTCGA	GCTGCAGGAC	ACCATCAGCG	850
	GCGTCAAGGA	GATTTTGGAC	GGCGAGTGCG	ACGACATG		888

35 2) INFORMATION FOR SEQ ID NO: 857

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857

50

50	TGATTATGGA	ATTGATCAAC	AATGTCGCCA	AGAAACACGG	TGGGTTCTCC	50
	GTGTTTCGCTG	GTGTTGGTGA	ACGTACGAGG	GAAGGTAACG	AACTGTACCA	100
	TGAAATGATG	GAAACGGGTG	TCATCAAGCG	CCGTCAACTG	GAAGACGGAA	150
	CATTTGACTT	CTCGGGCTCT	AAAGCTGCTT	TGGTGTACGG	ACAAATGAAC	200
55	GAACCACCAG	GTGCTAGAGC	CCGTGTTGCA	CTCACGGGAT	TGACCGTTGC	250
	CGAGTATTTT	CGTGATGAAG	AGGGGCAGGA	TGTGCTACTC	TTCATCGATA	300
	ACATCTACCG	TTTCACCCAG	GCCGGTTCCG	AAGTGAGTGC	GCTGTTAGGA	350
	AGAATTCCAT	CCGCCGTGGG	TTATCAACCT	ACATTGGCCA	CTGATCTCGG	400
	AGCACTCCAG	GAACGCATTA	CTACAACCAA	CAAGGGTTCG	ATTACATCAG	450
60	TCCAGGCAGT	ATACGTCCCA	GCCGATGATA	TCACTGATCC	CGCTCCAGCT	500

480

	ACCACTTTCT	CGCACTTGGA	TGCCACTACA	GTGCTTTCTC	GTTCAATTGC	550
	GGAGTTGGGT	ATTTACCCTG	CGGTCGACCC	GCTTGACTCA	ACGTCACGTA	600
	TGCTGTCGGC	CAACATTGTA	GGACAGGAAC	AGTACGATGC	CGCACGTGGT	650
	GTACAGAAAA	TTTTACAGGA	CTACAAATCA	CTGCAGGATA	TCATTGCCAT	700
5	TCTGGGTATG	GACGAGCTGT	CTGAGCAGGA	CAAGTTCGTT	GTAGCACGCG	750
	CCCGTAAGGT	ACAGCGTTTC	CTGTCTCAGC	CGTTCCAAGT	GGCTGAGGTG	800
	TTCACCGGCA	AGCCTGGGAG	GTTCTGTTGAA	CTACAGGATA	CCATCAGCGG	850
	TGTCAAGGAA	ATCTGGAAGG	TGAGTGTGAC	GATA		884

10

2) INFORMATION FOR SEQ ID NO: 858

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 871 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microtti*
 (B) STRAIN: Persing-1

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 858

	TGGAAGTATG	TAATAATGTG	GCCAAAAAGC	ATGGCGGTTA	CTCTGTTTTT	50
	GCAGGTGTAG	GTGAAAGGAC	GAGGGAGGGT	AATGAATTGT	ACCATGAAAT	100
30	GATGGAGACA	GGTGTTATAA	AGAAAAAGGC	ACTAGGTGGT	GGGAAGTTTG	150
	ATTTCAAGTG	ATCTAAAGCA	GCGCTGGTCT	ATGGACAAAT	GAACGAGCCA	200
	CCTGGGGGCC	GTGCTAGAGT	GGCACTAACT	GGATTAACAG	TCGCAGAATA	250
	TTTCCGTGAC	GAACAAGGAC	AAGACGTGTT	GTTGTTTATT	GATAATATTT	300
	ACCGATTTAC	TCAGGCAGGG	TCTGAGGTTT	CAGCCTTGCT	AGGCCGTATA	350
35	CCTTCAGCTG	TGGGATACCA	GCCTACATTG	GCAACAGATC	TTGGCTGTTT	400
	ACAAGAACGA	ATTACTACGA	CCAAATCTGG	TTCAATCACC	AGTGTACAAG	450
	CTGTGTATGT	GCCAGCAGAT	GATATTACTG	ATCCAGCGCC	TGCCACAAC	500
	TTTACTCACT	TGGACGCTAC	TACTGTACTT	AGCAGGCCAA	TTGCTGAACT	550
	CGGTATTTAT	CCAGCGGTAG	ACCCGTTGGA	TTCAACAAGC	CGTATGCTAA	600
40	GCGCGAACAT	TGTGGGAAAT	GAACACTATA	GTGTAGCCCG	TTCCGTGCAG	650
	AAGATACTGC	AAGATTACAA	ATCGCTTCAG	GACATTATTG	CCATTTTGGG	700
	TATGGATGAA	CTGTCGGAAC	AAGACAAAAA	TATAGTAGCC	CGAGCAAGGA	750
	AGATGCAAAG	GTTCTTATCA	CAGCCATTCC	AAGTGGCGGA	AGTTTTTACT	800
	GGTAAACCGG	GAAGATTTGT	GGAATTGGAA	GATACAATTG	CCGGGGCACG	850
45	AGATATAATT	GCGGGTAATT	G			871

2) INFORMATION FOR SEQ ID NO: 859

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Leishmania guyanensis*

(B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859

5	TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
	CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
	GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCGGCG	150
	GCAACATCTC	CGTGCCGGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
	GTGCTGGGCG	ACGCGATTGA	CCACCGCGGC	CCCGTGTGCG	AGAAGATGCG	250
10	CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
	ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
	TGCAAGGGCG	GCAAGATCGG	CCTGTTCCGG	GGTGCCGGTG	TGGGCAAGAC	400
	TGTGATCATC	ATGGAGCTGA	TCAACAACGT	CGCGAAGGGG	CACGGCGGCT	450
	TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
15	TACCTGGAGA	TGATGCAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
	GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
	GCGTTGCGCA	GTCTGCGCTG	ACGATGGCCG	AGTACTTCCG	CGACGTGGAG	650
	GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
	GAACTCCGAG	GTGTCTGCGC	TGCTGGGCCG	CATCCCGGCC	GCCGTGGGTT	750
20	ACCAGCCGAC	GCTTGCGGAG	GATCTTGGCA	TGCTGCAGGA	GCGCATTACG	800
	TCGACGACGA	AGGGATCGAT	TACGTCTGTG	CAGGCTGTGT	ACGTGCCTGC	850
	GGATGATATC	ACGGACCCCG	CGCCCGCGAC	GACGTTCTCG	CACCTGGACG	900
	CGACGACTGT	GCTGGACCGC	GCGGTGGCGG	AGTCGGGCAT	CTACCCTGCC	950
	GTGAACCCGC	TGGAGTGCGC	GTCGCGCATC	ATGGACCCCG	ATGTGATCGA	1000
25	CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCAAGT	1050
	ACAAGGAGCT	GCAGGACATC	ATTGCGGTGC	TTGGCATCGA	CGAGCTGAGC	1100
	GAGGAGGACA	AGGTCGTGGT	GGACCGCGCG	CGCAAGGTGA	CGCGGTTCTT	1150
	GTCGCGACCG	TTCCAGGTTG	CGGAGGTGTT	CACCGGCATG	ACGGGCCACT	1200
	ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
30	TCGTA					1255

2) INFORMATION FOR SEQ ID NO: 860

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1222 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Leishmania mexicana*

(B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860

50	CTCGGAGGGC	GTCCCGCCCG	TGCTGACGGC	GCTGGATGTG	ACGGAGGACC	50
	TTGGCCGCGA	TGAGCCGCTG	ACGCTGGAGA	TCGTGCAGCA	CCTGGACGCG	100
	AACACCGGCC	GCTGCATTGC	GATGCAGACG	ACGGACCTGC	TGAAGCTGAA	150
	GTCGAAGGTT	GTGTCGACCG	GCGGCAACAT	CTCTGTGCCG	GTGGGCCGTG	200
	AGACGCTGGG	CCGCATCTTC	AACGTGCTGG	GCGACGCGAT	CGACCAGCGC	250
55	GGCCCCGTGG	GTGAGAAGAT	GCGCATGGCG	ATCCACGCCG	AGGCCCCGAA	300
	GCTGGCGGAT	CAGGCCGCGG	AGGACACGAT	CCTGACGACC	GGCATCAAGG	350
	TGATCGACCT	GATTCTGCCC	TACTGCAAGG	GTGGCAAGAT	CGGCCTGTTT	400
	GGCGGCGCCG	GTGTGGGCAA	GACCGTGATC	ATCATGGAGC	TGATTAACAA	450
	CGTCGCGAAG	GGCCACGGTG	GTTTCTCGGT	GTTTGCCGGC	GTTGGCGAGC	500
60	GCACGCGCGA	GGGCACGGAC	CTGTACCTGG	AGATGATGCA	GTCGAAGGTG	550

	ATTGACCTGA	AGGGCGAGTC	GAAGTGCGTG	CTTGTGTACG	GGCAGATGAA	600
	CGAGCCCCCG	GGTGCGCGCG	CGCGCGTTGC	GCAGTCTGCG	CTGACGATGG	650
	CGGAGTACTT	CCGAGACGTG	GAGGGCCAGA	ATGTGCTGCT	GTTTCATCGAC	700
	AACATCTTCC	GCTTCACGCA	GGCGAACTCC	GAGGTCTCTG	CGCTGCTGGG	750
5	CCGCATTCCG	GCCGCCGTGG	GCTACCAGCC	GACGCTTGCG	GAGGATCTTG	800
	GTATGCTGCA	GGAGCGCATC	ACGTCGACGA	CGAAGGGGTC	GATCACGTCC	850
	GTGCAGGCCG	TGTACGTGCC	TGCGGATGAT	ATCACGGATC	CGGCGCCCCG	900
	GACGACGTTT	TCGCACCTGG	ACGCGACGAC	TGTGCTGGAC	CGCGCGGTGG	950
	CGGAGTCGGG	GATCTACCCT	GCCGTGAACC	CGCTGGAGTG	CGCGTCGCGT	1000
10	ATCATGGACC	CCGATGTGAT	CGACGTGGAC	CACTACAACG	TTGCGCAGGA	1050
	TATCGTGCAG	ATGCTGACCA	AGTACAAGGA	GCTGCAGGAT	ATCATTGCGG	1100
	TGCTTGGTAT	CGACGAGCTG	AGCGAGGAGG	ACAAGGTCGT	GGTGGACCGC	1150
	GCGCGCAAGG	TGACCCGGTT	CCTGTCGCAG	CCGTTCCAGG	TTGCGGAGGT	1200
	GTTCACGGGC	ATGACGGGCC	AC			1222
15						

2) INFORMATION FOR SEQ ID NO: 861

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861

	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	ACCTTGGCCG	CGATGAGCCG	50
35	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	GCGAACACCG	GCCGCTGCAT	100
	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	GAAGTCGAAG	GTTGTGTCTGA	150
	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	GTGAGACGCT	GGGCCGCATC	200
	TTCAACGTTC	TGGGCGACGC	GATCGACCAG	CGCGGCCCCG	TGGGCGAGAA	250
	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	GAAGCTGGCG	GATCAGGCCG	300
40	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	AGGTGATCGA	CCTGATTCTG	350
	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	TTCGGCGGTG	CCGGTGTGGG	400
	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	CAACGTCGCG	AAGGGCCACG	450
	GTGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	AGCGCACGCG	CGAGGGCACG	500
	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	GTGATTGACC	TGAAGGGCGA	550
45	GTCGAAGTGC	GTGCTTGTGT	ACGGGCAGAT	GAACGAGCCC	CCGGGTGCGC	600
	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	TGGCGGAGTA	CTTCCGCGAC	650
	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	GACAACATCT	TCCGCTTCAC	700
	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	GGGCCGCATT	CCGGCCGCCG	750
	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	GCAGGAGCGC	800
50	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	TCCGTGCAGG	CCGTGTACGT	850
	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	CGCGACGACG	TTCTCGCACC	900
	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	GGGCATCTAC	950
	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	ACCCCGATGT	1000
	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	CAGATGCTGA	1050
55	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	CATCGACGAG	1100
	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	AGGTGACCCG	1150
	GTTCTGTGCG	CAGCCGTTCC	AGGTTGCGGA	GGTGTTACAG	GGCATGACGG	1200
	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	TGGCCT	1246

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2) INFORMATION FOR SEQ ID NO: 862

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 1265 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 30815

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862

	GGCGTGCCGC	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	ACCTTGGCCG	50
	CGATGAGCCG	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	GCGAACACGG	100
20	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	GAAGTCGAAG	150
	GTCGTGTCGA	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	GTGAGACGCT	200
	GGGCCGCATC	TTCAAYGTTC	TGGGCGACGC	GATCGACCAG	CGCGGCCCCG	250
	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	GAAGCTGGCG	300
	GATCAGGCCG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	AGGTGATCGA	350
25	CCTGATTCTG	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	TTCGGCGGGT	400
	CCGGTGTGGG	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	CAACGTCGCG	450
	AAGGGCCACG	GCGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	AGCGCACGCG	500
	CGAGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	GTGATTGACC	550
	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	GAACGAGCCC	600
30	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	TGGCGGAGTA	650
	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATC	GACAAATCT	700
	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	GGGCCGCATT	750
	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	800
	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	TCCGTGCAGG	850
35	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	CGCGACGACG	900
	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	950
	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	1000
	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	1050
	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	1100
40	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	1150
	AGGTGACCCG	GTTCTGTGCG	CAGCCGTTCC	AGGTTGCGGA	GGTGTTACG	1200
	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	1250
	TGGCCTGCTG	ATGGG				1265

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2) INFORMATION FOR SEQ ID NO: 863

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1191 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bordetella pertussis*

- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863

	ATGGCAAAAG	GCAAGTTTGA	ACGTACCAAG	CCGCACGTGA	ACGTGGGTAC	50
	GATTGGTCAC	GTTGACCACG	GCAAAACGAC	GTTGACGGCG	GCGATCACGA	100
	CGGTGCTGTC	GAACAAGTTC	GGCGGCGAGG	CTCGCGGCTA	CGACCAGATT	150
5	GACGCGGCGC	CGGAAGAGAA	GGCGCGTGGG	ATCACGATCA	ACACCTCGCA	200
	CGTTGAGTAC	GAGACGGAGA	CGCGTCACTA	CGCGCACGTT	GATTGCCCCG	250
	GTCACGCTGA	CTACGTGAAG	AACATGATCA	CGGGTGCTGC	GCAGATGGAC	300
	GGCGCGATCC	TGGTGGTGTC	GGCCGCAGAC	GGCCCGATGC	CGCAGACGCG	350
	CGAGCACATT	TTGCTGTCTC	GCCAGGTTGG	CGTGCCGTAC	ATCATCGTGT	400
10	TCCTGAACAA	GGCGGACATG	GTTGATGACG	CGGAGCTGCT	CGAGCTGGTG	450
	GAGATGGAAG	TCCGCGAACT	GCTGAGCAAG	TACGATTTC	CGGGCGATGA	500
	CACGCCGATC	GTGAATGGTG	CGGCCAAGCT	GGCGCTGGAA	AGCGACAACG	550
	GCGACCTGGG	CGAGCAGGCG	ATTCTGTCTC	TGGCGCAAGC	GCTGGACACG	600
	TACATTCCGA	CGCCGGAGCG	CGCGGTCTGAC	GGTGCGTTCC	TGATGCCGGT	650
15	GGAAGACGTG	TTCTCGATCT	CGGGCCGTGG	CACGGTGGTG	ACTGGCCGTA	700
	TCGAGCGCGG	CGTGGTGAAG	GTTGGCGAGG	AAATCGAAAT	CGTGGGCATC	750
	AAGCCGACGG	TGAAGACGAC	CTGCACGGGC	GTGGAGATGT	TCCGCAAGCT	800
	GCTGGACCAG	GGCCAGGCGG	GCGACAACGT	GGGTATCTTG	CTGCGCGGCA	850
	CCAAGCGTGA	AGACGTCTGAG	CGTGGCCAGG	TGCTGGCCAA	GCCGGGTTCT	900
20	ATCAACCCGC	ACACGGACTT	CACGGCCGAG	GTGTACATTC	TGTCCAAGGA	950
	AGAGGGTGGC	CGTCACACGC	CGTTCTTCAA	CGGCTATCGT	CCGCAGTTCT	1000
	ACTTCCGCAC	GACGGACGTG	ACCGGCACGA	TCGACCTGCC	GGCGGACAAG	1050
	GAAATGGTGC	TGCCGGGCGA	CAACGTGTCG	ATGACCGTCA	AGCTGCTGGC	1100
	CCCGATCGCC	ATGGAAGAAG	GTCTGCGTTT	CGCCATCCGT	GAAGGCGGTC	1150
25	GTACCGTCGG	TGCCGGCGTC	GTCGCCAAGA	TCATCAAGTA	A	1191

2) INFORMATION FOR SEQ ID NO: 864

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Trypanosoma brucei*
 (B) STRAIN: LVH/75/USAMRU-K/18
 (C) ACCESSION NUMBER: extracted from U10562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864

45

	ATGGGAAAGG	AAAAGGTGCA	CATGAATCTT	GTGGTGGTGG	GCCACGTCGA	50
	TGCCGGTAAA	TCCACTGCAA	CGGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
	TTGACAAACG	TACGATCGAG	AAGTTCGAGA	AAGAAGCTGC	CGACATTGGT	150
	AAGGCCTCAT	TCAAGTACGC	ATGGGTGCTG	GACAAGCTGA	AGGCTGAGCG	200
50	CGAACGTGGT	ATCACGATCG	ACATTGCACT	GTGGAAATTC	GAGTCACCCA	250
	AGTCTGTCTT	CACTATTATT	GATGCTCCTG	GGCACCCTGA	CTTCATCAAG	300
	AACATGATCA	CCGGCACATC	GCAAGCCGAC	GCAGCCATCC	TCATCATTGC	350
	CTCTGCGCAG	GGTGAGTTCT	AGGCTGGTAT	CTCCAAGGAT	GGACAGACCC	400
	GCGAGCACGC	GTTGCTGGCC	TTCACCTTGG	GTGTGAAGCA	GATGGTTGTG	450
55	TGCTGCAACA	AAATGGACGA	CAAGACTGTG	AACTACGGAC	AGGAGCGGTA	500
	TGACGAGATT	GTGAAGGAGG	TGTCTGCTTA	CATCAAGAAG	GTTGGGTACA	550
	ACGTGGAGAA	GGTGCGCTTC	GTCCCCATCT	CCGGATGGCA	GGGCGACAAC	600
	ATGATTGAGA	AATCCGAGAA	GATGCCATGG	TACAAGGGTC	CAACGCTCCT	650
	GGAGGCACTA	GACATGCTGG	AGCCACCAGT	GCGTCCGAGC	GACAAGCCCC	700
60	TGCGTCTGCC	ACTGCAGACG	TGTACAAAGA	TCGGTGGTAT	TGGCACCGTG	750

	CCCGTTGGTC	GTGTGGAGAC	CGGCGTGATG	AAGCCTGGTG	ATGTGGTGAC	800
	GTTTGCCCCC	GCCAACGTGA	CGACCGAGGT	GAAATCGATC	GAGATGCACC	850
	ACGAGCAGCT	CGCTGAGGCG	ACCCCCGGTG	ACAACGTCGG	CTTTAACGTG	900
	AAGAACGTTT	CTGTAAAGGA	CATCCGCCGT	GGCAACGTCT	GCGGTAACAC	950
5	CAAGAACGAC	CCCCCAAAGG	AGGCCGCCGA	CTTCACGGCA	CAGGTGATCA	1000
	TCCTGAACCA	CCCCGGACAG	ATTGGAAACG	GTTATGCGCC	CGTGCTGGAC	1050
	TGCCACACAT	CGCACATTGC	CTGCAAGTTC	GCGGAGATCG	AGTCGAAGAT	1100
	CGACCGTCGC	TCTGGCAAGG	AGCTGGAGAA	GGCTCCCAAG	TCGATCAAGT	1150
	CTGGCGACGC	CGCGATCGTG	CGCATGGTGC	CGCAGAAGCC	TATGTGCGTG	1200
10	GAGGTCTTCA	ACGACTACGC	GCCACTCGGC	CGCTTTGCCG	TGCGTGACAT	1250
	GCGCCAGACC	GTCGCTGTCG	GTATCATCAA	GGCCGTGACC	AAGAAGGACG	1300
	GTTCTGGTGG	TAAGGTGACG	AAGGCTGCGG	TGAAGGCTTC	GAAGAAATAA	1350

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2) INFORMATION FOR SEQ ID NO: 865

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865

30

	AAGCTCAAGG	CTGAGAGAGA	AAGAGGTATT	ACCATCGATA	TTGCTTTATG	50
	GCAATTCGAA	ACCCCAAAT	ACCACTACAC	TGTCATTGAT	GCCCCAGGTC	100
	ACAGAGATTT	CATCAAGAAT	ATGATTACTG	GTACCTCTCA	AGCTGATGTT	150
	GCTTTATTGG	TTGTCCCAGC	CGATCGTTTC	GAAGGTGCCT	TCTCCAAGGA	200
35	AGGTCAAACC	AGAGAACATG	CTTTATTGGC	CTTCACTTTG	GGTGTCAGAC	250
	AAATGATTGT	CGGTATTAAC	AAGATGGATA	CCTGTGAATA	CAAGCAATCT	300
	CGTTTTGATG	AAATCTTCAA	CGAAGTTGAT	GGTTACCTCA	AGAAGGTTGG	350
	TTACAACACC	GAGAAGATCC	CATTCGTTGC	CATTTCTGGT	TTCGTTGGTG	400
	ATAATATGGT	TGAGAGATCT	GACAAGATGC	CATGGTATAA	GGGTAAGACC	450
40	TTAGTCGAAG	CCCTCGACAC	TATGGAACCA	CCAAAGAGAC	CAACTGACAA	500
	GCCACTCCGT	CTCCCATTAC	AAGATGTTTA	CAAGATAGGT	GGTGTAGGTA	550
	CTGTCCCAGT	CGGTCGTGTT	GAGACTGGTA	TCATCAGACC	AGGTATGAAT	600
	GTTACCTTCG	CTCCAGCTGG	TGTTACCACT	GAAGTTAAGT	CAGTAGAAAT	650
	GCACCATGAG	CAGATGCCAG	AGGCCGTCCC	AGGTGACAAC	GTTGGTTTCA	700
45	ATGTTAAGAA	CGTCTCCATC	AAGGATATCA	AGAGAGGTTT	CGTTGCTTCT	750
	GATGCCAAGA	ATGACCCAGC	TAAGGGCTGT	GAAGACTTCA	CTGCTCAAGT	800
	TATCGTCCTC	AACCACCCAG	GTGAAATCAA	GAACGGTTAC	TCTCCAGTCG	850
	TTGACTGTCA	CACCGCTCAC	ATTTCCTGCA	AATTCCAGAC	TATCACTGCT	900
	AAGATGGACA	AGAGATCTGG	TAAGGTTTTG	GAAGAAAACC	CAAAGCTTAT	950
50	CAAGTCTGGT	GATGCTGCTT	TGGTTGTTAT	GCAACCTTTG	AAGCCACTTT	1000
	GTGTTGAGGC	CTTCACTGAC	TACCCACCTC	TAGGTCGTTT	CGCTGTCCGT	1050
	GA					1052

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2) INFORMATION FOR SEQ ID NO: 866

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 35552

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
15	TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCA	GTTGGTGATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTTCGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
20	TTCGGTGGCG	CTGGTGTAGG	TAAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
25	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

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2) INFORMATION FOR SEQ ID NO: 867

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Zoogloea ramigera*
(B) STRAIN: ATCC 25935

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867

	AAGGTATTCTG	ATGCCTTGAA	AATGGAAGGC	TCCGAGCTGA	CCCTGGAAGT	50
	ACAACAGCAG	CTGGGCGACG	GCATTGTCCG	TACCATTGCA	CTGGGTACCT	100
50	CCGACGGCCT	GCGTCGCGGC	ATGATGATCC	AGAACACCGG	CAAACCTATC	150
	ATGGTGCCAG	TCGGTAAAGC	AACCCTGGGT	CGCATCATGG	ACGTGCTGGG	200
	TAACCCGATC	GACGAATGCG	GCGCGGTGCG	TCACGACCAG	ATCGCTTCGA	250
	TCCACCGCGC	TCCTCCTGCG	TACGACGAAC	TGTCGCCATC	GCAAGATCTG	300
	CTGGAAACCG	GCATTAAAGT	TATTGACCTG	GTGTGCCCGT	TCGCCAAGGG	350
55	CGGTAAAGTC	GGTCTGTTCG	GCGGTGCAGG	TGTGGGCAAG	ACCGTGAACA	400
	TGATGGAACT	GATCAACAAC	ATCGCCAAAG	CACACTCGGG	TCTGTCCGTG	450
	TTTGCCGGTG	TGGGTGAGCG	TACCCGTGAA	GGTAACGACT	TCTACCACGA	500
	GATGGCTGAC	GCCAAAGTGG	TCGATCTGGA	AAATCCAGAG	AACTCCAAGG	550
	TTGCGATGGT	CTACGGTCAG	ATGAATGAAC	CACCAGGCAA	CCGTCTGCGC	600
60	GTGGCGCTGA	CCGGTCTGAC	CATGGCTGAA	GCATTCCGTG	ACGAAGGCAA	650

AGACGTTCTG	TTCTTCGTGG	ACAACATCTA	C C G C T T C A C C	CTGG C C C G G T A	700
CCGAAGTATC	GGCACTGCTG	GGCCGTATGC	CATCGGCTGT	GGGTTACCAG	750
CCTACGCTGG	CCGAAGAAAT	GGGTCGCCTG	CAAGAGCGCA	TCACTTCGAC	800
CAAGACCGGT	TCGATCAC				818

5

2) INFORMATION FOR SEQ ID NO: 868

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 20 (B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868

CTATCTTAGT	AGTATCTGCT	GCTGATGGCC	CAATGCCACA	AACTCGTGAA	50
25 CACATTCTTT	TATCACGTAA	CGTTGGTGTT	CCAGCATTAG	TTGTATTCTT	100
AAACAAAGTT	GACATGGTTG	ACGATGAAGA	ATTATTAGAA	TTAGTAGAAA	150
TGGAAGTTCG	TGACTTATTA	AGCGAATATG	ACTTCCCAGG	TGACGATGTA	200
CCTGTAATCT	CTGGTTCTGC	ATTAAAAGCT	TTAGAAGGCG	ACGCTGACTA	250
TGAGCAAAAA	ATCTTAGACT	TAATGCAAGC	TGTTGATGAC	TTCATTCCAA	300
30 CACCAGAACG	TGATTCTGAC	AAACCATTCA	TGATGCCAGT	TGAGGACGTA	350
TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	ACAGGCCGTG	TTGAACGTGG	400
TCAAATCAAA	GTCGGTGAAG	AAATCGAAAT	CATCGGTATG	CAAGAAGAAT	450
CAAGCAAAAC	AACTGTTACT	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	500
TACGCTGAAG	CTGGTGACAA	CATTGGTGCA	TTATTACGTG	GTGTTTCACG	550
35 TGATGACGTA	CAACGTGGTC	AAGTTTTAGC	TGCTCCTGGT	ACTATTACAC	600
CACATACAAA	ATTCAAAGCG	GATGTTTACG	TTTTATCTAA	AGATGAAGGT	650
GGTCGTCATA	CACCATTCTT	CACTAACTAC	CGCCCACAAT	TCTATTTCCG	700
TACTACTGAC	GTAAGTGGTG	TTGTTAACTT	ACCAGAAGGT	ACTGAAATGG	750
40 TTATGCCTGG	CGATAACGTT	GAAATGGA			778

2) INFORMATION FOR SEQ ID NO: 869

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 55 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869

TGGTCCTATG	CCTCAAACAC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
60 GTGTACCATA	CATCGTTGTT	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	100

	GAAGAATTAC	TAGAATTAGT	TGAAATGGAA	GTTCGTGACT	TATTGTGAGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGCGATGCT	TCATACGAAG	AAAAAATCAT	GGAATTAATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	300
5	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	400
	GAAATCGTTG	GTATTGCTGA	AGAAACTGCT	AAAACAACCTG	TAACTGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGTGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
10	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	600
	TTACGTTTTA	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA		640

15 2) INFORMATION FOR SEQ ID NO: 870

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 644 bases

(B) TYPE: Nucleic acid

20 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R754

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870

30	GTCCTATGCC	TCAAACACGT	GAACACATCT	TGTTATCACG	TAACGTTGGT	50
	GTACCATACA	TCGTTGTTTT	CTTAAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTACTA	GAATTAGTTG	AAATGGAAGT	TCGTGACTTA	TTGTCAGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCTGGTTC	TGCTTTGAAA	200
35	GCTCTTGAAG	GCGATGCTTC	ATACGAAGAA	AAAATCATGG	AATTAATGGC	250
	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGACACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ACGAAGTTGA	400
	AATCGTTGGT	ATTGCTGAAG	AAACTGCTAA	AACAACCTGTA	ACTGGTGTG	450
40	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
	GCATTGCTAC	GTGGTGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTTAAA	GCTGAAGTTT	600
	ACGTTTTAAC	AAAAGAAGAA	GGTGGACGTC	ACACACCATT	CTTC	644

45

2) INFORMATION FOR SEQ ID NO: 871

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 637 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

(B) STRAIN: R758

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871

	TCCTATGCCT	CAAACACGTG	AACACATCTT	GTTATCACGT	AACGTTGGTG	50
	TACCATACAT	CGTTGTTTTT	TTAAACAAAA	TGGATATGGT	TGATGACGAA	100
5	GAATTACTAG	AATTAGTTGA	AATGGAAGTT	CGTGACTTAT	TGTCAGAATA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCTGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	CGATGCTTCA	TACGAAGAAA	AAATCATGGA	ATTAATGGCT	250
	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGACACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
10	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	CGAAGTTGAA	400
	ATCGTTGGTA	TTGCTGAAGA	AACTGCTAAA	ACAACGTGTA	CTGGTGTGTA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTA	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTTAAAG	CTGAAGTTTA	600
15	CGTTTTAACA	AAAGAAGAAG	GTGGACGTCA	CACTCCA		637

2) INFORMATION FOR SEQ ID NO: 872

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872

35	GTCCTATGCC	TCAAACCTCGT	GAACACATCT	TGTTATCACG	TAACGTTGGC	50
	GTACCATACA	TCGTTGTTTT	CTTGAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTGCTA	GAATTAGTTG	AAATGGAAGT	TCGTGACCTA	TTGTCTGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCCGGTTC	TGCTTTGAAA	200
	GCTCTTGAAG	GAGATCCTTC	ATACGAAGAA	AAAATCATGG	AATTGATGGC	250
40	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGATACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ATGAAGTAGA	400
	AATCGTTGGT	ATTGCTGACG	AAACTGCTAA	AACAACGTGA	ACAGGTGTTG	450
	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
45	GCATTGCTAC	GTGGGGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTCAAA	GCTGAAGTTT	600
	ATGTTTTGAC	AAAAGAAGAA	GGTGGACGTC	ACACTCCATT	CTT	643

50

2) INFORMATION FOR SEQ ID NO: 873

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873

	GTCCTATGCC	TCAAACCTCGT	GAACACATCT	TGTTATCACG	TAACGTTGGC	50
	GTACCATAACA	TCGTTGTTTT	CTTGAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTGCTA	GAATTAGTTG	AAATGGAAGT	TCGTGACCTA	TTGTCTGAAT	150
10	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCCGGTTC	TGCTTTGAAA	200
	GCTCTTGAAG	GAGATCCTTC	ATACGAAGAA	AAAATCATGG	AATTGATGGC	250
	TGCAGTTGAC	GAATACGTTC	CAACTCCAGA	ACGTGATACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ATGAAGTAGA	400
15	AATCGTTGGT	ATTGCTGACG	AAACTGCTAA	AACAACTGTA	ACAGGTGTTG	450
	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
	GCATTGCTAC	GTGGGGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTCAAA	GCTGAAGTTT	600
20	ATGTTTTGAC	AAAAGAAGAA	GGTGGACGTC	ACACTCCATT	C	641

2) INFORMATION FOR SEQ ID NO: 874

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 35 (B) STRAIN: LSPQ 2514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874

	ACCAGCATT	GTAGTATTCT	TAAATAAAGT	TGACATGGTT	GACGATGAAG	50
40	AATTATTAGA	ATTAGTTGAA	ATGGAAGTAC	GTGACTTATT	ATCTGAATAC	100
	GACTTCCCAG	GTGACGATGT	ACCTGTAATC	GCTGGTTCAG	CATTAAAAGC	150
	TTTAGAAGGC	GATGCTCAAT	ACGAAGAAAA	AATCTTAGAA	TTAATGCAAG	200
	CAGTTGATGA	CTACATTCCA	ACTCCAGAAC	GTGATTCTGA	CAAACCATTC	250
	ATGATGCCAG	TTGAGGACGT	ATTCTCAATC	ACTGGTCGTG	GTACTGTTGC	300
45	TACAGGCCGT	GTTGAACGTG	GGCAAATCAA	AGTTGGTGAA	GAAGTTGAAA	350
	TCATTGGTAT	CCATGACACT	TCTAAAACAA	CTGTTACTGG	TGTAGAAATG	400
	TTCCGTAAAT	TATTAGACTA	CGCTGAAGCT	GGTGACAACA	TCGGTGCAAT	450
	ATTACGTGGT	GTTGCTCGTG	AAGACGTACA	ACGTGGTCAA	GTATTAGCTG	500
	CTCCAGGTTC	AATCACACCT	CACACAAAAT	TTAAAGCAGA	CGTATACGTT	550
50	TTATCTAAAG	ACGAAGGTGG	ACGTCACACT	CCATTCTTCA	CAAACATATCG	600
	TCCACAATTC	TATTTCCGTA	CTACTGACGT	AACTGGTGTT	GTTAACTTAC	650
	CAGAAGGTAC	TGAAATGGTT	ATGCCTGGCG	A		681

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2) INFORMATION FOR SEQ ID NO: 875

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 bases
 60 (B) TYPE: Nucleic acid

491

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: R591

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875

	ATTATCACGT	AACGTTGGTG	TACCAGCATT	AGTTGTATTC	TTAAACAAAG	50
	TTGACATGGT	AGACGACGAA	GAATTATTAG	AATTAGTTGA	AATGGAAGTT	100
	CGTGACTTAT	TAAGCGAATA	TGACTTCCCA	GGTGACGATG	TACCTGTAAT	150
15	CGCTGGTTCT	GCATTAAAAG	CATTAGAAGG	CGATGCTGAA	TACGAACAAA	200
	AAATCTTAGA	CTTAATGCAA	GCAGTTGATG	ATTACATTCC	AACTCCAGAA	250
	CGTGATTCTG	ACAAACCATT	CATGATGCCA	GTTGAGGACG	TATTCTCAAT	300
	CACTGGTCGT	GGTACTGTTG	CTACAGGCCG	TGTTGAACGT	GGTCAAATCA	350
	AAGTTGGTGA	AGAAGTTGAA	ATCATCGGTA	TGCACGAAAC	TTCTAAAACA	400
20	ACTGTTACTG	GTGTAGAAAT	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	450
	TGGTGACAAC	ATCGGTGCTT	TATTACGTGG	TGTTGCACGT	GAAGACGTAC	500
	AACGTGGTCA	AGTATTAGCT	GCTCCTGGTT	CTATTACACC	ACACACAAAA	550
	TTCAAAGCTG	AAGTATACGT	ATTATCTAAA	GATGAAGGTG	GACGTCACAC	600
	TCCATTCTTC	ACTAACTATC	GCCCACAATT	CTATTTCCGT	ACTACTGACG	650
25	TAAGTGGTGT	TGTAAACTTA	CCAGA			675

2) INFORMATION FOR SEQ ID NO: 876

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: CSG 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876

45	TCTTATTATC	ACGTAACGTT	GGTGTACCAG	CATTAGTTGT	ATTCTTAAAC	50
	AAAGTTGACA	TGGTAGACGA	CGAAGAATTA	TTAGAATTAG	TTGAAATGGA	100
	AGTTCGTGAC	TTATTAAGCG	AATATGACTT	CCCAGGTGAC	GATGTACCTG	150
	TAATCGCTGG	TTCTGCATTA	AAAGCATTAG	AAGGCGATGC	TGAATACGAA	200
	CAAAAAATCT	TAGACTTAAT	GCAAGCAGTT	GATGATTACA	TTCCAACCTC	250
50	AGAACGTGAT	TCTGACAAAC	CATTCATGAT	GCCAGTTGAG	GACGTATTCT	300
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	350
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCATC	GGTATGCACG	AAACTTCTAA	400
	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	450
	AAGCTGGTGA	CAACATCGGT	GCTTTATTAC	GTGGTGTGTC	ACGTGAAGAC	500
55	GTACAACGTG	GTCAAGTATT	AGCTGCTCCT	GGTTCTATTA	CACCACACAC	550
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	TAAAGATGAA	GGTGGACGTC	600
	ACACTCCATT	CTTCACTAAC	TATCGCCCAC	AATTCTATTT	CCGTACTACT	650
	GACGTAACTG	GTGTTGTAAA	CTTACCAGAA	GGTACAGAAA	TGGTTATGCC	700
	TGGC					704

60

2) INFORMATION FOR SEQ ID NO: 877

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 770 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 15 (B) STRAIN: ATCC 35984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877

	TCTTAGTTGT	ATCTGCTGCT	GACGGTCCAA	TGCCACAAAC	TCGTGAACAC	50
20	ATCTTATTAT	CACGTAACGT	TGGTGTACCA	GCATTAGTTG	TATTCTTAAA	100
	CAAAGTTGAC	ATGGTAGACG	ACGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTTCGTGA	CTTATTAAGC	GAATATGACT	TCCCAGGTGA	CGATGTACCT	200
	GTAATCGCTG	GTTCTGCATT	AAAAGCATT	GAAGGCGATG	CTGAATACGA	250
	ACAAAAAATC	TTAGACTTAA	TGCAAGCAGT	TGATGATTAC	ATTCCAACCTC	300
25	CAGAACGTGA	TTCTGACAAA	CCATTCATGA	TGCCAGTTGA	GGACGTATTC	350
	TCAATCACTG	GTCGTGGTAC	TGTTGCTACA	GGCCGTGTTG	AACGTGGTCA	400
	AATCAAAGTT	GGTGAAGAAG	TTGAAATCAT	CGGTATGCAC	GAAACTTCTA	450
	AAACAACCTGT	TACTGGTGTA	GAAATGTTCC	GTAAATTATT	AGACTACGCT	500
	GAAGCTGGTG	ACAACATCGG	TGCTTTATTA	CGTGGTGTTG	CACGTGAAGA	550
30	CGTACAACGT	GGTCAAGTAT	TAGCTGCTCC	TGGTTCTATT	ACACCACACA	600
	CAAAATTCAA	AGCTGAAGTA	TACGTATTAT	CTAAAGATGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCACTAA	CTATCGCCCA	CAATTCTATT	TCCGTACTAC	700
	TGACGTAAC	GGTGTTGTAA	ACTTACCAGA	AGGTACAGAA	ATGGTTATGC	750
	CTGGCGACAA	CGTTGAAATG				770

35

2) INFORMATION FOR SEQ ID NO: 878

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 716 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 50 (B) STRAIN: ATCC 35983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878

	TTGTATTCTT	AAACAAAGTT	GACATGGTAG	ACGACGAAGA	ATTATTAGAA	50
55	TTAGTTGAAA	TGGAAGTTCG	TGACTTATTA	AGCGAATATG	ACTTCCCAGG	100
	TGACGATGTA	CCTGTAATCG	CTGGTTCTGC	ATTAAAAGCA	TTAGAAGGCG	150
	ATGCTGAATA	CGAACAAAAA	ATCTTAGACT	TAATGCAAGC	AGTTGATGAT	200
	TACATTCCAA	CTCCAGAACG	TGATTCTGAC	AAACCATTCA	TGATGCCAGT	250
	TGAGGACGTA	TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	ACAGGCCGTG	300
60	TTGAACGTGG	TCAAATCAAA	GTTGGTGAAG	AAGTTGAAAT	CATCGGTATG	350

	CACGAACTT	CTAAAACAAC	TGTTACTGGT	GTAGAAATGT	TCCGTAAATT	400
	ATTAGACTAC	GCTGAAGCTG	GTGACAACAT	CGGTGCTTTA	TTACGTGGTG	450
	TTGCACGTGA	AGACGTACAA	CGTGGTCAAG	TATTAGCTGC	TCCTGGTTCT	500
	ATTACACCAC	ACACAAAATT	CAAAGCTGAA	GTATACGTAT	TATCTAAAGA	550
5	TGAAGGTGGA	CGTCACACTC	CATTCTTCAC	TAACTATCGC	CCACAATTCT	600
	ATTTCCGTAC	TACTGACGTA	ACTGGTGTTG	TAACTTACC	AGAAGGTACA	650
	GAAATGGTTA	TGCCTGGCGA	CAACGTTGAA	ATGACAGTTG	AATTAATCGC	700
	TCCAATCGCT	ATCGAA				716

10

2) INFORMATION FOR SEQ ID NO: 879

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R764

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879

	CGGTCCTATG	CCTCAAACCTC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
	GCGTACCATA	CATCGTTGTT	TTCTTGAACA	AAATGGATAT	GGTTGATGAC	100
30	GAAGAATTGC	TAGAATTAGT	TGAAATGGAA	GTTTCGTGACC	TATTGTCTGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCCGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGAGATCCT	TCATACGAAG	AAAAAATCAT	GGAATTGATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACTCCA	GAACGTGATA	CTGACAAACC	300
	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
35	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	400
	GAAATCGTTG	GTATTGCTGA	CGAAACTGCT	AAAACAACCTG	TAACAGGTGT	450
	TGAAATGTTC	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	600
40	TTATGTTTTG	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA		640

2) INFORMATION FOR SEQ ID NO: 880

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: PAO-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880

60	CGGCGCGATC	CTGGTTTGCT	CGGCTGCCGA	CGGCCCATG	CCGCAGACCC	50
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	GCGAGCACAT	CCTGCTGTCC	CGCCAGGTAG	GCGTTCCTTA	CATCGTCGTG	100
	TTCCTGAACA	AGGCCGACAT	GGTCGACGAC	GCCGAGCTGC	TGGAAGTGGT	150
	CGAGATGGAA	GTTCGCGATC	TGCTGAACAC	CTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CATCATCGGT	TCCGCGCTGA	TGGCGCTGGA	AGGCAAGGAT	250
5	GACAACGGCA	TCGGCGTAAG	CGCCGTGCAG	AAGCTGGTAG	AGACCCTGGA	300
	CTCCTACATT	CCGGAGCCGG	TTCGTGCCAT	CGACCAGCCG	TTCCTGATGC	350
	CGATCGAAGA	CGTGTTCTCG	ATCTCCGGCC	GCGGTACCGT	GGTAACCGGT	400
	CGTGTAAGC	GCGGCATCAT	CAAGGTCCAG	GAAGAAGTGG	AAATCGTCGG	450
	CATCAAGGCG	ACCACCAAGA	CTACCTGCAC	CGGCGTTGAA	ATGTTCCGCA	500
10	AGCTGCTCGA	CGAAGGTCGT	GCTGGTGAGA	ACGTTGGTAT	CCTGCTGCGT	550
	GGCACCAAGC	GTGAAGACGT	AGAGCGTGGC	CAGGTTCTGG	CCAAGCCGGG	600
	CACCATCAAG	CCGCACACCA	AGTTCGAGTG	CGAAGTGTAC	GTGCTGTCCA	650
	AGGAAGAAGG	TGGTCGTCAC	ACCCCGTTCT	TCAAGGGCTA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	YGTGACCGGT	AACTGCCAAC	TGCCGGAAGG	750
15	CGTAGAGATG	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTCACCCTGA	800
	TCGCTCCGAT	CGCCATGGAA	GATGGCCTGC	G		831

20 2) INFORMATION FOR SEQ ID NO: 881

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881

35	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
	GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCTG	CTTTGAAAGC	200
40	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
	ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	350
	TACAGGCCGT	GTTGAACGTG	GACAAGTTCG	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTTGAA	450
45	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
	GTTTAAACAA	AAGAAGAAGG	TGGACGTCAC	ACACCATTCT	TC	642

50

2) INFORMATION FOR SEQ ID NO: 882

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R775

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882

	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
10	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
	GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCTG	CTTTGAAAGC	200
	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
	ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	350
15	TACAGGCCGT	GTTGAACGTG	GACAAGTTCG	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTGAA	450
	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
20	GTTTTAACAA	AAGAAGAAGG	TGACGTCAT	ACACCA		636

2) INFORMATION FOR SEQ ID NO: 883

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 641 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883

40	GGTCCTATGC	CTCAAACACG	TGAACATATC	TTATTATCAC	GTAACGTTGG	50
	TGTACCATAC	ATCGTTGTAT	TCTTAAACAA	AATGGATATG	GTTGATGACG	100
	AAGAATTATT	AGAATTAGTA	GAAATGGAAG	TTCGTGACTT	ATTATCAGAA	150
	TACGATTTC	CAGGCGATGA	TGTTCCAGTT	ATCGCAGGTT	CTGCTTTGAA	200
	AGCTTTAGAA	GGCGACGAGT	CTTATGAAGA	AAAAATCTTA	GAATTAATGG	250
45	CTGCAGTTGA	CGAATATATC	CCAACCTCCAG	AACGTGATAC	TGACAAACCA	300
	TTCATGATGC	CAGTCGAAGA	CGTATTCTCA	ATCACTGGAC	GTGGTACTGT	350
	TGCTACAGGC	CGTGTTGAAC	GTGGTGAAGT	TCGCGTTGGT	GACGAAGTTG	400
	AAATCGTTGG	TATTAAAGAC	GAAACATCTA	AAACAACTGT	TACAGGTGTT	450
	GAAATGTTCC	GTAAATTATT	AGACTACGCT	GAAGCAGGCG	ACAACATCGG	500
50	TGCTTTATTA	CGTGGTGTAG	CACGTGAAGA	TATCGAACGT	GGACAAGTAT	550
	TAGCTAAACC	AGCTACAATC	ACTCCACACA	CAAAATTCAA	AGCTGAAGTA	600
	TACGTATTAT	CAAAAGAAGA	AGGCGGACGT	CACACTCCAT	T	641

55

2) INFORMATION FOR SEQ ID NO: 884

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 640 bases

60

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: R575

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884

	TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
	CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
15	TTTCCCAGGC	GATGATGTTC	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
	TAGAAGGCGA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
	GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTTCAT	300
	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
20	GTTGGTATTA	AAGACGAAAC	ATCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
	TATTACGTGG	TGTTGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
	AAACCAGCTA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
	ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCATTCTTC		640

25

2) INFORMATION FOR SEQ ID NO: 885

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 632 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R492

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885

	TGCCTCAAAC	TCGTGAACAC	ATCCTATTGT	CTCGTCAAGT	TGGTGTTTCCT	50
45	TACATCGTTG	TATTCTTGAA	CAAAGTAGAC	ATGGTTGATG	ACGAAGAATT	100
	ACTAGAATTA	GTTGAAATGG	AAGTTCGTGA	CCTATTAACA	GAATACGAAT	150
	TCCCTGGTGA	CGATGTTTCT	GTAGTTGCTG	GATCAGCTTT	GAAAGCTCTA	200
	GAAGGCGACG	CTTCATACGA	AGAAAAAATT	CTTGAATTAA	TGGCTGCAGT	250
	TGACGAATAC	ATCCCAACTC	CAGAACGTGA	CAACGACAAA	CCATTTCATGA	300
50	TGCCAGTTGA	AGACGTGTTC	TCAATTACTG	GACGTGGTAC	TGTTGCTACA	350
	GGTCGTGTTG	AACGTGGACA	AGTTCGCGTT	GGTGACGAAG	TTGAAGTTGT	400
	TGGTATTGCT	GAAGAACTT	CAAAAACAAC	AGTTACTGGT	GTTGAAATGT	450
	TCCGTAAATT	GTTAGACTAC	GCTGAAGCTG	GAGACAACAT	TGGTGCTTTA	500
	CTACGTGGTG	TTGCACGTGA	AGACATCCAA	CGTGGACAAG	TTTTAGCTAA	550
55	ACCAGGTACA	ATCACACCTC	ATACAAAATT	CTCTGCAGAA	GTATACGTGT	600
	TGACAAAAGA	AGAAGGTGGA	CGTCATACTC	CA		632

60 2) INFORMATION FOR SEQ ID NO: 886

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886

15	CGGCCCAATG	CCTCAAACCTC	GTGAACACAT	CCTATTGTCT	CGTCAAGTTG	50
	GTGTTTCCTTA	CATCGTTGTA	TTCTTGAACA	AAGTAGACAT	GGTTGATGAC	100
	GAAGAATTAC	TAGAATTAGT	TGAAATGGAA	GTTTCGTGACC	TATTAACAGA	150
	ATACGAATTC	CCTGGTGACG	ATGTTCTGT	AGTTGCTGGA	TCAGCTTTGA	200
20	AAGCTCTAGA	AGGCGACGCT	TCATACGAAG	AAAAAATTCT	TGAATTAATG	250
	GCTGCAGTTG	ACGAATACAT	CCCAACTCCA	GAACGTGACA	ACGACAAACC	300
	ATTCATGATG	CCAGTTGAAG	ACGTGTTCTC	AATTACTGGA	CGTGGTACTG	350
	TTGCTACAGG	TCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	400
	GAAGTTGTTG	GTATTGCTGA	AGAAACTTCA	AAAACAACAG	TTACTGGTGT	450
25	TGAAATGTTC	CGTAAATTGT	TAGACTACGC	TGAAGCTGGA	GACAACATTG	500
	GTGCTTTACT	ACGTGGTGTT	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	550
	TTAGCTAAAC	CAGGTACAAT	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	600
	ATACGTGTTG	ACAAAAGAAG	AAGGTGGACG	TCATACTCCA		640

30

2) INFORMATION FOR SEQ ID NO: 887

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Zoogloea ramigera*
 (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887

	ATCCTGGTTT	GCTCCGCAGC	TGACGGCCCA	ATGCCACAGA	CCCGCGAGCA	50
	CATCCTGCTG	GCCCGCCAAG	TTGGCGTTCC	ATACATCATC	GTGTTTCCTGA	100
50	ACAAGTGCGA	CCTGGTTGAC	GACGCAGAAC	TGCTGGAACT	GGTCGAAATG	150
	GAAGTGCGTG	AATTGCTGTC	GAAATACGAG	TTCCCAGGCG	ACGACGTACC	200
	AATCATCAAG	GGTTCGGCAC	GTATGGCGCT	GGAAGGCAAA	GAAGGCGAGA	250
	TGGGCGTTGA	CGCCATCATG	CGTCTGGCCG	ATGCACTGGA	CAGCTACATC	300
	CCTACGCCAG	AGCGCGCAGT	CGATGGCGCC	TTCCTGATGC	CAGTGGAAGA	350
55	CGTGTTCTCG	ATCTCGGGTC	GCGGTACCGT	TGTGACCGGT	CGTATCGAGC	400
	GCGGCGTGAT	CAAGGTCGGC	GAAGAGATCG	AAATCGTCGG	CATTATCGAC	450
	ACCGTCAAAA	CCACTTGCAC	CGGCGTGGAA	ATGTTCCGCA	AGCTGCTGGA	500
	CCAGGGTCAA	GCCGGCGACA	ACGTTGGTCT	GCTGCTGCGC	GGCACCAAGC	550
	GTGAAGACGT	ACAGCGTGGT	CAGGTTCTGG	CCAAGCCAGC	GTCGATCAAG	600
60	CCGCACAACC	ACTTCACCGG	CGAGATCTAC	GTTCTGTCTGA	AAGATGAAGG	650

CGGCCGTCAC	ACCCCGTTCT	TCAACAATA	TCGTCCACAG	TTCTACTTCC	- 700
GTACGACTGA	CGTGACCGGT	TCGATCGAAC	TGCCAGCAGA	CAAAGAAATG	750
GTCATGCCAG	GCGACAACGT	GTCGATCACC	GTCAAGCTGA	TCAACCCGAT	800
CGCGAT					806

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2) INFORMATION FOR SEQ ID NO: 888

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R503

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888

25	TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
	CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
	TTTCCCAGGC	GATGATGTTT	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
	TAGAAGGCCA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
	GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTCAT	300
30	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTA	AAGACGAAAC	ATCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
	TATTACGTGG	TGTAGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
35	AAACCAGCTA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
	ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCA		634

40 2) INFORMATION FOR SEQ ID NO: 889

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 14110

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889

55

60	TGTCTTCATC	CAGGAATTGA	TTGTGAGTCG	TTCCACATGC	TCACCTAGTT	50
	TTCGCTCGAT	CTTTTCACTA	ACGCAAACCA	TGTAGAACAA	CATTGCCAAG	100
	GCCCACGGTG	GTTACTCCGT	CTTCACTGGT	GTTGGTGAGC	GTACTCGTGA	150
	GGGTAACGAT	CTGTACCACG	AAATGCAGGA	GACTGGTGTC	ATTGAGCTCG	200
	AGGGTGAATC	CAAGGTCGCA	CTGGTGTTTC	GACAGATGAA	CGAGCCCCCC	250

	GGTGCCCGTG	CCCGTGTCGC	CCTTACCGGT	CTGACCATTG	CCGAGTACTT	300
	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	CTTCATTGAC	AACATTTTCC	350
	GTTTCACCCA	GGCCGGTTCT	GAGGTGTCTG	CCCTTCTCGG	TCGTATCCCC	400
	TCTGCCGTCG	GTTACCAGCC	CACCCTGGCC	GTCGACATGG	GTGGTATGCA	450
5	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	TATTACCTCC	GTC	493

2) INFORMATION FOR SEQ ID NO: 890

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890

25	TTGATTGTAC	GTCTTTACCT	TTCTGCCTGA	CTGTTTACGA	CAACTAACGA	50
	AAGCGTAGAA	CAACATTGCC	AAGGCTCACG	GTGGTTACTC	TGTCTTCACT	100
	GGTGTCGGTG	AACGTACTCG	TGAGGGTAAC	GATTTGTACC	ACGAAATGCA	150
	GGAAACTGGT	GTCATTACAG	TCGAGGGTGA	ATCCAAGGTC	GCCCTCGTGT	200
	TCGGTCAGAT	GAACGAGCCC	CCCGGTGCCC	GTGCCCCGTGT	CGCTCTTACT	250
30	GGTTTGACCA	TTGCCGAGTA	CTTCCGTGAC	GAGGAAGGTC	AGGACGTGCT	300
	TCTCTTCATT	GACAACATTT	TCCGTTTCAC	TCAGGCCGGT	TCTGAGGTGT	350
	CTGCCCTTCT	GGGTCGTATC	CCCTCTGCCG	TCGGTTACCA	GCCCACCCTT	400
	GCCGTCGACA	TGGGTATCAT	GCAGGAGCGT	ATTACCACCA	CCACCAAGGG	450
	TTCCATCACC	TCCGTC				466

35

2) INFORMATION FOR SEQ ID NO: 891

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891

	AGGAGCTGAT	CAACAACATC	GCCAAGGCTC	ACGGTGGTTA	CTCCGTCTTC	50
55	ACTGGTGTCG	GTGAGCGTAC	CCGTGAGGGT	AACGATCTGT	ACCACGAAAT	100
	GCAGGAGACC	TCGGTCATTC	AGCTCGAGGG	CGAGTCTAAG	GTGGCCCTGG	150
	TCTTTGGTCA	GATGAACGAG	CCCCCGGGTG	CTCGTGCCCG	TGTCGCTCTT	200
	ACTGGTCTTA	CCGTCGCCGA	GTA CTTCCTG	GACCAGGAGG	GTCAGGATGG	250
	TTAGTTCTCG	TCCACTCATG	CCGAAACATG	TGCGTGTTCC	GAGGCTAATC	300
60	AACGTGCCAG	TGCTGCTTTT	CATCGACAAC	ATTTTCCGAT	TCACACAGGC	350

500

CGGTTCCGAG	GTGTCTGCCC	TGCTGGGTCG	TATCCCCCTCT	GCCGTGGTT	400
ACCAGCCCAC	CCTCGCCGTC	GACATGGGTG	GCATGCAGGA	GCGTATCACC	450
ACCACCAAGA	AGGGCTCTAT	CACCTCCG			478

5

2) INFORMATION FOR SEQ ID NO: 892

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 481 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffei*
- (B) STRAIN: ATCC 58950

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892

GTCTTTATCC	AGGAGTTGAT	TGTACGTCTT	TACCTTTCTG	CCTGACTGTT	50
TACGACAACT	AACGAAAGCG	TAGAACAACA	TTGCCAAGGC	TCACGGTGGT	100
25 TACTCTGTCT	TCACTGGTGT	CGGTGAACGT	ACTCGTGAGG	GTAACGATTT	150
GTACCACGAA	ATGCAGGAAA	CTGGTGTCT	TCAGCTCGAG	GGTGAATCCA	200
AGGTCGCCCT	CGTGTTCCGT	CAGATGAACG	AGCCCCCGG	TGCCCGTGCC	250
CGTGTCGCTC	TTACTGGTTT	GACCATTGCC	GAGTACTTCC	GTGACGAGGA	300
AGGTCAGGAC	GTGCTTCTCT	TCATTGACAA	CATTTTCCGT	TTCACTCAGG	350
30 CCGGTTCTGA	GGTGTCTGCC	CTTCTGGGTC	GTATCCCCTC	TGCCGTCGGT	400
TACCAGCCCA	CCCTTGCCGT	CGACATGGGT	ATCATGCAGG	AGCGTATTAC	450
CACCACCACC	AAGGGTTCCA	TCACCTCCGT	C		481

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2) INFORMATION FOR SEQ ID NO: 893

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 1208 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
- (B) STRAIN: ATCC 14285

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893

CTCGTCCGTG	GTGCTAAGGC	CACTGACACT	GGTTSCCCCA	TTACCATCCS	50
CGTCGGCCCC	GGTACCCTCG	GTCGCATCAT	GAACGTCACC	GGTGACCCGA	100
TCGACGAGCG	CGGTCCCATC	AAGACCGACA	AGTTCCGTCC	CATCCACGCT	150
55 GAGGCTCCCG	AGTTCGTTGA	CCAGTCGACC	ACCGCTGAGG	TTCTCGTGAC	200
TGGTATCAAG	GTCGTCGATC	TGCTTGCTCC	CTACGCCCGT	GGTGGTAAGA	250
TTGGTCTGTT	TGGCGGTGCC	GGTGTTGGCA	AGACCGTGTT	CATCCAGGAG	300
CTCATCAACA	ACATCGCCAA	GGCCCACGGT	GGTTACTCCG	TCTTCACCGG	350
TGTCGGCGAG	CGTACCCGTG	AGGGTAACGA	TCTGTACCAC	GAAATGCAGG	400
60 AGACCTCTGT	CATTCAGCTT	GACGGTGACT	CCAAGGTCGC	CCTGGTGTTT	450

501

	GGTCAGATGA	ACGAGCCCCC	TGGTGCTCGT	GCCCGTGTCG	CCTTGACCGG	500
	TTTGACTGTC	GCTGAGTACT	TCCGTGACGA	GGAGGGCCAG	GATGGTATGT	550
	TTTGAATTAT	TTCCTTGTCG	TACAGTTCCA	AATCGAAGAA	TTACTAACTT	600
	GTCAGTGCTT	CTCTTCATCG	ACAACATTTT	CCGCTTCACC	CAGGCCGGTT	650
5	CTGAGGTGTC	TGCCCTTCTG	GGTCGTATTC	CCTCCGCTGT	CGGTTACCAG	700
	CCCACGCTCG	CCGTGGACAT	GGGTCTGATG	CAGGAGCGTA	TTACCACCAC	750
	CCGCAAGGGC	TCAATTACCT	CCGTCCAGGC	CGTCTACGTG	CCCGCTGACG	800
	ATCTGACGGA	TCCCGCCCCC	GCCACCACCT	TCGCCCATCT	GGACGCCACC	850
	ACTGTGCTGT	CCCGAGGTAT	CTCTGAGCTG	GGTATCTACC	CCGCTGTCTG	900
10	CCCCCTCGAC	TCCAAGTCGC	GTATGCTGGA	CCCCCGTATT	GTCGGTGACG	950
	ACCACTACGA	GACCGCCACT	CGCGTCCAGC	AGATCCTCCA	AGAGTACAAG	1000
	TCGCTGCAGG	ACATCATCGC	CATTCTGGGT	ATGGACGAGC	TGTCTGAGGC	1050
	CGACAAGCTT	ACAGTCGAGC	GTGCTCGTAA	GATCCAGCGT	TTCCTGAGCC	1100
	AGCCGTTCAC	GGTCGCGCAG	GTCTTCACTG	GTATCGAAGG	CCAGCTGGTC	1150
15	GATCTGAAGG	ACACTATCGC	TTCGTTCAAG	GCTATCCTGA	GCGGTGAGGG	1200
	TGACAGCC					1208

20 2) INFORMATION FOR SEQ ID NO: 894

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 534 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
(B) STRAIN: ATCC 48174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894

35	TTCAGGA	ACT	TATTGTA	AAGC	CGCCCTC	TTT	ATGCATT	GAG	GGTGA	AATAAG	50
	AAGGCTG	ACA	GGTAATA	AGAA	CAACATT	GCC	AAGGCTC	ACG	GTGGTTA	CTC	100
	CGTGTTCA	CT	GGTGTCG	GGTG	AGCGTAC	CCG	TGAAGGA	AAC	GATCTGT	ACC	150
	ATGAAATG	CA	GGAAACCC	GC	GTCATCC	AGC	TTGATGG	CGA	GTCTAAG	GTC	200
40	GCCCTTGT	GT	TCGGTCAG	AT	GAACGAG	CCC	CCTGGAG	CCC	GTGCCCC	GTG	250
	CGCTCTTA	CT	GGTCTTA	CCG	TTGCCGA	AATA	CTTCCGT	GAC	GAGGAGG	GCC	300
	AAGATGGT	AC	GCCTTTT	TAC	TCTTCTT	ATT	CTTCGGG	TCG	GA	CTACAGAA	350
	CTAACCTG	CT	CCAGTGCT	TTC	TCTTCATT	GTA	TAACATT	TTT	CGTTTCA	CAC	400
	AAGCCGGT	TC	TGAGGTGT	CT	GCCTTGCT	TG	GACGTAT	TCC	CTCTGCC	GTC	450
45	GGTTACC	AGC	CCACTCTC	GC	CGTCGAC	ATG	GGTGGTAT	GC	AGGAACG	TAT	500
	CACAACC	ACC	AACAAGGG	T	CCATTACT	TTC	CGTG				534

50 2) INFORMATION FOR SEQ ID NO: 895

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 448 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895

```

5      CAAGGCTCAC GGTGGTTACT CCGTCTTCAC TGGTGTCGGT GAGCGTACCC      50
      GTGAGGGTAA CGATCTGTAC CACGAAATGC AGGAGACCTC GGTCATTCAG      100
      CTCGAGGGCG AGTCTAAGGT GGCCCTGGTC TTTGGTCAGA TGAACGAGCC      150
      CCCGGGTGCT CGTGCCCGTG TCGCTCTTAC TGGTCTTACC GTCGCCGAGT      200
10     ACTTCCGTGA CCAGGAGGGT CAGGATGGTT AGTTCTCGTC CACTCATGCC      250
      GAAACATGTG CGTGTTCCGA GGCTAATCAA CGTGCCAGTG CTGCTTTTCA      300
      TCGACAACAT TTTCCGATTC ACCCAGGCCG GTTCCGAGGT GTCTGCCCTG      350
      CTGGGTCGTA TCCCCTCTGC CGTCGGTTAC CAGCCCACCC TCGCCGTCGA      400
      CATGGGTGGC ATGCAGGAGC GTATCACCAC CACCAAGAAG GGCTCTAT      448
15
  
```

2) INFORMATION FOR SEQ ID NO: 896

```

20     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 483 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25
      (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Aspergillus niger
30     (B) STRAIN: ATCC 9508
  
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896

```

      ATTCAGGAGC TGATTGTAAG TTGCCAATCC ATGAACTGGA GATTTGGTGT      50
35     GACCCATAGA ACTAACAAAT TATTTAGAAC AACATCGCCA AGGCTCACGG      100
      TGGTTACTCC GTCTTCTGTG GTGTCTGGTGA GCGTACTCGT GAGGGTAACG      150
      ATCTGTACCA CGAAATGCAG GAGACTGGTG TCATCCAGCT CGAGGGTGAC      200
      TCCAAGGTCG CTCTGGTCTT CGGTCAGATG AACGAGCCCC CGGGTGCCCG      250
      TGCCCGTGTC GCCCTTACCG GTCTGACCAT TGCCGAGTAC TTCCGTGACG      300
40     AGGAGGGTCA GGACGTGCTG CTCTTCATTG ACAACATTTT CCGTTTCACC      350
      CAGGCCGGTT CTGAGGTGTC TGCCCTTCTG GGTCGTATCC CCTCTGCCGT      400
      CGGTTACCAG CCCACTCTGG CCGTCGACAT GGGTGGTATG CAGGAGCGTA      450
      TTACCACCAC CACCAAGGGT TCCATTACCT CCG                      483
  
```

45

2) INFORMATION FOR SEQ ID NO: 897

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      (i) SEQUENCE CHARACTERISTICS:
50     (A) LENGTH: 1124 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
55
      (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Aspergillus fumigatus
      (B) STRAIN: ATCC 14110
60
  
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
5	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
10	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTC	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAACCTGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTY	CAACAAGCCC	600
15	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTGCGC	CGTGTCGAGA	CCGGTATCAT	CAAGCCCAGC	ATGGTCGTCA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
20	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCC	CCGTCCTCGA	950
	CTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
25	CGAGTCCTTC	ACTGACTACC	CCCC			1124

2) INFORMATION FOR SEQ ID NO: 898

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Penicillium marneffei*
 (D) STRAIN: WSA-214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898

45	CTCAAGGCTG	AGCGTGAGCG	TGGTATCACC	ATCGATATTG	CTCTCTGGAA	50
	GTTCCAGACT	GCCAAGTACG	AGGTTACCGT	CATTGACGCC	CCCGGTCACC	100
	GTGATTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	CGATTGCGCT	150
	ATTCTCATCA	TTGCCTCTGG	TACTGGTGAA	TTCGAGGCTG	GTATCTCCAA	200
	GGATGGCCAG	ACTCGTGAGC	ACGCTCTTTT	GGCTTTCACC	CTCGGTGTCC	250
50	GTCAGCTCAT	TGTTGCCCTC	AACAAGATGG	AACTTGCAA	GTGGTCTCAG	300
	GGTGAGTACT	CGTACCTGCG	TTTGGCCTTG	AATATCTTAC	TAATGCACCA	350
	TAGATCGTTA	CAACGAAATT	GTCAAGGAGA	CTTCCAACCT	CATCAAGAAG	400
	GTCGGATACA	ACCCTAAGAA	CGTTCCTTTC	GTTCTATCT	CCGGTTTCAA	450
	CGGTGACAAC	ATGCTTGAGC	CCTCCCCCAA	CTGCCCCCTG	TACAAGGGTT	500
55	GGGAGAAGGA	GACCAAGGCC	GGTAAGGTCA	CTGGTAAGAC	CCTCCTCGAG	550
	GCCATCGACG	CCATTGAGCC	CCCTACCCGT	CCCGCCAACA	AGGTTAGTCC	600
	CTCCTCGACT	ACTCAAACCC	TCCTCATAAG	TTCATGATTA	CGACTCGTTC	650
	ACAGCCCCTC	CGTCTTCCCC	TCCAGGATGT	CTACAAGATC	GGTGGTATTG	700
	GAACGGTTCC	CGTCGGTCGT	GTTGAGACTG	GTACCATCGT	TCCTGGTATG	750
60	GTTGTCACCT	TGTAAGTCAC	TCTCCTCGCT	TATCCTACCT	GAAATCATCA	800

	TGTGCTAACT	TGACACTCAG	CGCTCCCGCC	AACGTCACCA	CTGAAGTCAA	850
	GAGTGTTGAA	ATGCACCACC	AGCAGCTCAC	TGCCGGTCAG	CCCGGTGACA	900
	ACGTTGGTTT	CAACGTGAAG	AACGTCTCCG	TCAAGGAAAT	CCGTCGTGGT	950
	AACGTTGCTG	GTGACAGCAA	GAACGACCCC	CCTGCCGGTG	CTGCCTCCTT	1000
5	CAACGCCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAGGTC	GGTGCTGGTT	1050
	ACGCCCCAGT	CCTCGATTGC	CACACTGCCC	ACATTGCTTG	CAAGTTCGCT	1100
	GAGCTCCTCG	AGAAGATTGA	CCGTCGTACC	GGAAAGTCTG	TTGAGGACCA	1150
	CCCCAAGTTC	ATCAAGTCCG	GTGACGCTGC	CATCGTCAAG	ATGATTCCTT	1200
	CCAAGCCCAT	GTGTGTTGAG	GCTTTCACCG	AGTACCCTCC	TCTCGGTCGT	1250
10	TTCGCCGTTT	GCGAGTAAGT	TTTATCTCCG	TTGTCTATTT	TCCATCCTTC	1300
	CCTTCTCCTC	CGTCTTCCAT	ATATATTTTT	TCAGTTATAT	GTGACTAACC	1350
	ACAAATCACG	GGA				1363

15

2) INFORMATION FOR SEQ ID NO: 899

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1147 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Piedraia hortai*
- (B) STRAIN: ATCC 24292

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899

	CAAGCTGAAA	GCCGAGCGTG	AGCGTGGTAT	CACTATCGAC	ATTGCCCTCT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CCGTCATTGG	TACGTCGCAT	100
	TATCTCACTC	CTCACAGAAG	CACGCTCCTA	ACATCACACA	GACGCTCCCG	150
35	GTCACCGTGA	TTTCATCAAG	AACATGATCA	CTGGTACCTC	CCAGGCCGAC	200
	TGCGCTATCC	TCATTATCGC	TGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCC	TACACCCTCG	300
	GTGTGCGTCA	GCTCATCGTC	GCCATCAACA	AGATGGACAC	CACCAAGTGG	350
	TCTGAGGCCC	GTTACCAGGA	GATCATCAAG	GAGACCTCCA	ACTTCATCAA	400
40	GAAGGTCGGC	TACAACCCCA	AGACCGTCGC	TTTCGTCCCC	ATCTCTGGCT	450
	TCAACGGCGA	CAACATGCTT	GCCCCCTCCA	CCAAGTGGCC	CTGGTACAAG	500
	GGATGGGAGC	GTGAGGTCAA	GGGCAACAAG	CAGACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGGCATTG	AGCCCCCAAA	GCGTCCTTCC	GACAAGCCCC	600
	TCCGTCTTCC	TCTCCAGGAT	GTTTACAAGA	TCGGTGGTAT	CGGAAGTGT	650
45	CCTGTCGGCC	GTATCGAGAC	TGGTGTCTCT	AAGCCCGGTA	TGGTCGTTAC	700
	CTTCGCTCCC	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	750
	ACGAGCAGCT	CACTGAGGGT	CTTCCCGGTG	ACAACGTCGG	TTTCAACGTG	800
	AAGAACGTTT	CCGTCAAGGA	CATCCGCCGT	GGTAACGTTG	CCAGTGACTC	850
	CAAGAACGAC	CCCGCTCTGG	GTGCCGCTTC	TTTCGACGCC	CAGGTCATCG	900
50	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	GGTCCTCGAT	950
	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGATCA	AGGAGAAGAT	1000
	CGACCGCCGT	ACCGGCAAGT	CTGTTGAGGA	CGCCCCCAAG	TTCATCAAGT	1050
	CTGGTGACTC	TGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTT	1100
	GAGGCTTTCA	CCGACTACCC	TCCTCTGGGC	CGTTTCGCCG	TCCGTGA	1147

55

2) INFORMATION FOR SEQ ID NO: 900

- (i) SEQUENCE CHARACTERISTICS:
- 505

- (A) LENGTH: 1150 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
(B) STRAIN: ATCC 60735

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900

	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
15	GTTTCGAGACT	CCCAAGTACT	ATGTCACCGT	CATTGGTACG	TCGACTCGCG	100
	CGAGACTGGT	CGCAATTTCC	ACGTCGCTAA	CGTGCTTGAA	CAGACGCTCC	150
	CGGCCACCGT	GACTTCATCA	AGAACATGAT	CÀCTGGTACC	TCCCAGGCTG	200
	ACTGCGCTAT	CCTCATTATC	GCTGCCGGCA	CTGGTGAGTT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	300
20	CGGTGTTAAG	CAGCTCATCG	TCGCTATCAA	CAAGATGGAC	ACCACCAAGT	350
	GGTCTGAGGC	CCGTTTCCAG	GAGATCATCA	AGGAGACCTC	CAACTTCATC	400
	AAGAAGGTCG	GCTACAACCC	CAAGACCGTC	GCTTTCGTCC	CCATCTCTGG	450
	TTTCCACGGC	GACAACATGC	TTTCCCCCTC	CACCAACTGC	CCCTGGTACA	500
	AGGGCTGGGA	GAAGGAGACC	AAGGCTGGCA	AGTCCACCGG	CAAGACCCTC	550
25	CTTGAGGCCA	TCGACTCCAT	CGAGCCCCCC	AAGCGCCCCA	GCGACAAGCC	600
	CCTCCGCCTT	CCCCTTCAGG	ATGTGTACAA	GATCGGCGGT	ATCGGCACAG	650
	TCCCTGTCGG	CCGTATCGAG	ACTGGTGTCA	TCAAGCCCCG	CATGGTCGTG	700
	ACCTTCGCTC	CTTCCAACGT	CACCACCGAA	GTCAAGTCCG	TTGAGATGCA	750
	CCACGAGCAG	CTCTCCGAGG	GTGTCCCCCG	TGACAACGTC	GGCTTCAACG	800
30	TCAAGAACGT	CTCCGTCAAG	GAGATCCGTC	GTGGCAACGT	CGCCGGTGAC	850
	TCCAAGAACG	ACCCCCCTCT	GGGTGCCGCT	TCTTTCGATG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGCC	AGGTCGGTGC	TGGCTACGCC	CCCGTCCTCG	950
	ACTGCCACAC	CGCCACATT	GCCTGCAAGT	TCGCCGAGAT	CAAGGAGAAG	1000
	ATCGACCGCC	GTACCGGCAA	GTCTGTCTGAG	TCCGCCCCCA	AGTTCATCAA	1050
35	GTCTGGCGAC	TCTGCCATCG	TCAAGATGAT	TCCCTCCAAG	CCCATGTGCG	1100
	TTGAGGCTTT	CACCGACTAC	CCTCCTCTGG	GCCGCTTCGC	CGTCCGTGAC	1150

40 2) INFORMATION FOR SEQ ID NO: 901

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
(B) STRAIN: ATCC 32075

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 901

55

	TACCACTAAG	TGGTCCGAGA	CCCGATTCAA	TGAAATTATC	AAGGAAGTCA	50
	CCAATTTTCAT	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	100
	CCCATTTCTG	GTTTCGAGGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
60	GCAAGACCCT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250

	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
	TATTGGCACT	GTTCCTGTCG	GACGTGTTGA	GACTGGAGTC	ATCAAGCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCG	GTGACAACGT	450
5	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
	GCCCAGGTCA	TCGTCTCTCA	CCACCCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCACAT	TGCCTGCAAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACCGGAA	AGTCTGTTGA	GAACAACCCC	700
10	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
	G					751

15 2) INFORMATION FOR SEQ ID NO: 902

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1056 bases

(B) TYPE: Nucleic acid

20 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sporothrix schenckii*

(B) STRAIN: ATCC 7968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902

30	CGTGAGCGCG	GTATCACCAT	CGATATTGCT	CTGTGGAAGT	TCGAGACCCC	50
	CAAGTACTAC	GTCACCGTCA	TTGACGCCCC	CGGTCATCGC	GATTTTCATCA	100
	AGAACATGAT	CACTGGTACC	TCGCAGGCCG	ACTGCGCCAT	TCTCATCATT	150
	GCCGCTGGTA	CTGGTGAGTT	CGAGGCTGGT	ATCTCCAAGG	ATGGCCAGAC	200
35	TCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	GGGTGTGCGG	CAGCTGATCG	250
	TCGCCATCAA	CAAGATGGAC	ACGGCCAAGT	GGGCTGAGGC	TCGTTACCAG	300
	GAGATCATCA	AGGAGACCTC	CAACTTCATC	AAGAAGGTCG	GCTACAACCC	350
	CAAGACTGTT	GCCTTCGTCC	CCATCTCGGG	CTTCCACGGC	GACAACATGC	400
	TTACTCCCTC	GACCAACTGC	CCCTGGTACA	AGGGCTGGGA	GAAGGAGGGC	450
40	AAGAGCGGCA	AGGTTACCGG	TAAGACTCTG	CTGGACGCCA	TTGACGCCGT	500
	CGAGCCCCCC	AAGCGCCCCA	CGGACAAGCC	CCTGCGTCTG	CCCCTCCAGG	550
	ATGTCTACAA	GATCGGCGGT	ATCGGCACTG	TCCCTGTGCG	CCGTATCGAG	600
	ACTGGTGTCC	TGAAGCCCGG	CATGGTCGTC	ACCTTTGCCC	CGTCCAACGT	650
	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	CCACGAGCAG	CTTGTTGAGG	700
45	GTGTTCCCGG	CGACAACGTC	GGCTTCAACG	TCAAGAACGT	CTCCGTCAAG	750
	GAGATCCGTC	GTGGCAACGT	TGCCGGTGAC	TCCAAGAACG	ACCCCCCTC	800
	GGGCGCCGCC	ACCTTCAACG	CCCAGGTCAT	TGTCCTGAAC	CACCCCGGCC	850
	AGGTCGGCAA	CGGCTACGCC	CCGGTTCTGG	ACTGCCACAC	CGCCCACATT	900
	GCCTGCAAGT	TCACCGAGAT	CCTTGAGAAG	ATCGACCGCC	GTACCGGCAA	950
50	GTCGGTTGAG	AACAACCCCA	AGTTCATCAA	GTCGGGTGAC	GCCGCCATTG	1000
	TCAAGCTGAC	GCCCTCGAAG	CCCATGTGCG	TTGAGGCCTT	CACTGACTAC	1050
	CCCCCT					1056

55

2) INFORMATION FOR SEQ ID NO: 903

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1366 bases

60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*
(B) STRAIN: ATCC 58950

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903

	CAAGGCTGAG	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	50
	TCCAGACTGC	CAAGTACGAG	GTTACCGTCA	TTGACGCCCC	CGGTCACCGT	100
	GATTTTCATCA	AGAACATGAT	CACTGGTACC	TCCCAGGCCG	ATTGCGCTAT	150
15	TCTCATCATT	GCCTCTGGTA	CTGGTGAATT	CGAGGCTGGT	ATCTCCAAGG	200
	ATGGCCAGAC	TCGTGAGCAC	GCTCTTTTGG	CTTTCACCCCT	CGGTGTCCGT	250
	CAGCTCATTG	TTGCCCTCAA	CAAGATGGAC	ACTTGCAAGT	GGTCTCAGGG	300
	TGAGTACTCG	TACCTGCGTT	TGGCCTTGAA	TATCTTACTA	ATGCACCATA	350
	GATCGTTACA	ACGAAATTGT	CAAGGAGACT	TCCAACCTCA	TCAAGAAGGT	400
20	CGGATACAAC	CCTAAGAACG	TTCCTTTTCGT	TCCTATCTCC	GGTTTCAACG	450
	GTGACAACAT	GCTTGAGCCC	TCCCCCAACT	GCCCCTGGTA	CAAGGGTTGG	500
	GAGAAGGAGA	CCAAGGCCGG	TAAGGTCACT	GGTAAGACCC	TCCTCGAGGC	550
	CATCGACGCC	ATTGAGCCCC	CTACCCGTCC	CGCCAACAAG	GTTAGTCCCT	600
	CCTCGACTAC	TCAAACCCTC	CTCATAAGTT	CAGATTACTG	ACTCGTTCAC	650
25	AGCCCCCTCCG	TCTTCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATTGGA	700
	ACGGTTCCCG	TCGGTCGTGT	TGAGACTGGT	ACCATCGTTC	CTGGTATGGT	750
	TGTCACCTTG	TAAGTCACTC	TCCTCGCTTA	TCCTACCTGA	AATCATCATG	800
	TGCTAACTTG	ACACTCAGCG	CTCCCGCCAA	CGTCACCACT	GAAGTCAAGA	850
	GTGTTGAAAT	GCACCACCAG	CAGCTCACTG	CCGGTCAGCC	CGGTGACAAC	900
30	GTTGGTTTCA	ACGTGAAGAA	CGTCTCCGTC	AAGGAAATCC	GTCGTGGTAA	950
	CGTTGCTGGT	GACAGCAAGA	ACGACCCCCC	TGCCGGTGCT	GCCTCCTTCA	1000
	ACGCCCAGGT	CATCGTCCTC	AACCACCCCG	GTCAGGTCGG	TGCTGGTTAC	1050
	GCCCCAGTCC	TCGATTGCCA	CACTGCCAC	ATTGCTTGCA	AGTTCGCTGA	1100
	GCTCCTCGAG	AAGATTGACC	GTCGTACCGG	AAAGTCTGTT	GAGGACCACC	1150
35	CCAAGTTCAT	CAAGTCCGGT	GACGCTGCCA	TCGTCAAGAT	GATTCCTTCC	1200
	AAGCCCATGT	GTGTTGAGGC	TTTCACCGAG	TACCCTCCTC	TCGGTCGTTT	1250
	CGCCGTTCGC	GAGTAAGTTT	TATCTCCGTT	GTCTATTTTC	CATCCTTCCC	1300
	TTCTCCTCCG	TCTTCCATAT	ATATTTTTTC	AGTTATATGT	GACTAACCAC	1350
	AAATCACGGG	AATAGC				1366

40

2) INFORMATION FOR SEQ ID NO: 904

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 841 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Curvularia lunata*
(B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904

	CTATTATCGT	TGTTGCCGCT	TCCGACGGTC	AAATGCCCCA	GACTCGTGAG	50
60	CATCTGCTGC	TCGCCCCGCA	GGTCGGTGTC	CAGAAGATCG	TTGTCTTCGT	100

508

	CAACAAGGTC	GATGCTGTTG	AGGACAAGGA	GATGTTGGAG	CTCGTCGAGA	150
	TGGAGATGCG	CGAATTGCTC	AGCAGCTACG	GCTTCGAGGG	CGACGAGACT	200
	CCCATCATCA	TGGGATCTGC	CCTCTGCGCC	ATTGAGGGCC	GCGAACCTGA	250
	GATTGGTGTC	AACCGAATTG	ATGAGCTGCT	CGAGGCCGTT	GATACTTGGA	300
5	TCCCCACCCC	TCAGCGTGAG	ACCGACAAGC	CTTTCCTCAT	GGCCGTCGAG	350
	GATGTCTTCT	CCATTGCTGG	TCGTGGCACT	GTCGTCTCTG	GCCGTGTCGA	400
	GCGAGGTATC	CTGAAGCGCG	ATGCTGAAGT	TGAGCTCGTC	GGCAAGGGCA	450
	CCGCCCCCAT	CAAGACCAAG	GTTACCGATA	TCGAGACCTT	CAAGAAGTCC	500
	TGCGAGGAGT	CTCGCGCTGG	TGACAACTCC	GGTCTCCTTC	TTCGTGGTGT	550
10	CAAGCGTGAT	GAAGTCCGCC	GTGGTATGGT	CGTTTCCGTC	CCTGGACAGG	600
	TCAAGGCGCA	CAAGAAGTTC	CTTGTCTCCA	TGTACGTGTT	GAGCAAGGAG	650
	GAAGGTGGTC	GTCACACTGG	CTTCGGTGAG	AACTACAGGC	CGCAAATGTT	700
	CATCCGCACT	GCCGACGAGT	CGTGTGCCCT	GTACTGGCCA	GAAGGCACCG	750
	AGGACGCCCA	TGACAAGCTT	GTTATGCCCC	GTGACAACGT	CGAGATGGTT	800
15	TGCGAGCTCC	ATGCACCACA	CGTCTTGGAG	CCTGGTCAAC	G	841

2) INFORMATION FOR SEQ ID NO: 905

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Aspergillus niger*
- (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905

35	CGGTGCTATC	ATTGTCGTCG	CCGCCTCCGA	CGGTCAGATG	TACGTTAACC	50
	TTAAAAGAAT	AACTCTCCTT	CAGTATATAT	GCTTACACTG	GCGATCAACA	100
	GGCCCCAGAC	TCGTGAGCAC	TTGCTGCTTG	CTCGTCAGGT	CGGTGTCCAG	150
	AAGATCGTTG	TCTTCGTCAA	CAAGGTCGAT	GCTATCGATG	ACCCCGAGAT	200
	GCTGGAGCTC	GTTGAGCTGG	AAATGCGCGA	GCTTCTCAGC	ACCTACGGAT	250
40	TCGAGGGTGA	GGAGACCCCC	ATCGTCTTCG	GCTCTGCTCT	CTGCGCCATT	300
	GAGGACCGCC	GCCCCGACAT	CGGTACCGAG	CGTATCGACG	CTCTCCTCGA	350
	GGCCGTTGAC	ACCTGGATCC	CCACTCCCCA	GCGTGACCTT	GACAAGCCTT	400
	TCTTGATGTC	CATTGAGGAA	GTTTTCTCCA	TCCCCGGTCG	TGGTACCGTC	450
	GCCTCCGGCC	GTGTCGAGCG	TGGTCTCCTG	AAGCGTGATA	GCGAGGTTGA	500
45	GATCATCGGT	ACCACCAACG	AGGTCATCAA	GACCAAGGTT	ACCGACATTG	550
	AGACCTTCAA	GAAGTCCTGC	TCCGAGTCCC	GCGCCGGTGA	CAACTCCGGT	600
	CTCCTGCTCC	GTGGTGTCCG	CCGTGAGGAT	CTCCGCCGTG	GTATGGTCAT	650
	TGCCGCTCCT	GGCAGCGCCA	AGGCCAACAG	CAAGTTCATG	GTCTCCATGT	700
	ACGTCCTGAC	CGAGGCTGAR	GGTGGTCGCC	GTACCGGTTT	CGGTGTCCAG	750
50	TACCGTCCCC	AGCTGTTTCAT	CCGCACTGCC	GGTAAGTAAA	ATTGCATTCT	800
	ATTCCGCTAC	TAGGGAACCA	TCTCTAATTC	TATTTGCTAC	AGATGAGGCT	850
	GCTGAGTTCA	GCTTCCCCGA	CGGAGACCAG	TCCCGCCGTA	TCATGCCCGG	900
	TGACAACGTC	GAGATGATCG	TCAAGACCCA	CCGCCCCGTC	GCCGCCGAGG	950
55	CCGGTCAGCG	CTTCAAC				967

2) INFORMATION FOR SEQ ID NO: 906

(i) SEQUENCE CHARACTERISTICS:

509

- (A) LENGTH: 852 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906

	TGGTGCTATT	ATTGTTGTTG	CCGCTTCCGA	CGGTCAAATG	CCCCAGACTC	50
15	GTGAGCATCT	GCTGCTCGCC	CGTCAGGTCG	GTGTTCAGAA	GATCGTTGTC	100
	TTCGTTAACA	AGGTCGACGC	TGTCGAGGAC	AAGGAGATGT	TGGAGCTTGT	150
	CGAGATGGAG	ATGCGCGAAC	TGCTCAGCAG	CTATGGCTTC	GAGGGCGACG	200
	AGACCCCTAT	CATCATGGGT	TCTGCTCTCT	GCGCCATTGA	AGGCCGTCAA	250
	CCCGACATTG	GTGTCGAACG	AATTGACGAG	CTGCTCGAGG	CTGTTGATAC	300
20	TTGGATTCCC	ACCCCTCAGC	GTGAGACCGA	AAAGCCTTTC	CTCATGGCCG	350
	TCGAGGATGT	CTTCTCCATT	GCTGGTCGTG	GTACCGTCGT	CTCTGGCCGT	400
	GTCGAACGAG	GTATCCTGAA	GCGCGATGCT	GAAGTTGAGC	TTGTGGGCAA	450
	GGGCAGCGCA	CCCATCAAGA	CCAAGGTTAC	CGATATCGAG	ACCTTCAAGA	500
	AGTCTTGCGA	GGAGTCCCGC	GCTGGTGACA	ACTCCGGTCT	CCTTCTTCGT	550
25	GGTGTTAAGC	GTGATGAAGT	CCGCCGTGGT	ATGGTCGTTT	CCGTCCCTGG	600
	ACAGGTTAAG	GCGCACAAGA	AGTTCCTTGT	CTCCATGTAT	GTGCTGAGCA	650
	AGGAGGAAGG	TGGCCGACAC	ACTGGCTTCG	GTGAGAACTA	CAGGCCGCAA	700
	ATGTTTCATCC	GCACTGCCGA	CGAGTCGTGT	GCCCTGTACT	GGCCAGAAGG	750
	CACCGAGGAT	GCCCACGACA	AGCTTGTCAT	GCCCGGTGAC	AACGTCGAGA	800
30	TGGTTTGCGA	GCTCCATGCA	CCACACGTCT	TGGAGACTGG	TCAGCGCTTC	850
	AA					852

35 2) INFORMATION FOR SEQ ID NO: 907

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907

50

	GGTGCTATTG	TTGTCGTTGC	TGCTTCGGAT	GGTCATGATG	TATGGACAGG	50
	CCCTTTGCTA	CTGAATGGTT	TCAAGATCTC	GCGCTTACAC	GTATTATAAT	100
	AGGCCCCAGA	CCCGGGAGCA	CTTGCTGCTT	GCCCGTCAGG	TCGGTGTTCA	150
	GAAGATCGTC	GTTTTTGTCA	ACAAGATTGA	TGCCGTTGAG	GACCCTGAGA	200
55	TGTTGGAGCT	TGTCGAGTTG	GAAATGCGCG	AGCTCCTTAG	CAGCTACGGC	250
	TTCGAGGGCG	AAGAGACTCC	CATCATCTTC	GGTTCTGCTC	TGTGTGCTTT	300
	GGAGGACCGT	CGCCCCGACA	TTGGTGCCGA	GCGTATCGAC	GAGCTCATGA	350
	AGGCCGTTGA	CACCTGGATC	CCTACCCCTC	AGCGTGATCT	TGACAAGCCT	400
	TTCCTCATGT	CTGTCGAGGA	AGTCTTCTCC	ATCGCCGGTC	GTGGTACCGT	450
60	TGCCTCCGGC	CGTGTCGAAC	GTGGTATCCT	GAAGAAGGAC	AGCGAAGTCG	500

	AGATCATCGG	AGGTAGCTTC	GATGCTACCA	AGACCAAGGT	CACCGACATT	550
	GAGACCTTCA	AGAAGTCTTG	TGACGAGTCC	CGCGCTGGTG	ACAACTCTGG	600
	CTTGCTTCTC	CGTGGTATCC	GTCGTGAAGA	CGTCCGCCGC	GGAATGATCA	650
	TTGCTGCTCC	TGGCAGCACC	AAGGCCACG	ACCAGTTCTT	GGTGTCCATG	700
5	TACGTTCTCA	CTGAGGCTGA	GGGTGGTCGT	CGTACTGGCT	TCGGCTCCAA	750
	CTACCGCCCC	CAGGTGTTCTG	TTCGCACTGC	TGGTAAGTCA	AGCCTTTTGC	800
	TCACTTAACG	GTATTGATTA	AGTTCTAACT	GTTGTATCCT	AGATGAGGCT	850
	GCTGACCTCA	GCTTCCCCGA	CGGTGATGAG	TCCCGGAGGG	TGATGCCTGG	900
	TGACAACGTC	GAGATGGTCC	TCAAGACTCA	CCGCCCCATT	GCTGCTGAGG	950
10	CTGGCCAGCG	CTTCAA				966

2) INFORMATION FOR SEQ ID NO: 908

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908

30	GGTGCTATCA	TCGTCGTTGC	TGCTTCCGAT	GGTCAGATGC	CCCAGACCCG	50
	TGAGCACTTG	CTGCTCGCCC	GTCAGGTCGG	TGTTCAGAAG	ATCGTTGTCT	100
	TCGTCAACAA	GGTCGATGCT	GTCGAAGACC	CGGAGATGTT	GGAATCGTC	150
	GAGATGGAGA	TGCGTGAGTT	ACTCACCAGC	TACGGCTTCG	AGGGCGACGA	200
	GACACCCATC	ATCATGGGTT	CCGCTCTATG	CGCCATCGAG	GGCCGCCAGC	250
35	CCGAGATCGG	TGTTACCAAG	GTCGACGAGC	TAATGGACGC	TGTCGACTCA	300
	TGGATCCCCA	CCCCTCAGCG	TGAGACCGAG	AAGCCTTTCC	TCATGGCTGT	350
	TGAGGATGTC	TTCTCGATTG	CTGGACGTGG	TACCGTCGTT	TCGGGCCGTG	400
	TCGAGCGCGG	TATCTTGAAG	CGTGACGCTG	AAGTCGAGCT	TGTCGGCAAG	450
	GGCACCGCGC	CAATCAAGAC	CAAGGTCACT	GATATTGAGA	CCTTCAAGAA	500
40	GTCGTGCGAG	GAGTCGCGCG	CGGGTGATAA	CTCCGGTCTT	CTCCTCCGTG	550
	GTGTCAAGCG	TGATGACGTT	CGCCGCGGTA	TGGTTGTTTC	CGTTCCCGGA	600
	CAAGTCAAGG	CTCACAAGAA	GTTCTTGTC	TCCATGTACG	TTCTAAGCAA	650
	AGAGGAGGGT	GGTCGTCACA	CCGGCTTCGG	CGAGAACTAC	AGGCCGCAA	700
	TGTTTCATCCG	AACTGCCGAT	GAATCCTGCG	CACTTCACTT	CCCAGAGGGT	750
45	ACCGAGGATG	CGCACGACAA	GCTAGTTATG	CCCGGTGACA	ACGTCGAGAT	800
	GGTCTGCGAA	CTCCACCAGC	CCCACGTTCT	AGAGACCGGT	CAGCG	845

50 2) INFORMATION FOR SEQ ID NO: 909

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
(B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909

5
CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG 50
AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG 100
CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT 150
CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT 200
10 TGGAAATGCG TGAACCTTTG ACCACCTACG GTTTCGAGGG TGAAGAGACC 250
CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA 300
GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA 350
TCCCCACCCC CCAGCGTGAC CTTGACAAGC CCTTCTTGAT GTCCGTTGAG 400
GAAGTTTTCT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA 450
15 GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA 500
AGAACCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT 550
TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT 600
CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA 650
CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT 700
20 GAAGGTGGTC GTCGTACTGG ATTCGGCGCC AACTACCGTC CTCAAGCTTT 750
CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT 800
GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT 850
CAGTCCAAGC AGGTCATGCC CCGTGACAAC GTTGAGATGA TCTTGAAGAC 900
ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931
25

2) INFORMATION FOR SEQ ID NO: 910

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 931 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: *Penicillium marneffei*
(B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910

45 CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG 50
AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG 100
CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT 150
CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT 200
TGGAAATGCG TGAACCTTTG ACCACCTACG GTTTCGAGGG TGAAGAGACC 250
CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA 300
50 GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA 350
TCCCCACCCC CCAGCGTGAC CTTGACAAGC CCTTCTTGAT GTCCGTTGAG 400
GAAGTTTTCT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA 450
GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA 500
AGAACCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT 550
55 TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT 600
CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA 650
CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT 700
GAAGGTGGTC GTCGTACTGG ATTCGGCGCC AACTACCGTC CTCAAGCTTT 750
CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT 800
60 GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT 850

CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC 900
ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931

5

2) INFORMATION FOR SEQ ID NO: 911

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911

GACGGMKKCA TGCCGCARAC

20

20

2) INFORMATION FOR SEQ ID NO: 912

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912

GACGGCGKCA TGCCGCARAC

20

35

2) INFORMATION FOR SEQ ID NO: 913

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913

GACGGYSYCA TGCKKCAGAC

20

50

2) INFORMATION FOR SEQ ID NO: 914

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

513

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 914

5

GAARAGCTGC GGRCGRTAGT G

21

10 2) INFORMATION FOR SEQ ID NO: 915

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915

AAACGCCTGA GGRCGGTAGT T

21

25

2) INFORMATION FOR SEQ ID NO: 916

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 916

GCCGAGCTGG CCGGCTTCAG

20

40

2) INFORMATION FOR SEQ ID NO: 917

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917

TCGTGCTACC CGTYGCCGCC AT

22

55

2) INFORMATION FOR SEQ ID NO: 918

60 (i) SEQUENCE CHARACTERISTICS:

514

- (A) LENGTH: 1391 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(E) ACCESSION NUMBER: J01672

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918

	AGAGAAGCCT	GTCGGCACCG	TCTGGTTTGC	TTTTGCCACT	GCCCGCGGTG	50
15	AAGGCATTAC	CCGGCGGGAT	GCTTCAGCGG	CGACCGTGAT	GCGGTGCGTC	100
	GTCAGGCTAC	TGCGTATGCA	TTGCAGACCT	TGTGGCAACA	ATTTCTACAA	150
	AACACTTGAT	ACTGTATGAG	CATACAGTAT	AATTGCTTCA	ACAGAACATA	200
	TTGACTATCC	GGTATTACCC	GGCATGACAG	GAGTAAAAAT	GGCTATCGAC	250
	GAAAACAAAC	AGAAAGCGTT	GGCGGCAGCA	CTGGGCCAGA	TTGAGAAACA	300
20	ATTTGGTAAA	GGCTCCATCA	TGCGCCTGGG	TGAAGACCGT	TCCATGGATG	350
	TGGAAACCAT	CTCTACCGGT	TCGCTTTTAC	TGGATATCGC	GCTTGGGGCA	400
	GGTGGTCTGC	CGATGGGCCG	TATCGTCGAA	ATCTACGGAC	CGGAATCTTC	450
	CGGTAAAACC	ACGCTGACGC	TGCAGGTGAT	CGCCGCAGCG	CAGCGTGAAG	500
	GTAAAACCTG	TGCGTTTATC	GATGCTGAAC	ACGCGCTGGA	CCCAATCTAC	550
25	GCACGTAAAC	TGGGCGTCGA	TATCGACAAC	CTGCTGTGCT	CCCAGCCGGA	600
	CACCGGCGAG	CAGGCACTGG	AAATCTGTGA	CGCCCTGGCG	CGTTCTGGCG	650
	CAGTAGACGT	TATCGTCGTT	GACTCCGTGG	CGGCACTGAC	GCCGAAAGCG	700
	GAAATCGAAG	GCGAAATCGG	CGACTCTCAC	ATGGGCCTTG	CGGCACGTAT	750
	GATGAGCCAG	GCGATGCGTA	AGCTGGCGGG	TAACCTGAAG	CAGTCCAACA	800
30	CGCTGCTGAT	CTTCATCAAC	CAGATCCGTA	TGAAAATTGG	TGTGATGTTC	850
	GGTAACCCGG	AAACCACTAC	CGGTGGTAAC	GCGCTGAAAT	TCTACGCCTC	900
	TGTTTCGTCTC	GACATCCGTC	GTATCGGCGC	GGTGAAAGAG	GGCGAAAACG	950
	TGGTGGGTAG	CGAAACCCGC	GTGAAAGTGG	TGAAGAACAA	AATCGCTGCG	1000
	CCGTTTAAAC	AGGCTGAATT	CCAGATCCTC	TACGGCGAAG	GTATCAACTT	1050
35	CTACGGCGAA	CTGGTTGACC	TGGGCGTAAA	AGAGAAGCTG	ATCGAGAAAG	1100
	CAGGCGCGTG	GTACAGCTAC	AAAGGTGAGA	AGATCGGTCA	GGGTAAAGCG	1150
	AATGCGACTG	CCTGGCTGAA	AGATAACCCG	GAAACCGCGA	AAGAGATCGA	1200
	GAAGAAAGTA	CGTGAGTTGC	TGCTGAGCAA	CCCGAACTCA	ACGCCGGATT	1250
	TCTCTGTAGA	TGATAGCGAA	GGCGTAGCAG	AAACTAACGA	AGATTTTTTA	1300
40	TCGTCTTGTT	TGATACACAA	GGGTCGCATC	TGCGGCCCTT	TTGCTTTTTT	1350
	AAGTTGTAAG	GATATGCCAT	GACAGAATCA	ACATCCCGTC	G	1391

45 2) INFORMATION FOR SEQ ID NO: 919

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919

GGICCIGART CITMIGGIAA RAC

23

60

2) INFORMATION FOR SEQ ID NO: 920

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920

TCICCVATIT CICCITCIAI YTC

23

15

2) INFORMATION FOR SEQ ID NO: 921

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921

TIYRTIGAYG CIGARCAIGC

20

30

2) INFORMATION FOR SEQ ID NO: 922

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922

45 TARAAYTTIA RIGCIYKICC ICC

23

2) INFORMATION FOR SEQ ID NO: 923

50

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923

60

5 2) INFORMATION FOR SEQ ID NO: 924

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924

ACCTCAGTCG TCACGTTGGC G

21

20

2) INFORMATION FOR SEQ ID NO: 925

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925

AAGCAGATGG TTGTGTGCTG

20

35

2) INFORMATION FOR SEQ ID NO: 926

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926

CAGCTGCTCG TGGTGCATCT CGAT

24

50

2) INFORMATION FOR SEQ ID NO: 927

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927

5 ACGCGGAGAA GGTGCGCTT

19

2) INFORMATION FOR SEQ ID NO: 928

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928

20

GGTCGTTCTT CGAGTCACCG CA

22

25 2) INFORMATION FOR SEQ ID NO: 929

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacteroides fragilis*

(B) STRAIN: ATCC 25285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929

40

TTCAGCATGC	CATTTCAAAA	CAGGCCGAAG	CCGATATCGT	GATTATCGCT	50
GCTTGTGGGG	AGCGTGCAAA	TGAAGTTGTG	GAAATCTTTA	CCGAATTTCC	100
GGAATTGGTG	GACCCGCACA	CGGGACGTAA	GCTGATGGAG	CGTACCATTA	150
TTATCGCAAA	TACATCGAAC	ATGCCGGTAG	CAGCGCGTGA	AGCTTCTGTG	200
45 TATACGGCCA	TGACGATTGC	CGAATACTAT	CGTGCCATGG	GATTGAAAGT	250
CCTGCTGATG	GCAGACTCCA	CTTCCCGTTG	GGCGCAGGCA	TTGCGTGAGA	300
TGTCGAACCG	TATGGAGGAG	TTGCCCGGAC	CGGATGCATT	CCCGATGGAC	350
CTGTCCTCAA	TCATTTCTAA	CTTCTATGGC	CGTGCAGGCT	ACGTGAAACT	400
50 GAATAACGGC	GAGAGCGGTT	CTATTACCTT	TATCGGTACA	GTATCACC	448

2) INFORMATION FOR SEQ ID NO: 930

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacteroides distasonis*
(B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930

	GCTATCTCTA	AACAAGCGGA	AGCGGATATC	GTGATTATCG	CCGCCTGCGG	50
10	TGAGCGTGCG	AATGAGGTCG	TAGAGGTATT	TACGGAGTTC	CCGGAATTGG	100
	TAGACCCGCA	TACGGGACGT	AAATTGATGG	AACGTACGAT	CATTATCGCC	150
	AATACATCCA	ACATGCCGGT	AGCCGCTCGT	GAGGCATCCG	TATATACGGC	200
	GATGACCATC	GCCGAGTATT	ATCGCAGCAT	GGGTTTGAAG	GTTCTGTTGA	250
	TGGCCGACTC	TACTTCCCGC	TGGGCACAGG	CTTTGCGTGA	GATGTCCAAC	300
15	CGTTTGGAGG	AGTTGCCGGG	ACCGGATGCT	TTCCCGATGG	ACTTGTCCGC	350
	TATCGTGGCG	AACTTCTACG	CTCGTGCCGG	ATTCGTTCAT	TTGAATAACA	400
	ACGCTACAGG	CTCCGTCACT	TTCATCGGTA	CGGTATCG		438

20

2) INFORMATION FOR SEQ ID NO: 931

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 453 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas asaccharolytica*
(B) STRAIN: ATCC 25260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931

	CCTCCAGCAC	GCTATCTCTA	AGCAGGCGGA	GGCTGATATC	GTCATTATGG	50
	CAGCCTGCGG	TGAGCGTGCT	AATGAGGTGG	TGGAGATCTT	TGCCGAGTTC	100
	CCTGAGCTCG	AAGACCCACA	CACGGGACGC	AAGCTGATGG	AGCGTACGAT	150
40	CATCATCGCT	AACACGAGTA	ACATGCCAGT	GGCTGCTCGT	GAGGCTTCGG	200
	TCTACACCGC	TATGACCATC	GCTGAGTACT	ACCGCTCGAT	GGGTCTCAAA	250
	GTA CTCTAA	TGGCTGACTC	GACCTCTCGC	TGGGCACAGG	CACTGCGTGA	300
	GATGTCTAAC	CGTCTAGAGG	AGCTGCCTGG	ACCAGATGCA	TTCCCGATGG	350
	ACTTGTCCGC	TATCGTGGCA	AACTTCTACG	CTCGTGCCGG	CTTCGTCTAT	400
45	CTCAACAACG	GTGAGACAGG	TTCTGTAACC	TTCATCGGTA	CGGTCTCTCC	450
	AGC					453

50 2) INFORMATION FOR SEQ ID NO: 932

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932

5 CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC 50
GTGAACATAT CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA 100
TTCATGAACA AATGTGACAT GGTGACGAT GAAGAATTAC TAGAATTAGT 150
TGAAATGGAA ATTCGTGATC TATTAAGTGA ATATGAATTC CCTGGCGATG 200
10 ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA AGGTGAAGCT 250
GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
TCCAACCTCCW GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG 350
ATGTATTCTC AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTTGAA 400
CGTGGACAAG TTAAAGTTGG TGACGAAGTA GAAGTTATCG GTATCGAAGA 450
15 AGAAAGCAAA AAAGTAGTAG TAACTGGAGT AGAAATGTTC CGTAAATTAC 500
TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT ACGTGGTGT 550
GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT 600
TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG 650
AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT 700
20 TTCCGTAATA CTGACGTAAC TGGTATTGTT ACACTTCCAG AAGGTACTGA 750
AATGGTAAYG CCTGGTGATA ACATTGAGCT TGCAGTTGAA CTAATTGCAC 800
CAATCGCTAT CGAAGACGGT ACTAAATTCT CTATC 835

25

2) INFORMATION FOR SEQ ID NO: 933

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933

CATCATCGTI TTCMTGAACA ARTG

24

40

2) INFORMATION FOR SEQ ID NO: 934

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934

TCACGYTTRR TACCACGCAG IAGA

24

55

2) INFORMATION FOR SEQ ID NO: 935

60 (i) SEQUENCE CHARACTERISTICS:

520

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935

10 GGIAARWSIC ARYTITGYCA YAC

23

15 2) INFORMATION FOR SEQ ID NO: 936

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936

25

TCISIIYTCIG GIARRCAIGG

20

30 2) INFORMATION FOR SEQ ID NO: 937

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937

40

ATIIACIGARG YITTYGGIGA RTT

23

45 2) INFORMATION FOR SEQ ID NO: 938

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938

55

CYIGTIGYIS WIGCRTGIGC

20

60

2) INFORMATION FOR SEQ ID NO: 939

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1203 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: D10023
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939

15	ATGTCTCAAG	TTCAAGAACA	ACATATATCA	GAGTCACAGC	TTCAGTACGG	50
	GAACGGTTCG	TTGATGTCCA	CTGTACCAGC	AGACCTTTCA	CAGTCAGTCG	100
	TTGATGGAAA	CGGCAACGGT	AGCAGCGAAG	ATATTGAGGC	CACCAACGGC	150
20	TCCGGCGATG	GTGGCGGATT	GCAGGAGCAA	GCGGAAGCGC	AAGGTGAAAT	200
	GGAGGATGAA	GCATACGATG	AAGCTGCCTT	AGGTTCTGTTT	GTGCCAATAG	250
	AAAAACTGCA	AGTGAACGGG	ATTACTATGG	CGGATGTGAA	AAAACTAAGG	300
	GAGAGTGGGC	TTCACACTGC	TGAAGCGGTA	GCATATGCTC	CCAGAAAGGA	350
	TTTATTGGAA	ATCAAAGGTA	TATCGGAAGC	TAAGGCAGAT	AAGTTGCTAA	400
25	ACGAAGCGGC	AAGGCTAGTG	CCTATGGGAT	TTGTCACGGC	TGCTGATTTT	450
	CATATGAGAA	GATCGGAGCT	GATTTGTTTG	ACAACGGGTT	CTAAGAATTT	500
	GGACACTCTT	TTGGGTGGTG	GTGTGGAAAC	TGGTTCTATT	ACTGAGCTTT	550
	TCGGTGAATT	CAGGACAGGT	AAGTCCCAGC	TATGTCACAC	TTTGGCCGTG	600
	ACATGCCAAA	TTCCATTGGA	TATTGGTGGC	GGTGAAGGTA	AGTGTTTGTA	650
30	TATCGATACC	GAAGGTACTT	TCAGGCCGGT	AAGATTGGTA	TCCATAGCTC	700
	AGCGGTTCGG	ATTAGACCCG	GATGATGCTT	TGAACAACGT	TGCGTATGCA	750
	AGAGCCTATA	ACGCCGATCA	TCAGTTAAGA	CTTCTGGATG	CTGCTGCCCA	800
	AATGATGAGC	GAGTCTCGGT	TTTCCTTGAT	TGTGGTCGAT	TCTGTTATGG	850
	CTCTATACCG	TACGGATTTT	TCTGGTCGTG	GTGAACTAAG	CGCAAGGCAA	900
35	ATGCATTTAG	CCAAATTTAT	GCGTGCTTTG	CAAAGGCTGG	CCGACCAATT	950
	TGGTGTTGCA	GTCGTCGTTA	CTAACCAAGT	GGTCGCCCAA	GTTGATGGTG	1000
	GTATGGCTTT	TAATCCAGAT	CCAAAGAAGC	CTATCGGTGG	TAATATTATG	1050
	GCACATTCTT	CCACCACGCG	ATTAGGTTTC	AAAAAGGGTA	AGGGATGTCA	1100
	AAGATTATGC	AAAGTTGTTG	ACTCACCTTG	CTTACCAGAG	GCTGAATGTG	1150
40	TGTTCGCGAT	CTATGAAGAT	GGTGTTGGTG	ACCCAGAGA	AGAAGACGAG	1200
	TAG					1203

45 2) INFORMATION FOR SEQ ID NO: 940

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: GRF88
 (C) ACCESSION NUMBER: M87549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940

	CGATCCAATT	GCTGGTCTTA	AGATGCATTT	GATTGATCTA	GGTATTGCCA	50
	CTGAAGCTGA	AGTCAAAGCT	TACGACAAGT	CCGCTAGAAA	ATACGTTGAC	100
	GAACAAGTTG	AATTAGCTGA	TGCTGCTCCT	CCTCCAGAAG	CCAAATTATC	150
5	CATCTTGTTT	GAAGACGTCT	ACGTGAAAGG	TACAGAAACT	CCAACCCCTAA	200
	GAGGTAGGAT	CCCTGAAGAT	ACTTGGGACT	TCAAAAAGCA	AGGTTTTTGCC	250
	TCTAGGGATT	AATTAAATCG	TAAGGAAAAA	TAAAATAATA	GTGCTGTGAT	300
	CGCATGATAT	TCTTCCCTGG	AAGCGCCATT	TTATAGCAAG	AAATGTAAGT	350
	CAAGTATATT	TTAACTGTAT	ATACAACAAT	ATGACTCTTT	TTTATGCCTT	400
10	GTTGTTTTTC	TTCGGGTTTT	CCCACACATT	GTGTGGAGAG	ATAGTTATTA	450
	ACAGACCGAA	AATAGCCGCC	CAAGGATAAA	CTTTTATATA	AAGGGAAGGG	500
	TAGTTGACCC	AAAAATTTGG	ATTCTACTTT	CCAGATTTAC	TTTCACCCTT	550
	TTATATTTGC	TGTAGTCTGT	TATGCCAATC	AGGAAAGCAT	TTGAACAAAT	600
	ATGTCTGTTA	CAGGAACTGA	GATCGATAGT	GATACAGCAA	AAAATATTCT	650
15	TAGTGTAGAT	GAATTACAGA	ACTATGGTAT	TAATGCCTCA	GATCTTCAAA	700
	AATTGAAGTC	TGGTGGGATA	TACACAGTCA	ATGTATGTTA	TAATAACATT	750
	TTTAAAACCT	CTGCTGTAGA	GGTTCTTTCC	CCCTTTCTTT	TACTAACTAA	800
	TAATTTGGAA	AGGAACTTTT	ATAGACCGTT	TTGTCAACAA	CAAGAAGACA	850
	TCTATGTAAA	ATTAAAGGGT	TAAGTGAGGT	GAAAGTGGAA	AAAATTAAAG	900
20	AAGCTGCTGG	AAAAATCATA	CAGGTGGGAT	TTATCCCCGC	TACTGTACAA	950
	TTAGATATAA	GACAGCGTGT	GTACTCCTTA	TCAACTGGAT	CTAAGCAACT	1000
	AGATTCAATC	CTAGGTGGTG	GAATAATGAC	AATGAGTATC	ACTGAAGTAT	1050
	TTGGTGAATT	TAGGTGTGGT	AAGACACAGA	TGTCTCATA	TTTGTGTGTT	1100
	ACCACGCAGC	TTCCGAGGGA	AATGGGTGGT	GGTGAAGGGA	AAGTAGCATA	1150
25	TATTGATACA	GAAGGCACTT	TCAGGCCCGA	GAGGATTAAG	CAAATTGCAG	1200
	AAGGTTATGA	ATTGGATCCC	GAGTCATGTT	TGGCAAACGT	TTCATATGCT	1250
	AGAGCCTTGA	ATAGTGAACA	TCAAATGGAA	CTTGTTGAAC	AATTGGGTGA	1300
	AGAACTTAGT	TCTGGAGATT	ATCGCCTTAT	CGTGGTAGAT	TCTATAATGG	1350
	CAAACCTCAG	AGTAGACTAC	TGCGGTAGAG	GTGAACTAAG	CGAAAGACAG	1400
30	CAAAAGCTAA	ATCAACATCT	TTTCAAATTG	AATAGATTGG	CAGAGGAATT	1450
	TAATGTTGCA	GTATTTCTGA	CAAACCAAGT	TCAATCAGAC	CCAGGTGCTT	1500
	CTGCATTATT	TGCCTCGGCA	GATGGTAGGA	AACCAATTGG	AGGGCACGTT	1550
	CTGGCACATG	CGTCAGCAAC	AAGGATTTTG	TTGAGAAAAG	GGCGTGGTGA	1600
	CGAAAGAGTT	GCCAAGTTAC	AAGATTCCCC	AGATATGCCT	GAAAAAGAAT	1650
35	GTGTCTACGT	AATTGGTGAA	AAAGGTATTA	CCGATTCAAG	TGACTAGTTT	1700
	TTGTATACTT	TTTAAATGAA	GATGACATTG	CTCCTTTATT	AAACTTTTCT	1750
	TTTACTTTGT	GTTACTAATA	TTATTAATAT	CTTGTTATGA	TTCTTTGTTT	1800

2) INFORMATION FOR SEQ ID NO: 941

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 430 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Cryptococcus humicola*
 (B) STRAIN: ATCC 38294
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941

5	CGTCCTTATC	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCC	CACGGTGGTT	50
	TCTCCGTCTT	CACCGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGACCTG	100
	TACCACGAGA	TGCGTGAGAC	TGGTGTCAAT	AACCTCGAGG	GCGACTCCAA	150
20	GGTCGCTCTC	GTCTTCGGCC	AGATGAACGA	GCCCCCGGA	GCCCGTGCCC	200
	GTGTCGCCCT	TACCGGCCTC	ACCATCGCCG	AGTACTTCCG	TGACGAGGAG	250
	GGTCAGGACG	TGCTTCTCTT	CATCGACAAC	ATTTTCCGTT	TCACCCAGGC	300
	CGGTTCCGAG	GTGTCTGCCC	TTCTCGGTCG	TATCCCCTCG	GCCGTCGGTT	350
	ACCAGCCAC	CCTCGCTACC	GACATGGGTT	CCATGCAGGA	GCGTATCACC	400
25	ACCACCAAGA	AGGGTTCGAT	TACCTCCGTC			430

2) INFORMATION FOR SEQ ID NO: 942

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942

45	CGTGTACGAT	GCTCTTGAGG	TGCAAAATGG	TAATGAGCGT	CTGGTGCTGG	50
	AAGTTCAGCA	GCAGCTCGGC	GGCGGTATCG	TGCGTACCAT	CGCAATGGGT	100
	TCCTCCGACG	GTCTGCGTCG	CGGTCTGGAT	GTAAAAGACC	TCGAACACCC	150
	GATCGAAGTC	CCGGTAGGTA	AAGCGACTCT	GGGCCGTATC	ATGAACGTAC	200
	TGGGTGAACC	GGTCGACATG	AAAGGCGAGA	TCGGTGAAGA	AGAGCGTTGG	250
50	GCGATTACAC	GCGCAGCACC	TTCCTACGAA	GAGCTGTCAA	ACTCTCAGGA	300
	ACTGCTGGAA	ACCGGTATCA	AAGTTATCGA	CCTGATGTGT	CCGTTCGCTA	350
	AGGGCGGTAA	AGTTGGTCTG	TTCGGTGGTG	CGGGTGTAGG	TAAAACCGTA	400
	AACATGATGG	AGCTCATTCG	TAACATCGCG	ATCGAGCACT	CCGGTTACTC	450
	TGTGTTTGCG	GGCGTAGGTG	AACGTACTCG	TGAGGGGAAC	GACTTCTACC	500
55	ACGAAATGAC	CGACTCCAAC	GTTATCGATA	AAGTATCCCT	GGTGTATGGC	550
	CAGATGAACG	AGCCGCCGGG	AAACCGTCTG	CGCGTAGCTC	TGACCGGTCT	600
	GACCATGGCT	GAGAAATTCC	GTGACGAAGG	TCGTGACGTT	CTGCTGTTCG	650
	TTGACAACAT	CTATCGTTAC	ACCCTGGCCG	GTACGGAAGT	ATCCGCACTG	700
	CTGGGCCGTA	TGCCTTCAGC	GGTAGGTTAT	CAGCCGACCC	TGGCGGAAGA	750
60	GATGGGCGTT	CTGCAGGAAC	GTATCACCTC	CACCAAAC	GGTT	794

2) INFORMATION FOR SEQ ID NO: 943

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943

20	ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTGCAAAA TGGTAATGAG	50
	CGTCTGGTGC TGGAAAGTTCA GCAGCAGCTC GCGGCGGGTA TCGTACGTAC	100
	CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGCGGTCTG GATGTAAAAG	150
	ACCTCGAACA CCCGATTGAA GTCCCGGTAG GTAAAGCGAC TCTGGGCCGT	200
	ATCATGAACG TACTGGGTGA ACCGGTCGAC ATGAAAGGCG AGATCGGTGA	250
25	AGAAGAGCGT TGGGCGATTC ACCGCGCAGC ACCTTCCTAC GAAGAGCTGT	300
	CAAACCTCTCA GGAAGTCTG GAAACCGGTA TCAAAGTTAT CGACCTGATG	350
	TGTCCGTTTCG CTAAGGGCGG TAAAGTTGGT CTGTTCCGGTG GTGCGGGTGT	400
	AGGTAAAACC GTAAACATGA TGGAGCTCAT TCGTAACATC GCGATCGAGC	450
	ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT	500
30	AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC	550
	CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG	600
	CTCTGACCGG TCTGACCATG GCTGAGAAAT TCCGTGACGA AGGTCGTGAC	650
	GTTCTGCTGT TCGTTGACAA CATCTATCGT TACACCCTGG CCGGTACGGA	700
	AGTATCCGCA CTGCTGGGCC GTATGCCTTC AGCGGTAGGT TATCAGCCGA	750
35	CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC CTCCACCAAA	800
	ACTGGTTCTA TCAC	814

40 2) INFORMATION FOR SEQ ID NO: 944

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 11775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944

55

	GTGTACGATG CTCTTGAGGT GCAAAATGGT AATGAGCGTC TGGTGCTGGA	50
	AGTTCAGCAG CAGCTCGGCG GCGGTATCGT GCGTACCATC GCAATGGGTT	100
	CCTCCGACGG TCTGCGTCGC GGTCTGGATG TAAAAGACCT CGAACACCCG	150
	ATCGAAGTCC CGGTAGGTAA AGCGACTCTG GGCCGTATCA TGAACGTACT	200
60	GGGTGAACCG GTCGACATGA AAGGCGAGAT CGGTGAAGAA GAGCGTTGGG	250

	CGATTCACCG	CGCAGCACCT	TCCTACGAAG	AGCTGTCAAA	CTCTCAGGAA	300
	CTGCTGGAAA	CCGGTATCAA	AGTTATCGAC	CTGATGTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTTGGTCTGT	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTAA	400
	ACATGATGGA	GCTTATTCGT	AACATCGCGA	TCGAGCACTC	CGGTTACTCT	450
5	GTGTTTGCGG	GCGTAGGTGA	ACGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
	CGAAATGACC	GACTCCAACG	TTATCGACAA	AGTATCCCTG	GTGTATGGCC	550
	AGATGAACGA	GCCGCCGGGA	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCTG	AGAAATTCCG	TGACGAAGGT	CGTGACGTTC	TGCTGTTCGT	650
	TGACAACATC	TATCGTTACA	CCCTGGCCGG	TACGGAAGTA	TCCGCACTGC	700
10	TGGGCCGTAT	GCCTTCAGCG	GTAGGTTATC	AGCCGACCCT	GGCGGAAGAG	750
	ATGGGCGTTC	TGCAGGAACG	TATCACCTCC	ACCAAAACCG	GTTCTATC	798

15 2) INFORMATION FOR SEQ ID NO: 945

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 812 bases

(B) TYPE: Nucleic acid

20 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945

30	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
35	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	GCGATCGAGC	450
40	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CTTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTATTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	CCGGTACCGA	700
45	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

50

2) INFORMATION FOR SEQ ID NO: 946

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

55 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946

	GCGACGCTAT	CCCGCATGTT	TACGATGCCC	TGAAATTGGA	CGAGAACGGT	50
	CTGACTCTGG	AAGTTCAACA	ACTTCTGGGT	GACGGCGTTG	TCCGTACTAT	100
	TGCAATGGGT	AGTTCAGACG	GCCTGAAACG	CGGCATGTCT	GTAAGCAATA	150
10	CTGGTGCGCC	AATCACTGTG	CCGGTAGGTA	AAGGTACTTT	GGGTCGTATT	200
	GTCGACGTAT	TGGGTACGCC	TGTTGATGAA	GCAGGTCCGA	TCGATAACCGA	250
	CAAGAGCCGT	GCCATTACAC	AAACTGCTCC	GAAATTTCGAC	GAGTTGTCTG	300
	CAACTACCGA	ATTGTTGGAA	ACCGGTATTA	AAGTGATCGA	CTTGCTGTGT	350
	CCGTTTGCTA	AAGGCGGTAA	AGTAGGTCTG	TTCGGTGGTG	CCGGTGTAGG	400
15	CAAAACCGTG	AACATGATGG	AATTGATCAA	CAACATCGCC	AAAGCGCACA	450
	GCGGTCTGTC	CGTGTTTCGA	GGTGTGGGCG	AGCGTACCCG	TGAAGGTAAC	500
	GACTTCTACC	ACGAGATGAA	AGATTCCAAC	GTATTGGATA	AAGTGGCAAT	550
	GGTTTACGGT	CAGATGAACG	AACCTCCGGG	CAACCGTTTG	CGCGTCGCAT	600
	TGACCGGTTT	GACCATGGCG	GAATACTTCC	GTGACGAAAA	AGACGAAAAC	650
20	GGTAAAGGTC	GCGACGTATT	GTTCTTCGTT	GACAAACATCT	ACCGTTACAC	700
	TCTGGCCCGT	ACCGAAGTAT	CTGCACTGTT	GGGCCGTATG	CCTTCTGCAG	750
	TGGGTTACCA	ACCGACATTG	GCTGAAGAAA	TGGGTCGTTT	GCAAGAGCGT	800
	ATTACCTCTA	CCCAAACCGG	TTCCATTACT	TC		832

25

2) INFORMATION FOR SEQ ID NO: 947

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*
 (B) STRAIN: ATCC 9913

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947

	TCCGCGCGAT	GCCATTCCGC	ATGTTTACGA	CGCCCTGAAA	TTGGATGCAA	50
	ACGGCCTGAC	TTTGGAAGTA	CAACAGCTTC	TGGGCGACGG	CGTGGTTCGT	100
45	ACTATTGCAA	TGGGTAGTTC	GGACGGTCTG	AAACGCGGCA	TGACTGTAAG	150
	CAATACAGAT	GCGCCGATTA	CTGTGCCGGT	AGGTAAAGGT	ACTTTGGGAC	200
	GTATTGTCGA	TGTGTTGGGT	ACACCTGTTG	ATGAAGCAGG	TCCGATTGAT	250
	ACCGACAAAC	ACCGTGCTAT	CCATCAGACA	GCTCCGAAAT	TCGATGAGTT	300
	GTCTGCTACT	ACCGAGCTGC	TGGAAACAGG	CATTAAAGTG	ATTGACTTGC	350
50	TGTGTCCGTT	TGCCAAAGGC	GGTAAAGTAG	GTCTGTTCGG	TGGTGCCGGT	400
	GTAGGCAAAA	CCGTCAACAT	GATGGAATTG	ATTAACAACA	TCGCCAAAGC	450
	GCATAGTGGT	TTGTCCGTGT	TCGCCGGTGT	GGGGGAACGT	ACCCGTGAAG	500
	GTAACGACTT	CTACCACGAG	ATGAAAGATT	CCAACGTATT	GGACAAAGTG	550
	GCGATGGTTT	ACGGTCAGAT	GAACGAACCT	CCGGGTAAAC	GTCTGCGTGT	600
55	AGCCTTGACC	GGTTTGACGA	TGGCCGAATA	CTTCCGTGAT	GAAAAAGACG	650
	AAAGCGGCAA	AGGTCGCGAC	GTATTGTTCT	TCGTGGACAA	CATTTACCGT	700
	TACACTCTGG	CCGGTACAGA	AGTATCCGCA	TTGCTCGGTC	GTATGCCTTC	750
	AGCAGTAGGT	TACCAACCGA	CATTGGCTGA	AGAAATGGGT	CGTCTGCAAG	800
	AGCGTATTAC	CCTCTACTCA	AACAGGCTCC	ATTACTTCTA		840

60

2) INFORMATION FOR SEQ ID NO: 948

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948

	GCAGCTGGCG	ACAAGCTACC	TGAGATCAAT	AATGCACTTG	TAGTCTATAA	50
20	AAATGACGAA	AAAAAATCAA	AAATCGTCCT	TGAAGTAGCT	CTTGAGCTTG	100
	GTGATGGAGT	GGTTCGGACC	ATCGCTATGG	AATCAACGGA	TGGGTTGACT	150
	CGTGGCATGG	AAGTGCTAGA	TACTGGCCGT	CCAATTTCTG	TGCCAGTCGG	200
	CAAAGAAACA	CTTGGTCGCG	TCTTTAACGT	TTTGGGAGAT	ACCATTGACT	250
	TGGATGCTCC	TTTTGCGGAT	GATGCAGAGC	GCCAGCCAAT	CCATAAGAAA	300
25	GCTCCAACCT	TTGATGAGTT	GTCTACTTCT	TCAGAGATCT	TAGAGACAGG	350
	TATCAAGGTT	ATCGACCTGT	TAGCCCCTTA	TCTGAAAGGT	GGTAAAGTTG	400
	GACTCTTCGG	TGGTGCCGGA	GTTGGTAAGA	CCGTCCTGAT	TCAAGAATTG	450
	ATCCACAACA	TTGCCAAGA	ACACGGTGGT	ATTTCTGTAT	TTACTGGCGT	500
	TGGGGAACGT	ACCCGTGAAG	GGAATGACCT	TTATTGGGAA	ATGAAAGAGT	550
30	CTGGTGTTAT	CGAGAAAACA	GCCATGGTCT	TCGGTCAGAT	GAATGAGCCG	600
	CCAGGAGCGC	GTATGCGGGT	TGCTTTGACT	GGTTTGACGA	TTGCAGAATA	650
	CTTCCGTGAT	GTGGAAGGTC	AAGATGTCTT	GCTCTTCATT	GACAACATCT	700
	TCCGTTTCAC	GCAGGCAGGT	TCTGAAGTTT	CTGCCCTTTT	GGGTCGGATG	750
	CCGTCAGCCG	TTGGTTACCA	ACCAACACTT	GCGACAGAAA	TGGGGCAATT	800
35	GCAAGAGCGT	ATCACATCGA	CTAAGAAGGG	TTCTGTAACC	TCT	843

2) INFORMATION FOR SEQ ID NO: 949

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949

55	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTGG	100
	GAGATGGTAT	GGTCCGTACT	ATCGCCATGG	AATCAACAGA	TGGTTTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAATGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTACAGAA	GATGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300

	GCTCCA	ACTT	TTGATGA	ATT	GTCTAC	CTCT	TCTGAA	ATCC	TTGAAAC	CAGG	350
	GATTAAG	GTT	ATCGAC	CCTT	TTGCC	CCCTTA	CCTTAA	AAGGT	GGTAAG	GTTG	400
	GACTTT	TCGG	TGGTG	CCCGA	GTTGGT	AAAA	CCGTCT	TAAT	CCAAGA	ATTG	450
	ATTCACA	ACA	TTGCC	CAAGA	ACACGG	TGGT	ATTTCA	GATAT	TTACCG	GTTG	500
5	TGGGGA	ACGT	ACTCGT	GAGG	GTAATG	ACCT	TTACTG	GGGA	ATGAA	AGAAT	550
	CAGGTG	TTAT	CGAGAA	AAACA	GCCATG	GATAT	TTGGTC	CAGAT	GAATG	AGCCG	600
	CCAGGAG	CAC	GTATGC	GTGT	TGCCCT	AACT	GGTTTG	GACAA	TCGCC	GAATA	650
	CTTCCG	TGAT	GTGGA	AGGCC	AAGACG	TGCT	TCTCTT	TATC	GATAAT	ATCT	700
	TCCGTT	TCAC	TCAGG	CTGGT	TCAGA	AGTAT	CTGCC	CTTTT	GGGTC	GTATG	750
10	CCATCAG	CCG	TTGGT	TACCA	ACCAAC	ACTT	GCTACG	GAAA	TGGGT	CAATT	800
	GCAAGAG	CGT	ATTACAT	CAA	CTAAA	AAGGG	TTCTGT	AACC	T		841

15 2) INFORMATION FOR SEQ ID NO: 950

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 bases

(B) TYPE: Nucleic acid

20 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus mitis*

(B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950

30	GCTACCTGAG	ATCAATAATG	CACTTGTAGT	CTATAAAAAT	GACGAAAATA	50
	AATCAAAAAT	CGTCCTTGAA	GTAGCTCTTG	AGCTTGGTGA	TGGAGTGGTT	100
	CGGACCATCG	CTATGGAATC	AACGGATGGG	TTGACTCGTG	GCATGGAAGT	150
	GCTAGATACT	GGTCGTCCAA	TTTCTGTGCC	AGTCGGCAAA	GAAACACTTG	200
35	GTCGCGTCTT	TAACGTTTTG	GGAGATACCA	TTGACTTGGA	TGCTCCTTTT	250
	GCGGATGATG	CAGAGCGCCA	GCCAATCCAT	AAGAAAGCTC	CAACCTTTGA	300
	TGAGTTGTCT	ACTTCATCAG	AGATCTTAGA	GACAGGTATC	AAGGTTATCG	350
	ACCTGTTAGC	ACCTTATCTG	AAAGGTGGTA	AAGTCGGACT	CTTCGGTGGT	400
	GCCGGAGTTG	GTAAGACCGT	CCTGATTCAG	GAATTGATCC	ACAACATTGC	450
40	CCAAGAGCAT	GGTGGTATTT	CCGTGTTTAC	CGGTGTTGGG	GAACGTACCC	500
	GTGAAGGGAA	TGACCTTTAC	TGGGAAATGA	AGGAGTCTGG	CGTTATCGAG	550
	AAAACAGCCA	TGGTCTTCGG	TCAGATGAAT	GAGCCACCAG	GAGCGCGTAT	600
	GCGGGTTGCT	TTGACTGGTT	TGACGATTGC	AGAGTACTTC	CGTGATGTAG	650
	AAGGTCAAGA	TGTCTTGCTC	TTCATTGACA	ACATCTTCCG	TTTCACGCAG	700
45	GCAGGTTCTG	AAGTCTCTGC	CCTTTTGGGT	CGGATGCCAT	CAGCCGTTGG	750
	TTACCAACCA	AACTTGCGA	CTGAAATGGG	AACTCCAA	GAGCGTATTA	800
	CATCGACTAA	GAAAGGTTCT	GTAACCTT			827

50

2) INFORMATION FOR SEQ ID NO: 951

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 844 bases

55 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus oralis*

(B) STRAIN: ATCC 35037

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951

	GCAGCAGGGG	AAACACTTCC	TGAGATTAAT	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTGG	100
	GTGATGGTAT	GGTCCGTACG	ATCGCCATGG	AATCAACAGA	TGGTTTGA	150
10	CGTGGAATGG	AAGTTTTGGA	CACAGGCCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACTATTGACT	250
	TGGATGCTCC	TTTCGCTGAA	GACGCTGAGC	GTCAGCCAAT	TCATAAGAAA	300
	GCTCCAACCTT	TTGATGAATT	GTCTACCTCA	TCTGAAATCT	TGGAAACAGG	350
	GATTAAGGTT	ATCGACCTTC	TTGCCCCCTTA	CCTTAAAGGT	GGGAAAGTTG	400
15	GACTCTTCGG	TGGTGCCGGA	GTTGGTAAAA	CTGTCTTGAT	CCAAGAGTTG	450
	ATTCACAACA	TTGCCCAAGA	ACATGGTGGT	ATTTCAGTAT	TTACCGGTGT	500
	TGGAGAACGT	ACCCGTGAGG	GGAACGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTAT	TTGGTCAGAT	GAATGAGCCA	600
	CCTGGAGCAC	GTATGCGTGT	TGCTCTTACT	GGTTTGACAA	TCGCCGAATA	650
20	CTTCCGTGAT	GTAGAAGGCC	AAGATGTGCT	TCTCTTTATC	GACAATATCT	700
	TCCGTTTCAC	TCAAGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGGATG	750
	CCTTCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CTAAGAAGGG	TTCTGTAACC	TCTA	844

25

2) INFORMATION FOR SEQ ID NO: 952

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-06

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952

	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
45	GAGATGGTAT	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGA	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	250
	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300
	GCTCCAACCTT	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	350
50	GATCAAGGTT	ATTGACCTTC	TTGCCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	400
	GACTTTTCGG	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	450
	ATTCACAACA	TTGCCCAAGA	GCACGGTGGT	ATTTCAGTAT	TTACTGGTGT	500
	TGGGGAACGT	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	600
55	CCAGGAGCAC	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	750
	CCATCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
60	GCAAGAACGT	ATCACATCAA	CCAAGAAGGG			830

2) INFORMATION FOR SEQ ID NO: 953

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 15 (B) STRAIN: StrR-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953

	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
20	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAAACT	200
	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACCT	300
25	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
	TTGCCCAAGA	GCACGGTGGT	ATTTCAGTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
30	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
35	ATCACATCAA	CTAAGAAGGG	TTC			823

2) INFORMATION FOR SEQ ID NO: 954

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954

55	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
	GAGATGGTAT	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300

	GCTCCAACTT	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	350
	GATCAAGGTT	ATTGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	400
	GACTTTTCGG	TGGTGCCGGA	GTTGGTAAAA	CTGTCTTAAT	CCAAGAATTG	450
	ATTCACAACA	TTGCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTGCTGGTGT	500
5	TGGGGAACGT	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	600
	CCAGGAGCAC	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	750
10	CCATCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CCAAGAAGGG	TTCTGTAACC	TCTA	844

15 2) INFORMATION FOR SEQ ID NO: 955

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 bases

(B) TYPE: Nucleic acid

20 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955

30	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAAACT	200
35	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACTT	300
	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
40	TTGCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
45	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
	ATCACATCAA	CCAAGAAGGG	TTCTGTAACC	TCTA		834

50 2) INFORMATION FOR SEQ ID NO: 956

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 bases

55 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia microti*

(B) STRAIN: Persing-1

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956

	TTGTATATCA	CAGGCACTCA	GCAAATATTC	CGATACTGAC	GTAATTATAT	50
	ACGTGGGTTG	TGGTGAACGT	GGGAATGAAA	TGGCTGAGAT	TCTATGCGAA	100
	TTCCCTGAAC	TATCTACTGT	AGTTAATGAT	GAAAAGGTGG	CCATTATGGA	150
10	ACGTACATGC	TTAGTTGCCA	ATACTTCTAA	TATGCCAGTG	GCCGCTAGAG	200
	AAGCTAGTAT	ATACACTGGT	ATTACAATTG	CTGAATATTT	CCGTGATATG	250
	GGTTACAAC	GCACTCTTAT	GGCCGATTCC	ACTAGCCGAT	GGGCAGAGGC	300
	TCTAAGGGAA	ATTTCTGGTA	GATTGGCTGA	AATGCCTGCA	GATTCTGGCT	350
	ATCCGGCCTA	TTTATCGTCA	AGGTTGTCAG	CTTTTTATGA	ACGTGCAGGT	400
15	GGGATAACTG	TCTAATTAAT	TTAGGCTTGA	TTAAGTGCTT	AGG TTCACCA	450
	ACACGAACCG	GATCTATTAC	GGTTGTAGGA	GCAGTTTCTC	CACCA	495

20 2) INFORMATION FOR SEQ ID NO: 957

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Entamoeba histolytica*

(B) STRAIN: HM1-1MSS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957

35	AGTTATTTCA	CAAGCATTA	GTAAATATAG	TAATTCAGAT	GTTATTATTT	50
	ATGTAGGATG	TGGTGAACGA	GGAAATGAAA	TGGCAGAAGT	TCTTCGAGAT	100
	TTTCCAGCTC	TTTCTATTAA	AGTAGGAGAT	AAAGAAGAAT	CTATTATGAC	150
	AAGAACAGCA	CTTGTTGCTA	ATACATCTAA	TATGCCTGTT	GCAGCACGTG	200
40	AAGCATCAAT	TTATACTGGA	ATTACATTAT	CAGAATATTA	TAGAGATATG	250
	GGATATAATG	TTGCTATGAT	GGCAGATTCA	ACATCAAGAT	GGGCTGAAGC	300
	ACTTAGAGAA	ATTTTCAGGAC	GTCTTGCAGA	AATGCCAGCT	GATTCTGGAT	350
	ATCCAGCATA	TCTTGCAGCA	CGTTTAGCAT	CATTTTATGA	ACGTGCAGGT	400
	ATGGTTGAAT	GTTTAGGATC	ACCAAAAAGA	ATAGGGTCAG	TTTCTATTGT	450
45	AGGAGCTGTT	TCACCACCT				469

50 2) INFORMATION FOR SEQ ID NO: 958

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*

(B) STRAIN: ATCC 10953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958

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5  TACAACACCA ACTTGCTAAA TGGGCAGATG CAGAAGTAGT TGTTTATGTT      50
   GGTGTGTTGGG AACGTGGAAA TGAAATGACC GATGTACTTA TGGAATTCCC      100
   AGAAATTATT GACCCTAAGA CAGGACAATC TTTAATGAAG AGAACAGTTC      150
   TTATAGCTAA TACTTCTAAT ATGCCAGTTG CTGCTCGTGA GGCTTCAATC      200
   TATACTGGTA TAACTATTGC AGAATATTTT AGAGATATGG GATATTCAGT      250
10  GGCACCTTATG GCAGATTCAA CAAGTCGTTG GGCAGAAGCA CTTTCGTGAAA      300
   TGTCAGGACG TTTGGAAGAA ATGCCAGGTG ATGAAGGATA TCCAGCATAT      350
   CTATCAAGTA GAATAGCAGA GTTTTATGAA AGAGCAGGGC TTGTTGAATG      400
   TCTAGGTAAT GGAGAAGAAG GAGCATTAAC TGTAATTGGA GCAGTATCTC      450
   CA                                     452

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15

2) INFORMATION FOR SEQ ID NO: 959

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
- (B) STRAIN: ATCC 50119

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959

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35  TGTAATTAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAC TCGTCATCT      50
   ATGTCGGCTG CGGCGAGCGC GGTAATGAGA TGGCCGAGGT GTCATGGAG      100
   TTCCCGACCC TGACGACCGT GATCAATGGT CGCGAGGAGT CGATCATGAA      150
   GCGCACCTGC CTCGTGGCGA ACACTTCGAA CATGCCAGTC GCAGCCCGTG      200
   AGGCCTCTAT TTACACCGGC ATCACCTGCG CCGAGTACTA CCGTGATATG      250
   GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC      300
40  GCTTCGTGAG ATTTCTGGGTC GTCTGGCGGA GATGCCGGCC GATGGTGGCT      350
   ACCCTGCCTA TCTCAGCGCT CGTCTCGCCT CCTTCTACGA GCGCGCCGGC      400
   CTCGTCACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATTGT      450
   CGGTGCCGTG TCTCCGCCG                                     469

```

45

2) INFORMATION FOR SEQ ID NO: 960

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 30815

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960

	TGTAATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
5	TTCCCGACCC	TGACGACCGT	GATCGATGGT	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACTTCGAA	CATGCCAGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTACACCGGC	ATCACCTTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTCGGGTC	GTTTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
10	ACCCTGCCTA	TCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGCG	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATTGT	450
	CGGTGCCGTG	TCTCCGCCG				469

15

2) INFORMATION FOR SEQ ID NO: 961

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 469 bases
20	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Leishmania guyanensis</i>
(B)	STRAIN: ATCC 50126

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961

	TGTCATCAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCGGAC	TGTGTCATCT	50
	ATGTCGGCTG	CGGTGAACGC	GGTAACGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TTCCCGACCC	TGACGACTGT	GATCGATGGT	CGCGAAGAGT	CCATCATGAA	150
35	GCGCACCTGC	CTCGTGGCGA	ACACCTCGAA	CATGCCCGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTATACCGGC	ATCACCTTGG	CTGAGTACTA	CCGTGATATG	250
	GGCAAGCACA	TTGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTGCGTGAG	ATTTCGGGTC	GATTGGCGGA	GATGCCGGCT	GATGGTGGCT	350
	ACCCTGCCTA	CCTCAGCGCC	CGCCTCGCCT	CCTTCTACGA	GCGCGCCGGT	400
40	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
	CGGTGCAGTG	TCTCCACCG				469

45 2) INFORMATION FOR SEQ ID NO: 962

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 469 bases
	(B) TYPE: Nucleic acid
50	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Leishmania donovani</i>
(B)	STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962

60

	TGTCATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAT	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TTCCCGACCC	TGACGACCGT	GATCGATGGC	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACCTCGAA	CATGCCAGTC	GCAGCCCGTG	200
5	AGGCCTCTAT	TTACACCGGC	ATCACCTTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCTGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTCGGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCCGCCTA	CCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
10	CGGTGCCGTG	TCTCCACCG				469

2) INFORMATION FOR SEQ ID NO: 963

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963

30	TGTGATCAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCGGAC	TGCGTCATCT	50
	ACGTCGGCTG	TGGTGAGCGC	GGGAACGAGA	TGGCCGAGGT	GCTCATGGAT	100
	TTCCCGACTT	TGACGACTGT	GATCGATGGT	CGCGAGGAGT	CCATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACCTCCAA	CATGCCAGTT	GCAGCCCGTG	200
	AGGCTTCTAT	CTATACCGGC	ATCACACTGG	CTGAGTACTA	TCGTGATATG	250
35	GGCAAGCACA	TTGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GTTGCGTGAG	ATTTCGGGTC	GGCTGGCGGA	GATGCCGGCC	GATGGTGGTT	350
	ACCCCGCCTA	CCTCAGTGCC	CGTCTCGCCT	CCTTCTACGA	GCGCGCTGGC	400
	CTCGTGACCT	GTATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACAATTGT	450
	TGGTGCGGTG	TCTCCACCG				469

40

2) INFORMATION FOR SEQ ID NO: 964

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964

60	GGTCATTAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCTGAC	TGCGTCATCT	50
	ACGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100

	TTCCCGACCC	TGACGACCAT	GATCGATGGT	CGGGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACCTCGAA	CATGCCCGTC	GCAGCCCGTG	200
	AGGCCTCTAT	CTACACCGGC	ATCACCTCTG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCTGAGGC	300
5	GCTTCGTGAG	ATTTCGGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCCGCCTA	CCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
	CGGTGCCGTG	TCTCCGCCG				469

10

2) INFORMATION FOR SEQ ID NO: 965

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 469 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*

(B) STRAIN: ATCC 50129

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965

	TGTAATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
30	TTCCCGACCC	TGACGACCGT	GATCGATGGT	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACTTCGAA	CATGCCAGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTACACCGGC	ATCACCTCTG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTCGGGTC	GTTTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
35	ACCCTGCCTA	TCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATTGT	450
	CGGTGCCGTG	TCTCCGCCG				469

40

2) INFORMATION FOR SEQ ID NO: 966

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 449 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus anaerobius*

(B) STRAIN: ATCC 27337

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966

	CACCAGTTCG	CCAAGTGGGC	AGATGCTCAG	ATAGTTGTAT	ACGTTGGTTG	50
	TGGAGAACGT	GGTAACGAGA	TGACAGACGT	TCTAAATGAA	TTCCCAGAAC	100
	TGATTGACCC	TCATACAGGC	GAATCTCTAA	TGAAGAGAAC	AGTTCTTATA	150
60	GCTAATACGT	CAAATATGCC	AGTTGCAGCC	AGAGAGGCAA	GTATATATAC	200

	AGGTATTACA	ATAGCTGAAT	ATTTTAGAGA	CATGGGATAT	TCAGTAGCGG	250
	TAATGGCCGA	CTCTACATCA	AGATGGGCAG	AGGCCCTAAG	AGAGATGTCA	300
	GGTCGTCTAG	AAGAAATGCC	TGGTGATGAA	GGTTATCCAG	CCTATCTAGG	350
	TTCTAGAGCT	GCAGAGTTCT	ATGAAAGAGC	AGGTAAGGTA	ATATGTAAGG	400
5	GTAGCGATAA	TAGAGAGGGA	GCCCTTACAA	TAATAGGTGC	CGTGTCCACC	449

2) INFORMATION FOR SEQ ID NO: 967

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Bordetella pertussis*
 (B) STRAIN: ATCC 9797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967

25	CTGGTGGTGT	CGGCCGCAGA	CGGCCCGATG	CCGCAGACGC	GCGAGCACAT	50
	TTTGCTGTCG	CGCCAGGTTG	GCGTGCCGTA	CATCATCGTG	TTCCTGAACA	100
	AGGCGGACAT	GGTTGATGAC	GCGGAGCTGC	TCGAGCTGGT	GAAGATGGAA	150
	GTCCGCGAAC	TGCTGAGCAA	GTACGATTTC	CCGGGCGATG	ACACGCCGAT	200
	CGTGAAGGGT	TCGGCCAAGC	TGGCGCTGGA	AGGCGACAAG	GGCGAACTGG	250
30	GCGAGCAGGC	GATTCTGTCG	CTGGCGCAAG	CGCTGGACAC	GTACATTCCG	300
	ACGCCGGAGC	GCGCGGTCGA	CGGTGCGTTC	CTGATGCCGG	TGGAAGACGT	350
	GTTCTCGATC	TCGGGCCGTG	GCACGGTGGT	GACTGGCCGT	ATCGAGCGCG	400
	GCGTGGTGAA	GGTTGGCGAG	GAAATCGAAA	TCGTGGGCAT	CAAGCCGACG	450
	GTGAAGACGA	CCTGCACGGG	CGTGGAGATG	TTCCGCAAGC	TGCTGGACCA	500
35	GGGCCAGGCG	GGCGACAACG	TGGGTATCTT	GCTGCGCGGC	ACCAAGCGTG	550
	AAGACGTCGA	GCGTGGCCAG	GTGCTGGCCA	AGCCGGGTTC	GATCAACCCG	600
	CACACGGACT	TCACGGCCGA	GGTGTACATT	CTGTCCAAGG	AAGAGGGTGG	650
	CCGTCACACG	CCGTTCTTCA	ACGGCTATCG	TCCGCAGTTC	TACTTCCGCA	700
	CGACGGACGT	GACCGGCACG	ATCGACCTGC	CGGCGGACAA	GGAAATGGTG	750
40	CTGCCGGGCG	ACAACGTGTC	GATGACCGTC	AAGCTGCTGG	CCCCGATCGC	800
	CATGGAAGAA	GGTCTGCGTT	TCGCCA			826

45 2) INFORMATION FOR SEQ ID NO: 968

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Bordetella pertussis*
 (B) STRAIN: BD180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968

60

	CGATCCTGGT	GGTGTGCGCC	GCAGACGGCC	CGATGCCGCA	GACGCGCGAG	50
	CACATTTTGC	TGTCGCGCCA	GGTTGGCGTG	CCGTACATCA	TCGTGTTTCT	100
	GAACAAGGCG	GACATGGTTG	ATGACGCGGA	GCTGCTCGAG	CTGGTGGAGA	150
	TGGAAGTCCG	CGAACTGCTG	AGCAAGTACG	ATTTCCCGGG	CGATGACACG	200
5	CCGATCGTGA	AGGGTTCGGC	CAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
	ACTGGGCGAG	CAGGCGATTC	TGTCGCTGGC	GCAAGCGCTG	GACACGTACA	300
	TTCCGACGCC	GGAGCGCGCG	GTCGACGGTG	CGTTCCTGAT	GCCGGTGGAA	350
	GACGTGTTCT	CGATCTCGGG	CCGTGGCACG	GTGGTGACTG	GCCGTATCGA	400
	GCGCGGCGTG	GTGAAGGTTG	GCGAGGAAAT	CGAAATCGTG	GGCATCAAGC	450
10	CGACGGTGAA	GACGACCTGC	ACGGGCGTGG	AGATGTTCCG	CAAGCTGCTG	500
	GACCAGGGCC	AGGCGGGCGA	CAACGTGGGT	ATCTTGCTGC	GCGGCACCAA	550
	GCGTGAAGAC	GTCGAGCGTG	GCCAGGTGCT	GGCCAAGCCG	GGTTCGATCA	600
	ACCCGCACAC	GGACTTCACG	GCCGAGGTGT	ACATTCTGTC	CAAGGAAGAG	650
	GGTGGCCGTC	ACACGCCGTT	CTTCAACGGC	TATCGTCCGC	AGTTCTACTT	700
15	CCGCACGACG	GACGTGACCG	GCACGATCGA	CCTGCCGGCG	GACAAGGAAA	750
	TGGTGCTGCC	GGGCGACAAC	GTGTCGATGA	CCGTCAAGCT	GCTGGCCCCG	800
	ATCGCCATGG	AAGAAGG				817

20

2) INFORMATION FOR SEQ ID NO: 969

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus columbae*
 (B) STRAIN: ATCC 51263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969

	CCTATGCCAC	AAACTCGTGA	ACACATTCTT	TTATCACGTA	ACGTTGGTGT	50
	GCCATACATC	GTTGTTTTCT	TAAACAAAGT	TGATATGGTT	GACGACGAAG	100
	AATTATTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	AACTGAATAT	150
40	GACTTCCCAG	GAGACGATGT	TCCTGTAATC	GCTGGTTCTG	CATTAAAAGC	200
	TTTAGAAGGC	GACCCTGCTT	ACGAAGAAAA	AATCTTAGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACATCCCA	ACTCCAGAAC	GTGACAACGA	CAAACCATTC	300
	ATGATGCCAG	TTGAAGACGT	GTTCTCAATT	ACTGGTCGTG	GTAAGTTGAA	350
	TACAGGTCGT	GTTGAACGTG	GACAAGTTCG	TGTTGGTGAC	GAAGTTGAAA	400
45	TCGTTGGTAT	CGCTGACGAA	ACTTCTAAAA	CAACAGTTAC	TGGTGTGAA	450
	ATGTTCCGTA	AATTATTAGA	TTACGCTGAA	GCTGGAGACA	ACATCGGTGC	500
	ATTATTACGT	GGTGTGGCTC	GTGAAGACAT	CCAACGTGGT	CAAGTATTAG	550
	CTAAACCAGG	TTCAATCACT	CCACATACAA	AATTCATGCT	TGAAGTGTAC	600
50	GTTTTAACTA	AAGAAGAAGG	TGGACGTCAT	ACTCCAT		637

50

2) INFORMATION FOR SEQ ID NO: 970

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus flavescens*
(B) STRAIN: ATCC 49997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970

	TATGCCTCAA	ACACGTGAAC	ACATCTTGTT	ATCACGTAAC	GTTGGTGTAC	50
10	CATACATCGT	TGTTTTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTACTAGAAT	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATATGA	150
	CTTCCCAGGC	GACGATGTTT	CTGTAATCGC	TGGTTCTGCT	TTGAAAGCTC	200
	TTGAAGGCGA	TGCTTCATAC	GAAGAAAAAA	TCATGGAATT	AATGGCTGCA	250
	GTTGACGAAT	ACGTTCCAAC	TCCAGAACGT	GACACTGACA	AACCATTTCAT	300
15	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGAAAC	TGCTAAAACA	ACTGTAAGTG	GTGTTGAAAT	450
	GTTCCGTAAA	TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGTCAT	500
	TGCTACGTGG	GGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTAGCT	550
20	AAAGCTGGTA	CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	600
	TTTAACAAAA	GAAGAAGGTG	GACGTCACAC	TCCA		634

25 2) INFORMATION FOR SEQ ID NO: 971

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 787 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971

40	GGACCAATGC	CACAAACTCG	TGAGCACATC	CTTCTTTCAC	GTCAGGTTGG	50
	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	AGTTGACTTG	GTTGACGACG	100
	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	TCCGTGACCT	ATTGTCAGAA	150
	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	ATCCAAGGTT	CAGCACTTAA	200
45	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	CATCGTTATG	GAATTGATGA	250
	ACACAGTTGA	TGAGTATATC	CCAGAACCAG	AACGTGACAC	TGACAAACCA	300
	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	ATCACTGGAC	GTGGTACAGT	350
	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	TAAAGTCAAC	GACGAAATCG	400
	AAATCGTTGG	TATCAAAGAA	GAAACTCAAA	AAGCAGTTGT	TACTGGTGTT	450
50	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	500
	TGTCCTTCTT	CGTGGTGTTT	AACGTGATGA	AATCGAACGT	GGACAAGTTA	550
	TCGCTAAACC	AGGTTCAATC	AACCCACACA	CTAAATTCAA	AGGTGAAGTC	600
	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	CACACTCCAT	TCTTCAACAA	650
	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	TGACGTTACA	GGTTCAATCG	700
55	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	CTGGTGATAA	CGTGACAATC	750
	GACGTTGAGT	TGATTCACCC	AATCGCCGTA	GAACAAG		787

60 2) INFORMATION FOR SEQ ID NO: 972

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972

15 TAGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA GCACATCCTG 50
 CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC TGAACAAATG 100
 CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTTGAA ATGGAAGTTC 150
 GTGAACTTCT GTCTCAGTAC GACTTCCCGG GCGACGACAC TCCGATCGTT 200
 20 CGTGGTTCTG CTCTGAAAGC GCTGGAAGGC GACGCAGAGT GGAAGCGAA 250
 AATCCTGGAA CTGGCTGGCT TCCTGGATTTC TTACATTCCG GAACCAGAGC 300
 GTGCGATTGA CAAGCCGTTT CTGCTGCCGA TCGAAGACGT ATTCTCCATC 350
 TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAACGCG GTATCATCAA 400
 AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGAGACT CAGAAGTCTA 450
 25 CCTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA AGGCCGTGCT 500
 GGTGAGAACG TAGGTGTTCT GCTGCGTGGT ATCAAACGTG AAGAAATCGA 550
 ACGTGGTCAG GTACTGGCTA AGCCGGGCAC CATCAAGCCG CACACCAAGT 600
 TCGAATCTGA AGTGTACATT CTGTCCAAAG ATGAAGGCGG CCGTCATACT 650
 CCGTTCTTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA CTACTGACGT 700
 30 GACTGGTACC ATCGAACTGC CGGAAGGCGT AGAGATGGTA ATGCCGGGCG 750
 ACAACATCAA AATGGTTGTT ACCCTGATCC ACCCGATCGC GATGGACGAC 800
 GGT 803

35 2) INFORMATION FOR SEQ ID NO: 973

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973

ACTGACGGCC CGATGCCGCA GACTCGTGAG CACATCCTGC TGGGTCGTCA 50
 GGTAGGCGTT CCGTACATCA TCGTGTTCCCT GAACAAATGC GACATGGTTG 100
 ATGACGAAGA GCTGCTGGAA CTGGTTGAAA TGGAAGTTCG TGAACCTCTG 150
 55 TCTCAGTACG ACTTCCCGGG CGACGACACT CCGATCGTTC GTGGTTCTGC 200
 TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG GGAAGCGAAA ATCCTGGAAC 250
 TGGCTGGCTT CCTGGATTCC TACATTCCGG AACCAGAGCG TGCRAATTGAC 300
 AAGCCGTTCC TGCTGCCGAT CGAAGACGTA TTCTCCATCT CCGGTCGTGG 350
 TACCGTTGTT ACCGGTCGTG TAGAACGCGG TATCATCAAA GTTGGTGAAG 400
 60 AAGTTGAAAT CGTTGGTATC AAAGAGACTC AGAAGTCTAC CTGTACTGGC 450

5 GTTGAAATGT TCCGCAAAC TCTGGACGAA GGCCGTGCTG GTGAGAACGT 500
AGGTGTTCTG CTGCGTGGTA TCAAACGTGA AGAAATCGAA CGTGGTCAGG 550
TACTGGCTAA GCCGGGCACC ATCAAGCCGC ACACCAAGTT CGAATCTGAA 600
GTGTACATTC TGTCCAAAGA TGAAGGCGGC CGTCATACTC CGTTCTTCAA 650
AGGCTACCGT CCGCAGTTCT ACTTCCGTAC TACTGACGTG ACTGGTACCA 700
TTGAACTGCC GGAAGGCGTA GAGATGGTAA TGCCGGGCGA CAACATCAAA 750
ATGGTTGTTA CC 762

10

2) INFORMATION FOR SEQ ID NO: 974

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*
(B) STRAIN: ATCC 11775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974

30 CCTGGTAGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GCGTTCCTG ACATCATCGT GTTCCTGAAC 100
AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TTGAAATGGA 150
AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACTCCGA 200
TCGTTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA 250
GCGAAAATCC TGGAAGTGGC TGGCTTCCTG GATTCCTACA TTCCGGAACC 300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA ACGCGGTATC 400
ATCAAAGTTG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GCGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGTCGTC 650
40 ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT 700
GACGTGACTG GTACCATCGA ACTGCCGGAA GCGGTAGAGA TGGTAATGCC 750
GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGA 804

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2) INFORMATION FOR SEQ ID NO: 975

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*
(B) STRAIN: ATCC 25922

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975

	GCGATCCTGG	TAGTTGCTGC	GACTGACGGC	CCGATGCCGC	AGACTCGTGA	50
	GCACATCCTG	CTGGGTCGTC	AGGTAGGCGT	TCCGTACATC	ATCGTGTTCC	100
5	TGAACAAATG	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTTGAA	150
	ATGGAAGTTC	GTGAACTTCT	GTCTCAGTAC	GACTTCCCGG	GCGACGACAC	200
	TCCGATCGTT	CGTGGTTCTG	CTCTGAAAGC	GCTGGAAGGC	GACGCAGAGT	250
	GGGAAGCGAA	AATCCTGGAA	CTGGCTGGCT	TCCTGGATTG	YTACATTCCG	300
	GAACCAGAGC	GTGCGATTGA	CAAGCCGTTC	CTGCTGCCGA	TCGAAGACGT	350
10	ATTCTCCATC	TCCGGTCGTG	GTACCGTTGT	TACCGGTCGT	GTAGAACGCG	400
	GTATCATCAA	AGTTGGTGAA	GAAGTTGAAA	TCGTTGGTAT	CAAAGAGACT	450
	CAGAAGTCTA	CCTGTACTGG	CGTTGAAATG	TTCCGCAAAC	TGCTGGACGA	500
	AGGCCGTGCT	GGTGAGAACG	TAGGTGTTCT	GCTGCGTGGT	ATCAAACGTG	550
	AAGAAATCGA	ACGTGGTCAG	GTACTGGCTA	AGCCGGGCAC	CATCAAGCCG	600
15	CACACCAAGT	TCGAATCTGA	AGTGATACATT	CTGTCCAAAG	ATGAAGGCGG	650
	TCGTCATACT	CCGTTCTTCA	AAGGCTACCG	TCCGCAGTTC	TACTTCCGTA	700
	CTACTGACGT	GACTGGTACC	ATCGAACTGC	CGGAAGGTGT	AGAGATGGTA	750
	ATGCCGGGCG	ACAACATCAA	AATGGTTGTT	ACCCTGATCC	ACCCGATCGC	800
	GATG					804
20						

2) INFORMATION FOR SEQ ID NO: 976

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
 (B) STRAIN: Mavi-1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976

	GGCGCGATCC	TGGTGGTTCG	CGCCACCGAC	GGCCCGATGC	CGCAGACCCG	50
40	TGAGCACGTG	CTGCTCGCCC	GTCAGGTCGG	TGTGCCCTAC	ATCCTGGTCG	100
	CCCTGAACAA	GGCCGACATG	GTCGACGACG	AGGAGCTCCT	CGAGCTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCCGCC	CAGGAGTTCG	ACGAGGACGC	200
	CCCGGTGGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGC	GACGCCAAGT	250
	GGGTCGAGTC	CGTCGAGCAG	CTGATGGAGG	CCGTCGACGA	GTCGATCCCG	300
45	GACCCGGTCC	GCGAGACGGA	GAAGCCGTTC	CTGATGCCGG	TGGAGGACGT	350
	CTTCACCATC	ACCGGGCGTG	GCACCGTGGT	CACCGGTCGT	GTCGAGCGCG	400
	GTGTGATCAA	CGTGAACGAG	GAAGTCGAGA	TCGTCGGCAT	CCGCCCCGAC	450
	AGCACCAAGA	CCACGGTCAC	CGGTGTGGAR	ATGTTCCGCA	AGCTGCTCGA	500
	CCAGGGCCAG	GCCGGTGACA	ACGTCGGTCT	GCTGCTGCGT	GGTATCAAGC	550
50	GTGAGGACGT	CGAGCGCGGC	CAGGTCGTGA	CCAAGCCCGG	CACCACCACG	600
	CCGCACACCG	AGTTCGAGGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACGC	TGCCGGAGGG	CACCGAGATG	750
	GTGATGCCCC	GTGACAACAC	CAACATCTCG	GTGAAGCTGA	TCCAGCCCGT	800
55	CGCCATGGAC	GACGGTSTGC	GGTTC			825

2) INFORMATION FOR SEQ ID NO: 977

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977

15	TATCCTTGTA	GTAGCTTCAA	CTGACGGACC	AATGCCACAA	ACTCGTGAGC	50
	ACATCCTTCT	TTCACGTCAG	GTTGGTGTTA	AACACCTTAT	CGTCTTCATG	100
	AACAAAGTTG	ACTTG GTTGA	CGACGAAGAA	TTGCTTGAAT	TGGTTGAAAT	150
	GGAAATCCGT	GACCTATTGT	CAGAATACGA	CTTCCCAGGT	GACGATCTTC	200
	CAGTTATCCA	AGGTTTCAGCA	CTTAAAGCTC	TTGAAGGTGA	CTCTAAATAC	250
20	GAAGACATCG	TTATGGAATT	GATGAACACA	GTTGATGAGT	ATATCCCAGA	300
	ACCAGAACGT	GACACTGACA	AACCATTGCT	TCTTCCAGTC	GAGGACGTAT	350
	TCTCAATCAC	TGGACGTGGT	ACAGTTGCTT	CAGGACGTAT	CGACCGTGGT	400
	ATCGTTAAAG	TCAACGACGA	AATCGAAATT	GTTGGTATCA	AAGAAGAAAC	450
	TCAAAAAGCA	GTTGTTACTG	GTGTTGAAAT	GTTCCGTAAA	CAACTTGACG	500
25	AAGGTCTTGC	TGGAGATAAC	GTAGGTGTCC	TTCTTCGTGG	TGTTCAACGT	550
	GATGAAATCG	AACGTGGACA	AGTTATCGCT	AAACCAGGTT	CAATCAACCC	600
	ACACACTAAA	TTCAAAGGTG	AAGTCTACAT	CCTTACTAAA	GAAGAAGGTG	650
	GACGTCACAC	TCCATTCTTC	AACAAC TACC	GTCCACAATT	CTACTTCCGT	700
	ACTACTGACG	TTACAGGTTC	AATCGAACTT	CCAGCAGGTA	CTGAAATGGT	750
30	AATGCCTGGT	GATAACGTGA	CAATCGACGT	TGAGTTGATT	CACCCAATCG	800
	CCGTAGAACA	AGGTACTACA				820

35 2) INFORMATION FOR SEQ ID NO: 978

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
 (B) STRAIN: M-Gor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978

50	GGCGCGATCC	TGGTGGTTCG	CGCCACCGAT	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACGTG	CTGCTCGCCC	GTCAGGTGGG	CGTGCCCTAC	ATCCTGGTGG	100
	CGCTGAACAA	GTCCGACGCG	GTCGACGACG	AGGAGCTGCT	CGAGCTCGTC	150
	GAGCTGGAGG	TCCGCGAGTT	GCTGGCCGCC	CAGGACTTCG	ACGAGGAAGC	200
55	TCCGGTGGTC	CGGGTCTCGG	CGCTGAAGGC	GCTCGAGGGC	GACGCCACCT	250
	GGGTGAAGTC	GGTAGAGGAC	TTGATGGACG	CGGTGACGA	GTCGATTCCG	300
	GACCCGGTCC	GCGACACCGA	CAAGCCGTTC	CTGATGCCCG	TCGAGGACGT	350
	CTTCACCATC	ACCGGTCGTG	GCACCGTCGT	CACCGGCCGT	GTGGAGCGCG	400
	GCGTGGTGAA	CGTGAACGAG	GAAGTCGAGA	TCGTCGGCAT	CAAGCCGACC	450
60	AGCACCAAGA	CCACGGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500

	CCAGGGTCAG	GCCGGTGACA	ACGTCGGTCT	GCTGCTGCGT	GGTGTCAAGC	550
	GTGAGGACGT	CGAGCGCGGC	CAGGTCGTCA	TCAAGCCCGG	CACCACCACT	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
5	GCACCACCGA	CGTGACCGGT	GTGGTGACGC	TGCCGGAGGG	CACCGAAATG	750
	GTGATGCCCG	GTGACAACAC	CAACATCTCG	GTGAAGCTGA	TCCAGCCCGT	800
	CGCCATGGAC	GACGGTCTGC	GG			822

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2) INFORMATION FOR SEQ ID NO: 979

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 821 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979

	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
30	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTTCAGC	ACTTAAAGCT	CTTGAAGGTG	ACTCTAAATA	250
	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TATATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTGC	TTCTTCCAGT	CGAGGACGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
35	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTTGAAA	TGTTCCGTAA	ACAACCTGAC	500
	GAAGGTCTTG	CTGGAGATAA	CGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATCGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTCTACA	TCCTTACTAA	AGAAGAAGGT	650
40	GGACGTCACA	CTCCATTCTT	CAACAACACT	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	TCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	A			821

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2) INFORMATION FOR SEQ ID NO: 980

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(B) STRAIN: ATCC 25177

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980

	GGTGCGATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	50
	CGAGCACGTT	CTGCTGGCGC	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	100
5	CGCTGAACAA	GGCCGACGCA	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCTGCC	CAGGAATTCG	ACGAGGACGC	200
	CCCGGTTGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	250
	GGGTTGCCTC	TGTCGAGGAA	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	300
	GACCCGGTCC	GCGAGACCGA	CAAGCCGTTC	CTGATGCCGG	TCGAGGACGT	350
10	CTTCACCATT	ACCGGCCGCG	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	400
	GCGTGATCAA	CGTGAACGAG	GAAGTTGAGA	TCGTGCGCAT	TCGCCCATCG	450
	ACCACCAAGA	CCACCGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500
	CCAGGGCCAG	GCGGGCGACA	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	550
	GCGAGGACGT	CGAGCGTGGC	CAGGTTGTCA	CCAAGCCCGG	CACCACCACG	600
15	CCGCACACCG	AGTTCGAAGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	750
	GTGATGCCCC	GTGACAACAC	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	800
	CGCCATGGAC	GAAGGTNTGC	GTTTCGCG			828
20						

2) INFORMATION FOR SEQ ID NO: 981

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: CSG 144

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981

	CGGCGGTATC	TTAGTAGTAT	CTGCTGCAGA	TGGCCCAATG	CCACAAACTC	50
40	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
	TTCTTAAACA	AAGCTGACAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTATCTGA	ATACGACTTC	CCTGGTGACG	200
	ATGTACCAGT	TATCGTTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACCCA	250
	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCTGTAG	ATGACTACAT	300
45	CCCAACTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCAACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATCACTGA	450
	AGAAAGCAAG	AAAACAACAG	TTACAGGTGT	AGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATCG	GTGCTTTATT	ACGTGGTGTT	550
50	GCACGTGAAG	ACGTACAACG	TGGACAAGTA	TTAGCAGCTC	CTGGCTCTAT	600
	TACTCCACAC	ACAAAATTCA	AAGCTGATGT	TTACGTTTTA	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
	TTCCGTACTA	CTGACGTAAC	TGGCGTTGTT	CACTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACGTAGAAAT	GACTGTTGAA	TTAATCGCTC	800
55	CAATCGCGAT	TGAAGACGG				819

2) INFORMATION FOR SEQ ID NO: 982

60

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982

15	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAGATC	GACTTGGTTG	ATGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTCTTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCT	CTTGAAGGTG	ATACTAAGTA	250
20	CGAAGACATC	ATCATGGAAT	TGATGAACAC	TGTTGATGAG	TACATCCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTCTTC	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTCGT	GTCAACGATG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	TCCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAGCTTGAC	500
25	GAAGGTCTTG	CAGGGGACAA	CGTAGGTGTA	CTTCTTCGTG	GTATCCAACG	550
	TGATGAAATC	GAACGTGGTC	AAGTTATCGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAGGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACT	CGTCCACAGT	TCTACTTCCG	700
	TACAACCTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
30	TAATGCCTGG	TGATAACGTA	ACTATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTTGAAC	AAGG				814

35 2) INFORMATION FOR SEQ ID NO: 983

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 983

50	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
55	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCC	CTTGAAGGTG	ACACTAAATA	250
	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TACATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTGC	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
60	CTCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACCTTGAC	500

	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
5	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC					810

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2) INFORMATION FOR SEQ ID NO: 984

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus mitis*

(B) STRAIN: ATCC 903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984

	TCCTTGTAGT	AGCTTCAACT	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCCTTCTTT	CACGTCAGGT	TGGTGTTAAA	CACCTTATCG	TCTTCATGAA	100
	CAAGATCGAC	TTGGTTGATG	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	150
30	AAATCCGTGA	CCTCTTGTCA	GAATACGACT	TCCCAGGTGA	CGATCTTCCA	200
	GTTATCCAAG	GTTCAAGCTCT	TAAAGCTCTT	GAAGGTGATA	CTAAGTACGA	250
	AGACATCATC	ATGGAATTGA	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	300
	CAGAACGTGA	TACTGACAAA	CCTCTTCTTC	TTCCAGTCGA	AGACGTATTC	350
	TCAATCACTG	GTCGTGGTAC	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	400
35	TGTTTCGTGTC	AACGATGAAA	TCGAAATCGT	TGGTATCAAA	GAAGAAATCC	450
	AAAAAGCAGT	TGTTACTGGT	GTTGAAATGT	TCCGTAAACA	GCTTGACGAA	500
	GGTCTTGCAG	GGGACAACGT	AGGTGTACTT	CTTCGTGGTA	TCCAACGTGA	550
	TGAAATCGAA	CGTGGTCAAG	TTATCGCTAA	ACCAGGTTCA	ATCAACCCAC	600
	ACACTAAATT	CAAGGGTGAA	GTTTACATCC	TTACTAAAGA	AGAAGGTGGA	650
40	CGTCACACTC	CATTCTTCAA	CAACTACCGT	CCACAGTTCT	ACTTCCGTAC	700
	AACTGACGTT	ACAGGTTCAA	TCGAACTTCC	AGCAGGTACT	GAAATGGTAA	750
	TGCCTGGTGA	TAACGTAAC	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	800
	GTTGAACAAG	GTACTAC				817

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2) INFORMATION FOR SEQ ID NO: 985

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus oralis*

(B) STRAIN: ATCC 35037

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 985

	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTTCTTT	CACGTCAGGT	50
	TGGTGTTAAA	CACCTTATTG	TCTTCATGAA	CAAAATTGAC	TTGGTAGACG	100
5	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	AAATCCGTGA	CCTCTTGTC	150
	GAATACGACT	TCCCAGGTGA	CGATCTTCCA	GTTATCCAAG	GTTCAGCTCT	200
	TAAAGCTCTT	GAAGGTGACT	CTAAATACGA	AGACATCATT	ATGGAATTGA	250
	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	CAGAACGTGA	CACTGAAAAA	300
	CCATTGCTTC	TTCCAGTCGA	AGACGTATTC	TCAATCACTG	GACGTGGTAC	350
10	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	TGTTCTGTGC	AACGACGAAA	400
	TCGAAATCGT	TGGTATCAAA	GAAGAACTC	AAAAAGCAGT	TGTTACTGGT	450
	GTTGAAATGT	TCCGTAAACA	ACTTGACGAA	GGTCTTGCCG	GAGATAACGT	500
	AGGTGTCCTT	CTTCGTGGTG	TTCAACGTGA	CGAAATCGAA	CGTGGACAAG	550
	TTATCGCTAA	ACCAGGTTCA	ATCAACCCAC	ACACTAAATT	TAAAGGTGAA	600
15	GTCTACATCC	TTACTAAAGA	AGAAGGTGGA	CGTCACACTC	CATTCTTCAA	650
	CAACTACCGT	CCACAATTCT	ACTTCCGTAC	TACTGACGTT	ACAGGTTCAA	700
	TCGAACTTCC	TGCAGGTACT	GAAATGGTAA	TGCCTGGTGA	TAACGTGACT	750
	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	GTAGAACAAG	GTACTACA	798

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2) INFORMATION FOR SEQ ID NO: 986

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 986

	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
	CTTCTTTCAC	GTCAGGTTGG	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	100
40	AGTTGACTTG	GTTGACGACG	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	150
	TCCGTGACCT	ATTGTCAGAA	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	200
	ATCCAAGGTT	CAGCACTTAA	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	250
	CATCGTTATG	GAATTGATGA	ACACAGTTGA	TGAGTATATT	CCAGAACCAG	300
	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	350
45	ATCACTGGAC	GTGGTACAGT	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	400
	TAAAGTCAAC	GACGAAATCG	AAATCGTTGG	TATCAAAGAA	GAAACTCAAA	450
	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	500
	CTTGCTGGAG	ATAACGTAGG	TGTCCTTCTT	CGTGGTGTTT	AACGTGATGA	550
	AATCGAACGT	GGACAAGTTA	TCGCTAAACC	AGGTTCAATC	AACCCACACA	600
50	CTAAATTCAA	AGGTGAAGTC	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCAACAA	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	700
	TGACGTTACA	GGTTCAATCG	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	750
	CTGGTGATAA	CGTGACAATC	GACGTTGAGT	TGATTCACCC	AATCGCCGTA	800
	GAACAAGGTA	CTACA				815

55

2) INFORMATION FOR SEQ ID NO: 987

60 (i) SEQUENCE CHARACTERISTICS:

549

- (A) LENGTH: 832 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
- (B) STRAIN: ATCC 8043

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987

	CGGACAATCT	TGGTTGTTTC	TGCTACGGAT	GGCCCAATGC	CTCAAACCTCG	50
15	TGAACACATT	TTACTTTCTC	GCCAAGTAGG	CGTGAAATAT	TTGATTGTTT	100
	TCTTGAACAA	AACAGATTTA	GTCGATGATG	AAGAATTAAT	TGATCTAGTA	150
	GAAATGGAAG	TTCGTGAACT	ATTAAGCGAA	TATGGATTTC	CAGGTGATGA	200
	TACACCTGTT	ATCAAAGGAT	CAGCATTAAA	AGCATTACAA	GGTGATCCTG	250
	ATGCAGAAGC	AGCTATCATG	GAATTGATGG	ACACAGTCGA	TGAATACATC	300
20	CCAACACCAG	AACGTGATAC	GGACAAACCA	TTATTGTTAC	CCGCCGAAGA	350
	TGTATTTTCA	ATTACTGGAC	GTGGAACAGT	AGCATCTGGT	CGGATTGACC	400
	GTGGGGCTGT	TAGAGTCGGT	GACGAAATCG	AAATCGTAGG	GATCAAACCA	450
	GAAACGCAAA	GAGCCGTAGT	AACAGGAGTT	GAAATGTTCC	GCAAAACGCT	500
	TGATTACGGT	GAAGCAGGGG	ATAACGTAGG	TGTGTTATTA	CGTGGGATTC	550
25	AAAGAGAAGA	CATCGAACGT	GGCCAAGTGA	TTGCCAAACC	TGGTTCAATT	600
	ACACCTCATA	CTAAATTCAA	AGCAGAAGTT	TAGGTTTTGA	CTAAAGAAGA	650
	AGGCGGACGT	CATACACCAT	TCTTCAATAA	TTATCGACCA	CAATTTTATT	700
	TCCGCACAAC	TGACGTAACA	GGAACAATTG	TTTTGCCAGA	AGGAACGGAA	750
	ATGGTCATGC	CTGGCGACAA	CGTAACGATC	GATGTAGAAT	TGATTCATCC	800
30	TGTTGCTATT	GAAACGGGA	CGACTTTCTC	CA		832

2) INFORMATION FOR SEQ ID NO: 988

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
- (B) STRAIN: ATCC 43186

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 988

50	TGGTGCGATC	TTAGTTGTTT	CTGCGACAGA	TGGACCAATG	CCTCAAACCTC	50
	GCGAGCATAT	CCTTTTATCA	CGTCAAGTTG	GTGTAAAATA	TTTGATTGTA	100
	TTTTTTGAATA	AAGTTGATTT	GGTCGATGAT	GAAGAATTGA	TCGATCTTGT	150
	AGAAATGGAA	GTTTCGTGAAT	TACTGAATGA	ATATGGTTTC	CCAGGTGATG	200
	ACACACCTGT	CATCAAAGGC	TCTGCATTGA	AAGCATTGCA	AGGTGACCCA	250
55	GAAGCAGAAG	CTGCGATCAA	TGAATTGATG	GAAACAGTGG	ATGACTATAT	300
	CCCAACACCA	GAACGTGATA	CCGACAAACC	ATTGCTTTTA	CCAGTTGAAG	350
	ATGTTTTTCTC	AATCACTGGT	CGCGGAACGG	TAGCATCTGG	TCGTATCGAC	400
	CGTGGAGCCG	TTCGTGTCGG	TGATGAAATC	GAGATCATCG	GAATCAAACC	450
	TGAAACGAAA	AAAGCGGTTG	TGACAGGGGT	AGAGATGTTC	CGTAAAACGT	500
60	TAGATTATGG	CGAAGCTGGA	GATAACGTAG	GAATCTTGTT	ACGTGGTATC	550

	CAAAGAGAAG	ATATTGAACG	TGGACAAGTA	ATTGCGAAAC	CTGGTTCAAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGAAGT	TTATGTATTG	ACGAAAGAAG	650
	AAGGCGGACG	TCATACACCA	TTCTTCAATA	ACTACCGCCC	ACAATTTTAT	700
	TTCCGCACAA	CAGATGTAAC	AGGTACGATC	GTGTTGCCAG	AAGGAACAGA	750
5	AATGGTCATG	CCTGGAGACA	ACGTAACCAT	CGAGGTAGAG	TTGATCCATC	800
	CAGTGGCAAT	CGAACAAGGA	ACGACTTTCT	CTATT		835

10 2) INFORMATION FOR SEQ ID NO: 989

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 989

25	TGCGATCTTA	GTAGTATCTA	CTACTGATGG	ACCAATGCCT	CAAACACGTG	50
	AGCACATTTT	GTTATCACGC	CAAGTAGGTG	TTAAATACTT	GATCGTCTTC	100
	TTGAACAAAG	TTGATTTAGT	CGACGATGAA	GAATTGATTG	ATTTAGTTGA	150
	AATGGAAGTA	CGTGAGTTAC	TTTCAGAATA	TGGTTTCCCA	GGCGATGATA	200
30	TTCTGTCTCT	TAAAGGTTCA	GCTCTGAAAG	CTTTAGAAGG	CGATCCTGAA	250
	CAAGAACAAG	TAATCATGGA	CCTAATGGAT	ACGGTTGACG	AATATATCCC	300
	AACACCAGAA	CGTGACACTG	ACAAACCAT	CTTGTTACCA	GTGGAAGATG	350
	TTTTCTCAAT	CACAGGACGT	GGGACTGTTG	CATCTGGTCG	TATTGATCGT	400
	GGGGAAGTTA	AAGTCGGTGA	CGAAGTTGAA	ATTATCGGGA	TCAAACCTGA	450
35	AGTTCAAAAG	GCTGTCGTAA	CTGGACTTGA	AATGTTCCGT	AAAACATTGG	500
	ATTATGGTGA	AGCTGGAGAT	AACGTTGGGG	TTCTATTACG	TGGTATTACA	550
	CGTGATGAAA	TCGAACGTGG	TCAAGTATTA	GCTAAACCAG	GTTCAATTAC	600
	ACCACATACG	AAATTCAGTG	CAGAAGTTTA	TGTGTTGACG	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTG	TTTAACAAC	ATCGTCCTCA	ATTCTACTTC	700
40	CGTACAACAG	ACGTTACCGG	TAATATCGTG	TTGCCAGAAG	GTACTGAAAT	750
	GGTCATGCCT	GGCGATAACG	TAACAATCGA	CGTTGAATTA	ATCCATCCAA	800
	TCGCCGTAGA	AAAAGGAACA	ACTTTCTCTA	TT		832

45

2) INFORMATION FOR SEQ ID NO: 990

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9440

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 990

551

GGATCCTGTA TATGCACAAA AACTAGGTGT TAACATCGAT GAATTACTAT 50
 TATCACAACC TGATACAGGG GAGCAAGGTT TAGAAATCGC AGAAGCACTT 100
 GTACGAAGTG GTGCGGTTGA TATTATCGTA ATTGACTCTG TAGCAGCTCT 150
 5 TGTA 154

2) INFORMATION FOR SEQ ID NO: 991

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 991

25 GCCATTGCAG AGGCACAGAA GCAGGGCGGT ATTGCAGCCT TCATTGATGC 50
 TGAGCACGCC TTCGACCGTT TCTATGCAGA GAAGTTAGGT GTGGATGTTG 100
 ATAACCTTTG GGTTCACAG CCAGACAATG GTGAGCAGGC TTTAGAGATT 150
 GCCGACCAGC TGATTCGCTC TTCCGCTATT GACATTCTCG TTGTCGACTC 200
 AGTTGCAGCC TTGACTCCAA AGAAGGAGAT TGAGGGTGAC ATGGGTGACT 250
 30 CTGCAGTAGG TTTACAAGCA CGACTGATGA GTCAGGCATT GCGTAAACTT 300
 ACCTCAACAA TCGCAAAAAC TAATACTTGC TGCATCTTCA TCAACCAGTT 350
 GCGTGAGAAG ATTGGTGTGA TGTTTGGTAA TCCA 384

35

2) INFORMATION FOR SEQ ID NO: 992

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R760

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 992

ACACGTGAAC ACATCTTGTT ATCACGTAAC GTTGGTGTAC CATACATCGT 50
 TGTTTTCTTA AACAAAATGG ATATGGTTGA TGACGAAGAA TTACTAGAAT 100
 TAGTTGAAAT GGAAGTTCGT GACTTATTGT CAGAATATGA CTTCCCAGGC 150
 55 GACGATGTTT CTGTAATCGC TGGTTCTGCT TTGAAAGCTC TTGAAGGCGA 200
 TGCTTCATAC GAAGAAAAAA TCATGGAATT AATGGCTGCA GTTGACGAAT 250
 ACGTTCCAAC TCCAGAACGT GACACTGACA AACCATTTCAT GATGCCAGTC 300
 GAAGACGTAT TCTCAATCAC TGGACGTGGT ACTGTTGCTA CAGGCCGTGT 350
 TGAACGTGGA CAAGTTCGCG TTGGTGACGA AGTTGAAATC GTTGGTATTG 400
 60 CTGAAGAAAC TGCTAAAACA ACTGTAAC TGTTTGAAT GTTCCGTAAA 450

TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGCAT	TGCTACGTGG	500
TGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	AAAGCTGGTA	550
CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	TTTAACAAAA	600
GAAGAAGGTG	GACGTCATAC	ACCA			624

5

2) INFORMATION FOR SEQ ID NO: 993

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 20 (C) ACCESSION NUMBER: extracted from U40453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 993

ATGGAAAACA	ATAAAAAAGT	ATTGAAGAAA	ATGGTATTTT	TTGTTTTAGT	50
25 GACATTTCTT	GGACTAACAA	TCTCGCAAGA	GGTATTTGCT	CAACAAGACC	100
CCGATCCAAG	CCAAC TTCAC	AGATCTAGTT	TAGTTAAAAA	CCTTCAAAAT	150
ATATATTTTC	TTTATGAGGG	TGACCCTGTT	ACTCACGAGA	ATGTGAAATC	200
TGTTGATCAA	CTTTTATCTC	ACGATTTAAT	ATATAATGTT	TCAGGGCCAA	250
ATTATGATAA	ATTAAAAACT	GAAC TTAAGA	ACCAAGAGAT	GGCAACTTTA	300
30 TTTAAGGATA	AAAACGTTGA	TATTTATGGT	GTAGAATATT	ACCATCTCTG	350
TTATTTATGT	GAAAATGCAG	AAAGGAGTGC	ATGTATCTAC	GGAGGGGTAA	400
CAAATCATGA	AGGGAATCAT	TTAGAAATTC	CTAAAAAGAT	AGTCGT TAAA	450
GTATCAATCG	ATGGTATCCA	AAGCCTATCA	TTTGATATTG	AAACAAATAA	500
AAAAATGGTA	ACTGCTCAAG	AATTAGACTA	TAAAGTTAGA	AAATATCTTA	550
35 CAGATAATAA	GCAACTATAT	ACTAATGGAC	CTTCTAAATA	TGAAACTGGA	600
TATATAAAGT	TCATACCTAA	GAATAAGAA	AGTTTTTGGT	TTGATTTTTT	650
CCCTGAACCA	GAATTTACTC	AATCTAAATA	TCTTATGATA	TATAAAGATA	700
ATGAAACGCT	TGACTCAAAC	ACAAGCCAAA	TTGAAGTCTA	CCTAACAACC	750
AAGTAA					756

40

2) INFORMATION FOR SEQ ID NO: 994

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 994

55 TGGACTAACA ATCTCGCAAG AGG

23

2) INFORMATION FOR SEQ ID NO: 995

60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 995
10 ACATTCTCGT GAGTAACAGG GT 22

15 2) INFORMATION FOR SEQ ID NO: 996

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 996
 ACAAATCATG AAGGGAATCA TTTAG 25

30 2) INFORMATION FOR SEQ ID NO: 997

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 997
 CTAATTCTTG AGCAGTTACC ATT 23

45 2) INFORMATION FOR SEQ ID NO: 998

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 998
 GGAGGGGTAA CAAATCATGA AGG 23
60

2) INFORMATION FOR SEQ ID NO: 999

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 999

15 TTGACCTTGT TGATGACGAA GAG

23

2) INFORMATION FOR SEQ ID NO: 1000

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1000

30 TTAGTGTGTG GGTGATTGA ACT

23

35 2) INFORMATION FOR SEQ ID NO: 1001

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1001

AAGAGTTGCT TGAATTAGTT GAG

23

50 2) INFORMATION FOR SEQ ID NO: 1002

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 894 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (B) STRAIN: ATCC 700294

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1002

	AACATGATCA	CTGGTGCCGC	TCAAATGGAC	GGAGCTATCC	TTGTAGTTGC	50
	TTCAACTGAT	GGACCAATGC	CACAAACTCG	TGAGCACATC	CTTCTTTCAC	100
	GTCAGGTTGG	TGTTAAACAC	CTTATCGTGT	TCATGAACAA	AGTTGACCTT	150
10	GTTGATGACG	AAGAGTTGCT	TGAATTAGTT	GAGATGGAAA	TTCGTGACCT	200
	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	CCTTCCAGTT	ATCCAAGGTT	250
	CAGCTCTTAA	AGCTCTTGAA	GGCGACACTA	AATTTGAAGA	CATCATCATG	300
	GAATTGATGG	ATACTGTTGA	TTCATACATT	CCAGAACCAG	AACGCGACAC	350
	TGACAAACCA	TTGCTTCTTC	CAGTCGAAGA	CGTATTCTCA	ATTACAGGTC	400
15	GTGGTACAGT	TGCTTCAGGA	CGTATCGACC	GTGGTACTGT	TCGTGTCAAC	450
	GACGAAATCG	AAATCGTTGG	TATCAAAGAA	GAAACTAAAA	AAGCTGTTGT	500
	TACTGGTGTT	GAAATGTTCC	GTAACAACACT	TGACGAAGGT	CTTGCAGGAG	550
	ACAACGTAGG	TATCCTTCTT	CGTGGTGTTT	AACGTGACGA	AATCGAACGT	600
	GGTCAAGTTA	TTGCTAAACC	AAGTTCAATC	AACCCACACA	CTAAATTCAA	650
20	AGGTGAAGTA	TATATCCTTT	CTAAAGACGA	AGGTGGACGT	CACACTCCAT	700
	TCTTCAACAA	CTACCGTCCA	CAATTCTACT	TCCGTACAAC	TGACGTAACA	750
	GGTTCAATCG	AACTTCCAGC	AGGTACAGAA	ATGGTTATGC	CTGGTGATAA	800
	CGTGACAATC	AACGTTGAGT	TGATCCACCC	AATCGCCGTA	GAACAAGGTA	850
	CTACTTTCTC	AATCCGTGAA	GGTGGACGTA	CTGTTGGTTC	AGGT	894

25

2) INFORMATION FOR SEQ ID NO: 1003

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1003

	AATGGATCCT	GTATATGCAC	AAAAATTAGG	CGTTAACATA	GATGAATTAC	50
45	TATTATCACA	GCCTGATACA	GGGGAGCAAG	GATTAGAAAT	CGCGGAAGCA	100
	CTTGACGAA	GTGGTGCGGT	TGACATTATC	GTAATTGACT	CTGTAGCAGC	150
	TCTTGATACCG	AAAGCAGAGA	TTGAAGGCGA	CATGGGTGAC	TCACACGTAG	200
	GTTTACAAGC	ACGTTTAATG	TCACAAGCAC	TTCGTAAGCT	TTCAGGAGCA	250
	ATCAACAAAT	CAAAAACAAT	TGCAATCTTT	ATTAACCAAA	TTCGTGAAAA	300
50	AGTTGGGGTT	ATGTTCTGGAA	ACCCAGAAAC	AA		332

55

2) INFORMATION FOR SEQ ID NO: 1004

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1004

10	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
15	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTT	AAGTAATACA	500
20	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
25	CTCAAGCTGG	TAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTTGG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
30	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CC				1212

35

2) INFORMATION FOR SEQ ID NO: 1005

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1005

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
55	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
60	GCACACCTGT	CTACAACTGG	GATAGAGCAT	ATTTCCGTAA	TATTACTCTG	350

	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
5	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTGC	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATACT	GGAACCTGGTC	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
10	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATAACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
15	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	TC				1212

20

2) INFORMATION FOR SEQ ID NO: 1006

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1213 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-03

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1006

	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACCTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
40	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
45	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTC	AAGTAATACA	500
	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCCAACG	GTGGAATTTA	CCACAAACCC	ATGTATATCA	600
50	ATAAGGTCGT	CTTCAGTGAC	GGTAGTAAAA	AAGAATTTTC	AGATGTAGGT	650
	ACACGAGCTA	TGAAAGAAAC	AACTGCTTAC	ATGATGACCG	AAATGATGAA	700
	AACTGTCTTG	GCATACGGAA	CTGGTCGTGG	AGCCTATCTC	CCATGGTTAG	750
	CGCAAGCTGG	TAAGACAGGT	ACTTCTAACT	ACACAGATGA	TGAAATTGAA	800
	AAACACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGTTG	850
55	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTGTC	TGAAGGAAGC	AATCCAGAGG	ATTGGAATAT	1000
	ACCAGAGGGG	CTCTACAGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1050
	GTTCTACGTG	GAGCTCACCT	GCTCCACAAC	AACCCCATC	AACTGAAAGT	1100
60	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAACT	CAACCACTCC	1150

AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT 1200
CAAATACAAC CCC 1213

5

2) INFORMATION FOR SEQ ID NO: 1007

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-04

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1007

ACCAAGAAGC TCAAAAACAT CTGTGGGATA TCTACAACTC CGATCAATAC 50
GTCTCTTACC CTGACGATGA TTTGCAAGTC GCATCTACGG TCGTAGATGT 100
TTCAAATGGT AAAGTCATCG CCCAACTTGG AGCTCGTCAC CAAGCAAGTA 150
ACGTTTCATT TGGTACCAAC CAAGCTGTGG AAACCAATCG TGACTGGGGT 200
TCTGCTATGA AACCAATCAC CGATTATGCA CCTGCCATAG AATACGGTGT 250
TTATGATTCC ACTGCAACTA TGGTTAATGA TATTCCTTAT AACTATCCGG 300
GAACAAGCAC ACCTGTCTAC AACTGGGATA GAGCATATTT CGGTAATATT 350
ACTCTGCAAT ATGCTCTTCA ACAATCACGA AATGTCACAG CCGTTGAGAC 400
TTTGAATAAG GTCGGTCTAG ATAGAGCTAA AACCTTCCTT AATGGTCTTG 450
GTATCGACTA TCCAAGCATG CATTATGCAA ACGCCATTTC AAGTAATACA 500
ACAGAATCTA ATAAACAATA CGGAGCAAGT AGTGAAAAAA TGGCTGCTGC 550
TTATGCTGCC TTTGCAAATG GTGGCACTTA CTATAAACCA ATGTATATCC 600
ATAAAGTCGT CTTCAGTGAT GGAAGTAAAA AAGAGTTCTC TAATGTCGGA 650
ACTCGTGCCA TGAAGGAAAC GACAGCCTAT ATGATGACCG ACATGATGAA 700
AACAGTCTTG ACTTATGGAA CTGGGCGTGG AGCCTATCTT CCTTGGCTTC 750
CTCAAGCTGG TAAACAGGA ACCTCTAACT ATACAGATGA GGAAGTTGAA 800
AACCACATCA AGAACACTGG CTATGTAGCT CCAGATGAAA TGTTTGTTGG 850
TTATACTCGT AAGTATTCTA TGGCTGTATG GACAGGTTAT TCGAATCGTT 900
TAACTCCTAT CGTTGGAGAT GGTTTCCTAG TTGCAGCTAA AGTTTATCGC 950
TCAATGATAA CGTATCTATC AGAAGATACT CATCCAGAAG ACTGGACGAT 1000
GCCAGACGGA CTTTTCAAGG ACGGGGAATT TGTATTCAAA AATGGAGCTC 1050
GCCCAATATG GACTGAACCC TCTACTCAAC AATCCTCAAC AGCTGAAAGT 1100
TCAAGCTCAT CATCAGATAG TTCAACTTCA CAGTCTAGCT CAACCACTCC 1150
AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT 1200
CAAATACAAC CCCTGATC 1218

50 2) INFORMATION FOR SEQ ID NO: 1008

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1008

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5      GTAGACCAAG AAGCTCAAAA ACATCTGTGG GATATCTACA ACTCCGATCA      50
      ATACGTCTCT TACCCTGACG ATGATTTGCA AGTCGCATCT ACGGTCGTAG      100
      ATGTTTCAAA TGGTAAAGTC ATCGCCCAAC TTGGAGCTCG TCACCAAGCA      150
      AGTAACGTTT CATTTGGTAC CAACCAAGCT GTGGAAACCA ATCGTGACTG      200
10     GGGTTCTGCT ATGAAACCAA TCACCGATTA TGCACCTGCC ATAGAATACG      250
      GTGTTTATGA TTCCACTGCA ACTATGGTTA ATGATATTCC TTATAACTAT      300
      CCGGGAACAA GCACACCTGT CTACAACCTGG GATAGAGCAT ATTTCCGGTAA      350
      TATTACTCTG CAATATGCTC TTCAACAATC ACGAAATGTC ACAGCCGTTG      400
      AGACTTTGAA TAAGGTCGGT CTAGATAGAG CTAACACCTT CCTTAATGGT      450
15     CTTGGTATCG ACTATCCAAG CATGCATTAT GCAAACGCCA TTTCAAGTAA      500
      TACAACAGAA TCTAATAAAC AATACGGAGC AAGTAGTGAA AAAATGGCTG      550
      CTGCTTATGC TGCCTTTGCA AATGGTGGCA CTTACTATAA ACCAATGTAT      600
      ATCCATAAAG TCGTCTTCAG TGATGGAAGT AAAAAAGAGT TCTCTAATGT      650
      CGGAACTCGT GCCATGAAGG AAACGACAGC CTATATGATG ACCGACATGA      700
20     TGAAAACAGT CTTGACTTAT GGAACCTGGC GTGGAGCCTA TCTTCCTTGG      750
      CTTCTCAAG CTGGTAAAC AGGAACCTCT AACTATACAG ATGAGGAAGT      800
      TGAAAACCAAC ATCAAGAACA CTGGCTATGT AGCTCCAGAT GAAATGTTTG      850
      TTGGTTATAC TCGTAAGTAT TCTATGGCTG TATGGACAGG TTATTCGAAT      900
      CGTTTAACTC CTATCGTTGG AGATGGTTTC CTAGTTGCAG CTAAAGTTTA      950
25     TCGCTCAATG ATAACGTATC TATCAGAAGA TACTCATCCA GAAGACTGGA      1000
      CGATGCCAGA CGGACTTTTC AGAAACGGGG AATTTGTATT CAAAAATGGA      1050
      GCTCGCCCAA TATGGACTGA ACCCTCTACT CAACAATCCT CAACAGCTGA      1100
      AAGTTCAAGC TCATCATCAG ATAGTTCAAC TTCACAGTCT AGCTCAACCA      1150
      CTCCAAGCAC AAATAATAGT ACGACTACCA ATCCTAACAA TAATACGCAA      1200
30     CAATCAAATA CAACCCCTGA TCA      1223
  
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2) INFORMATION FOR SEQ ID NO: 1009

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35     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1214 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
40     (D) TOPOLOGY: Linear
  
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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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45     (A) ORGANISM: Streptococcus pneumoniae
      (B) STRAIN: StrR-06
  
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1009

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50     ACCAAGAAGC TCAAAAACAT CTGTGGGATA TCTACAATC CGATCAATAC      50
      GTCTCTTACC CTGACGATGA TTTGCAAGTC GCATCTACGG TCGTAGATGT      100
      TTCAAATGGT AAAGTCATCG CCCAACTTGG AGCTCGTCAC CAAGCAAGTA      150
      ACGTTTCATT TGGTACCAAC CAAGCTGTGG AAACCAATCG TGAAGGGGT      200
      TCTGCTATGA AACCAATCAC CGATTATGCA CCTGCCATAG AATACGGTGT      250
55     TTATGATTCC ACTGCAACTA TGGTTAATGA TATTCCTTAT AACTATCCGG      300
      GAACAAGCAC ACCTGTCTAC AACTGGGATA GAGCATATTT CGGTAATATT      350
      ACTCTGCAAT ATGCTCTTCA ACAATCACGA AATGTCACAG CCGTTGAGAC      400
      TTTGAATAAG GTCGGTCTAG ATAGAGCTAA AACCTTCCTT AATGGTCTTG      450
      GTATCGACTA TCCAAGCATG CATTATGCAA ACGCCATTTC AAGTAATACA      500
60     ACAGAATCTA ATAAACAATA CGGAGCAAGT AGTGAAAAAA TGGCTGCTGC      550
  
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	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
5	CTCAAGCTGG	TAAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTTGG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
10	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CCCT				1214
15						

2) INFORMATION FOR SEQ ID NO: 1010

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1223 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - 30 (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1010

	CCAAGAAGCT	CAAAAACATC	TGTGGGATAT	CTACAACTCC	GATCAATACG	50
35	TCTCTTACCC	TGACGATGAT	TTGCAAGTCG	CATCTACGGT	CGTAGATGTT	100
	TCAAATGGTA	AAGTCATCGC	ACAACCTGGT	GCTCGTCATC	AAGCAAGTAA	150
	TGTTTCATTC	GGTACCAACC	AGGCCGTAGA	AACCAATCGT	GACTGGGGAT	200
	CATCAATGAA	ACCAATCACT	GACTATGCTC	CCGCTTTAGA	ATATGGAGTC	250
	TATGACTCTA	CTGCTTCTAT	TGTACATGAT	GTCCCTTATA	ACTATCCTGG	300
40	CACTGATACT	CCACTCTACA	ACTGGGATCA	TGTCTACTTT	GGAAACATTA	350
	CAATCCAGTA	TGCTCTTCAA	CAATCACGAA	ATGTCACAGC	CGTTGAGACT	400
	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	ACCTTCCTTA	ATGGTCTTGG	450
	TATCGACTAT	CCAAGCATGC	ATTATGCAAA	CGCCATTTCA	AGTAACACAA	500
	CTGAATCCAA	CAAAAAATAT	GGTGCAAGTA	GTGAAAAAAT	GGCTGCTGCC	550
45	TACGCTGCTT	TTGCTAATGG	TGGTATTTAT	CACAAACCAA	TGTATATCAA	600
	TAAAATCGTC	TTAGTGATG	GTAGCGAAAA	AGAATTTTCT	GATGCTGGTA	650
	CACGAGCTAT	GAAAGAGACT	ACTGCCTATA	TGATGACTGA	AATGATGAAA	700
	ACTGTTTTAA	CTTACGGAAC	AGGACGTGGA	GCCTACCTAC	CATGGCTTCC	750
	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	800
50	AGTATATCAA	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	850
	TATACCCGTA	AATATGCAAT	GGCTGTTTGG	ACAGGATACT	CAAATCGTCT	900
	AACTCCAATC	ATCGGAGATG	GTTTCCTTGT	TGCTGGTAAA	GTCTATCGTT	950
	CAATGATAAC	TTACCTTTCT	GAAGATGACC	AACCTGGAGA	TTGGACAATG	1000
	CCAGATGGCT	TGTATAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	1050
55	TTCTACGTGG	AGCTCACCTG	CTCCACAACA	ACCCCATCA	ACTGAAAGTT	1100
	CAAGCTCATC	ATCAGATAGT	TCAACTTCAC	AGTCTAACTC	AACCACTCCA	1150
	AGCACAAATA	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	1200
	AAATACAACC	CCTGATCAAC	AAA			1223

2) INFORMATION FOR SEQ ID NO: 1011

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 1207 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-08

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1011

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
20	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGA CTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACA ACTGG	GATAGAGCAT	ATTTCGGTAA	TATTACTCTG	350
25	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCA	AATGGTGGCA	CTTACTATAA	ACCAATGTAT	ATCCATAAAG	600
30	TCGTCTTCAG	TGATGGAAGT	AAAAAAGAGT	TCTCTAATGT	CGGAACTCGT	650
	GCCATGAAGG	AAACGACAGC	CTATATGATG	ACCGACATGA	TGAAAACAGT	700
	CTTGACTTAT	GGA ACTGGGC	GTGGAGCCTA	TCTTCCTTGG	CTTCCTCAAG	750
	CTGGTAA AAC	AGGAACCTCT	AACTATA CAG	ATGAGGAAGT	TGAAAACCAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
35	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATT CGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
	CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	GCTCGCCCAA	1050
	TATGGACTGA	ACCCTCTACT	CAACAATCCT	CAACAGCTGA	AAGTTCAAGC	1100
40	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCC					1207

45

2) INFORMATION FOR SEQ ID NO: 1012

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1201 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 55 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-09
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1012

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
5	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACCTG	GATAGAGCAT	ATTTCGGTAA	TATTACTCTG	350
	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
10	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
15	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTGGAAT	CGTTTAACTC	900
20	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
	CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	GCTCGTTCTA	1050
	CGTGGAACCT	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
25	AAATAATAGT	ACGACTACCG	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	C					1201

30 2) INFORMATION FOR SEQ ID NO: 1013

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1013

45	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATCTAC	AACTCCGATC	50
	AATACGTCTC	TTACCCTGAC	GATGATTTGC	AAGTCGCATC	TACGGTCGTA	100
	GATGTTTCAA	ATGGTAAAGT	CATCGCACAA	CTTGGTGCTC	GTCATCAAGC	150
	AAGTAATGTT	TCATTCCGGT	CCAACCAGGC	CGTAGAAACC	AATCGTGACT	200
50	GGGGATCATC	AATGAAACCA	ATCACTGACT	ATGCTCCCGC	TTTAGAATAT	250
	GGAGTCTATG	ACTCTACTGC	TTCTATTGTA	CATGATGTCC	CTTATAACTA	300
	TCCTGGCACT	GATACTCCAC	TCTACAACCT	GGATCATGTC	TACTTTGGAA	350
	ACATTACAAT	CCAGTATGCT	CTTCAACAAT	CACGAAATGT	CACAGCCGTT	400
	GAGACTTTGA	ATAAGGTCGG	TCTAGATAGA	GCTAAAACCT	TCCTTAATGG	450
55	TCTTGGTATC	GACTATCCAA	GCATGCATTA	TGCAAACGCC	ATTTCAAGTA	500
	ACACAACCTGA	ATCCAACAAA	AAATATGGTG	CAAGTAGTGA	AAAAATGGCT	550
	GCTGCCTACG	CTGCTTTTGC	TAATGGTGGT	ATTTATCACA	AACCAATGTA	600
	TATCAATAAA	ATCGTCTTTA	GTGATGGTAG	CGAAAAAGAA	TTTTCTGATG	650
	CTGGTACACG	AGCTATGAAA	GAGACTACTG	CCTATATGAT	GAAGTAAATG	700
60	ATGAAAACCTG	TTTAACTTA	CGGAACAGGA	CGTGGAGCCT	ACCTACCATG	750

	GCTTCCACAA	GCAGGTAAGA	CAGGTACTTC	TAACTATACT	GACGAAGAAA	800
	TTGAAAAGTA	TATCAAGAAC	ACTGGCTACG	TAGCTCCAGA	TGAAATGTTT	850
	GTGGGTTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
5	ATCGCTCTAT	GATGACCTAC	CTGTCTGAAG	GAAGCAATCC	AGAGGATTGG	1000
	AATATAACCAG	AGGGGCTCTA	CAGAAATGGA	GAATTCGTAT	TTAAAAATGG	1050
	TGCTCGTTCT	ACGTGGAGCT	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAGCTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
10	ACAATCAAAT	ACAACCCCTG				1220

2) INFORMATION FOR SEQ ID NO: 1014

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1199 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1014

30	CAAAAACATC	TGTGGGATAT	TTACAATACA	GACGAATACG	TTGCCTATCC	50
	AGACGATGAA	TTGCAAGTCG	CTTCTACCAT	TGTTGATGTT	TCTAACGGTA	100
	AAGTCATTGC	CCAGCTAGGA	GCACGCCATC	AGTCAAGTAA	TGTTTCCTTC	150
	GGAATTAACC	AAGCAGTAGA	AACAAACCGC	GACTGGGGAT	CAACTATGAA	200
	ACCGATCACA	GACTATGCTC	CTGCCTTGGA	GTACGGTGTC	TACGATTCAA	250
35	CTGCTACTAT	CGTTCACGAT	GAGCCCTATA	ACTACCCTGG	GACAAATACC	300
	CCTGTTTATA	ACTGGGATAG	GGGCTACTTT	GGCAACATCA	CCTTGCAATA	350
	CGCCCTGCAA	CAATCGCGAA	ACGTCCCAGC	CGTGGAAGT	CTAAACAAGG	400
	TCGGACTCAA	CCGCGCCAAG	ACTTTCCTAA	ATGGTCTCGG	AATCGACTAC	450
	CCAAGTATTC	ACTACTCAAA	TGCCATTTCA	AGTAACACAA	CCGAATCAGA	500
40	CAAAAAATAT	GGAGCAAGTA	GTGAAAAGAT	GGCTGCTGCT	TACGCTGCCT	550
	TTGCAAATGG	TGGAACCTAC	TATAAACCAA	TGTATATCCA	TAAAGTCGTC	600
	TTTAGTGATG	GGAGTGAAAA	AGAGTTCTCT	AATGTCGGAA	CTCGTGCCAT	650
	GAAGGAAACG	ACAGCCTATA	TGATGACCGA	CATGATGAAA	ACTGTCTTAG	700
	TATACGGAAT	CGGACGTGGA	GCCTACCTAC	CTTGGCTTCC	ACAAGCAGGT	750
45	AAAACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	AGTATATCAA	800
	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	TATACCCGCA	850
	AATATGCAAT	GGCTGTATGG	ACAGGCTATT	CTAACCGTCT	GACACCACTT	900
	GTAGGCGATG	GCCTTACGGT	CGCTGCTAAA	GTTTACCGCT	CTATGATGAC	950
	CTACCTGTCT	GAAGGAAGCA	ATCCAGAGGA	TTGGAATATA	CCAGAGGGGC	1000
50	TCTACAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	TTCTACGTGG	1050
	AACTCACCTG	CTCCACAACA	ACCCCATCA	ACTGAAAGTT	CAAGCTCATC	1100
	ATCAGATAGT	TCAACTTCAC	AGTCTAGCTC	AACCACTCCA	AGCACAAATA	1150
	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	AAATACAAC	1199

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2) INFORMATION FOR SEQ ID NO: 1015

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1211 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-12

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1015

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
15	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACCTG	GATAGAGCAT	ATTTCGGTAA	TATTACTCTG	350
20	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
25	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACCTG	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
30	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
35	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	T				1211

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2) INFORMATION FOR SEQ ID NO: 1016

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1222 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-13

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1016

	GTAGACCAAG	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	50
	ATACGTCTCT	TACCCTGACG	ATGATTGCA	AGTCGCATCT	ACGGTCGTAG	100
	ATGTTTCAAA	TGGTAAAGTC	ATCGCACAA	TTGGTGCTCG	TCATCAAGCA	150
60	AGTAATGTTT	CATTCGGTAC	CAACCAGGCC	GTAGAAACCA	ATCGTGACTG	200

	GGGATCATCA	ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	250
	GAGTCTATGA	CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	300
	CCTGGCACTG	ATACTCCACT	CTACAACTGG	GATCATGTCT	ACTTTGGAAA	350
	CATTACAATC	CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	400
5	AGACTTTGAA	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	450
	CTTGGTATCG	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	500
	CACAACTGAA	TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAATGGCTG	550
	CTGCCTACGC	TGCTTTTGCT	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	600
	ATCAATAAAA	TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	650
10	TGGTACACGA	GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	700
	TGAAAACCTGT	TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	750
	CTTCCACAAG	CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	800
	TGAAAAGTAT	ATCAAGAACA	CTGGCTACGT	AGCTCCAGAT	GAAATGTTTG	850
	TGGGTTATAC	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTGGAAT	900
15	CGTTTAACTC	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	950
	TCGCTCTATG	ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	1000
	ATATACCAGA	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	1050
	GCTCGTTCTA	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	1100
	AAGTTCAAGC	TCATCATCAG	ATAGTTCAAC	TTACACAGTCT	AGCTCAACCA	1150
20	CTCCAAGCAC	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	1200
	CAATCAAATA	CAACCCCTGA	TC			1222

25 2) INFORMATION FOR SEQ ID NO: 1017

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1017

40	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	50
	AATACGTTGC	CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	100
	GATGTTTCTA	ACGGTAAAGT	CATTGCCAG	CTAGGAGCAC	GCCATCAGTC	150
	AAGTAATGTT	TCCTTCGGAA	TTAACCAAGC	AGTAGAAACA	AACCGCGACT	200
45	GGGGATCAAC	TATGAAACCG	ATCACAGACT	ATGCTCCTGC	CTTGGAGTAC	250
	GGTGTCTACG	ATTCAACTGC	TACTATCGTT	CACGATGAGC	CCTATAACTA	300
	CCCTGGGACA	AATACCCCTG	TTTATAACTG	GGATAGGGGC	TACTTTGGCA	350
	ACATCACCTT	GCAATACGCC	CTGCAACAAT	CGCGAAACGT	CCCAGCCGTG	400
	GAAACTCTAA	ACAAGGTCGG	ACTCAACCGC	GCCAAGACTT	TCCTAAATGG	450
50	TCTCGGAATC	GACTACCCAA	GTATTCATA	CTCAAATGCC	ATTTCAAGTA	500
	ACACAACCGA	ATCAGACAAA	AAATATGGAG	CAAGTAGTGA	AAAGATGGCT	550
	GCTGCTTACG	CTGCCTTTGC	AAATGGTGGG	ACTTACTATA	AACCAATGTA	600
	TATCCATAAA	GTCGTCTTTA	GTGATGGGAG	TGAAAAAGAG	TTCTCTAATG	650
	TCGGAACCTG	TGCCATGAAA	GAAACAACCTG	CTTACATGAT	GACCGAAATG	700
55	ATGAAAACCTG	TCCTGGCATA	CGGAAGTGGT	CGTGGAGCCT	ATCTCCCATG	750
	GTTAGCGCAA	GCTGGTAAGA	CAGGTACTTC	TAACCTACACA	GATGATGAAA	800
	TTGAAAAACA	CATCAAGAAC	ACTGGCTATG	TAGCTCCAGA	TGAAATGTTT	850
	GTTGGTTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTGCAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
60	ATCGCTCAAT	GATAACGTAT	CTATCAAAAG	ATACTCATCC	AGAAGACTGG	1000

	ACGATGCCAG	ACGGACTTTT	CAGAAACGGG	GAATTTGTAT	TCAAAAATGG	1050
	AGCTCGTTCT	ACGTGGAAC	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAACTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
5	ACAATCAAAT	ACAACCCCTG	ATCAACAAA			1229

2) INFORMATION FOR SEQ ID NO: 1018

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1018

25	ATGTAGACCA	AGAGGCTCAA	AAACGTCTGT	GGGATATCTA	CAACTCCGAT	50
	CAATACGTCT	CTTACCCTGA	CGATGATTG	CAAGTCGCAT	CTACGGTCGT	100
	AGATGTTTCA	AATGGTAAAG	TCATCGCCCA	ACTTGGAGCT	CGTCACCAAG	150
	CAAGTAACGT	TTCATTTGGT	ACCAACCAAG	CTGTGGAAAC	CAACCGTGAC	200
	TGGGGATCAA	GCATGAAACC	AATCACTGAT	TATGCCCCAG	CCTTAGAATA	250
30	TGGTGTATAT	GATTCCACTG	CAACTATGGT	TAATGATATT	CCTTATAACT	300
	ATCCGGGCAC	AAGCACACCT	GTCTACAACT	GGGATCGAGC	ATATTTTGGT	350
	AATATTAGCC	TGCAATATGC	CCTTCAACAA	TCTCGTAACG	TGCCTGCCGT	400
	TGAAACACTA	AACAAGGTTG	GTTTAGATAG	AGCCAAAAC	TTCCTAAATG	450
	GTTTGGGAAT	TGACTATCCA	AGTATTCACT	ACTCAAATGC	TATTTCAAGT	500
35	AATACAAC	AATCTAGTAA	ACAGTACGGG	GCAAGCAGTG	AGAAAATGGC	550
	TGCGGCTTAC	GCTGCATTCT	CTAATGGCGG	TATTTACCAC	AAACCAATGT	600
	ACATCAATAA	AGTTGTCTTT	AGTGATGGTA	GCGAAAAAGA	ATTTTCTGAT	650
	GCTGGTACAC	GAGCTATGAA	AGAGACTACT	GCCTATATGA	TGACTGAAAT	700
	GATGAAAAC	GTTTTAACTT	ACGGAACAGG	ACGTGGAGCC	TACCTACCAT	750
40	GGCTTCCACA	AGCAGGTAAG	ACAGGTACTT	CTAACTATAC	TGACGACGAA	800
	ATTGAAAAGT	ATATCAAGAA	CACTGGCTAC	GTAGCTCCAG	ATGAAATGTT	850
	TGTGGGTTAT	ACTCGTAAGT	ATTCTATGGC	TGTATGGACT	GGATACTCAA	900
	ATCGTTTAAC	TCCAATCATT	GGAGATGGTT	TCCTAGTTGC	TGCCAAAGTT	950
	TATCGCTCAA	TGATATCGTA	TCTATCAGAA	GATGACCATC	CTGGAGATTG	1000
45	GACAATGCCT	GAGGGAGTAT	ACAGAAGTGG	AGAATTTCGTA	TTTAAAAATG	1050
	GTGCTCGTTC	TACGTGGAGC	TCCCCTGCTC	CACAACAACC	CCCATCAACT	1100
	GAAAGTTCAA	GCTCATCATC	AGATAGTTCA	ACTTCACAGT	CTAGCTTAAC	1150
	CACTCCAAGC	ACAAATAATA	GTACGACTAC	CAATCCTAAC	AACAATACGC	1200
	AACAATCAAA	TACAACCCCT	GATCA			1225

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2) INFORMATION FOR SEQ ID NO: 1019

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 5 (B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1019

	GCCTCTATTT	CAAAGGAGAT	GCCTGGCATT	AGTATTTCTA	CTTCTTGGA	50
10	TCGAAAGGTT	TTGGAAACTT	CCCTTTCTTC	TATAGTAGGG	AGTGTATCCA	100
	GTGAAAAGC	TGGTCTCCCA	GCGGAAGAAG	CAGAATCCTA	TCTTAAAAAA	150
	GGCTATTCTC	TAAATGACCG	TGTTGGAACC	TCCTATTTGG	AAAAGCAATA	200
	TGAAGAGACC	TTACAAGGAA	AACGCTCGGT	AAAAGAAATC	CATCTGGATA	250
	AATATGGCAA	TATGGAAAGC	GTGGACACAA	TTGAGGAAGG	TAGTAAGGGA	300
15	AACAATATCA	AACTGACCAT	TGATTTGGCC	TTCCAAGATA	GCGTGGATGC	350
	TTTGCTGAAA	AGTTATTTCA	ATTCCGAGCT	AGGAAATGGT	GGAGCTAAAT	400
	ATTCTGAAGG	TGTCTATGCA	GTCGCCCTTA	ACCCAAAAAC	AGGTGCTGTT	450
	TTATCCATGT	CAGGGATCAA	ACATGACCTG	AAAACGGGAG	AGTTGACTCC	500
	TGATTCCTTG	GGAACGGTAA	CCAATGTCTT	TGTCCCAGGT	TCGGTTGTCA	550
20	AGGCTGCGAC	CATCAGCTCA	GGTTGGGAAA	ATGGTGTTTT	ATCAGGAAAC	600
	CAAACCTTAA	CAGATCAGCC	TATTGTTTTT	CAAGGTTTCA	CTCCAATTTA	650
	TTCTTGGTAT	AAATTGGCAT	ATGGATCTTT	TCCTATTACA	GCTGTGGAAG	700
	CCTTGAGTA	TTCATCCAAT	GCTTACATGG	TTCAAACCGC	TCTTGGAATC	750
	ATGGGCCAGA	CCTATCAACC	AAATATGTTT	GTTGGAACCA	GCAATTTGGA	800
25	AACAGCTATG	GGAAAACCTC	GTGCGACCTT	TGGCGAATAT	GGCTTGGGGG	850
	CTGCGACCGG	AATTGACCTA	CCAGATGAAT	CTACTGGATT	TGTTCCCAA	900
	GAGTATAGCT	TTGCTAATTA	CATCACCAAT	TCCTTTGGGC	AGTTTGATAA	950
	CTATACGCCC	ATGCAGTTGG	CTCAGTATGT	AGCAACTATT	GCAAATAATG	1000
	GTGTTTCGTG	GGCTCCTCGT	ATTGTTGAAG	GCATTTATGG	TAATAATGAT	1050
30	AAGGGAGGAC	TGGGTGACTT	GATTCAGCAA	CTGCAACCGA	CAGAGATGAA	1100
	TAAGGTCAAT	ATATCCGACT	CCGATATGAG	CATCTTGCAC	CAAGGTTTTT	1150
	ATCAGGTTGC	CCATGGTACT	AGTGGATTGA	CAACTGGACG	TGCCTTTTCA	1200
	AATGGTGCCT	TGGTATCCAT	TAGCGGAAAA	ACAGGTACAG	CCGAAAGCTA	1250
	TGTGGCAGAT	GGTCAGCAAG	CAACCAATAC	CAATGCGGTG	GCCTATGCCC	1300
35	CATCTGATAA	TCCCCAAATC	GCTGTCGCAG	TGGTCTTTCC	TCATAATACC	1350
	AATCTAACAA	ATGGTGTAGG	ACCTTCCATT	GCGCGTGACA	TTATCAATCT	1400
	GTATCAAAAA	TACCATCCAA	TGAAC TAGAA	AGGAAATTA		1439

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2) INFORMATION FOR SEQ ID NO: 1020

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-02

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1020

	GCCTCTATTT	CAAAGGAGAT	GCCTGGCATT	AGTATTTCTA	CTTCTTGGA	50
	TCGAAAGGTT	TTGGAAACTT	CCCTTTCTTC	TATAGTAGGG	AGTGTATCCA	100
	GTGAAAAGC	TGGTCTCCCA	GCGGAAGAAG	CAGAATCCTA	TCTTAAAAAA	150
60	GGCTATTCTC	TAAATGACCG	TGTTGGAACC	TCCTATTTGG	AAAAGCAATA	200

	TGAAGAGACC	TTACAAGGAA	AACGCTCGGT	AAAAGAAATC	CATCTGGATA	250
	AATATGGCAA	TATGGAAAGC	GTGGACACAA	TTGAGGAAGG	TAGTAAGGGA	300
	AACAATATCA	AACTGACCAT	TGATTTGGCC	TTCCAAGATA	GCGTGGATGC	350
	TTTGCTGAAA	AGTTATTTCA	ATTCCGAGCT	AGGAAATGGT	GGAGCTAAAT	400
5	ATTCTGAAGG	TGTCTATGCA	GTCGCCCTTA	ACCCAAAAAC	AGGTGCTGTT	450
	TTATCCATGT	CAGGGATCAA	ACATGACCTG	AAAACGGGAG	AGTTGACTCC	500
	TGATTCCTTG	GGAACGGTAA	CCAATGTCTT	TGTCCCAGGT	TCGGTTGTCA	550
	AGGCTGCGAC	CATCAGCTCA	GGTTGGGAAA	ATGGTGTTTT	ATCAGGAAAC	600
	CAAACCTTAA	CAGATCAGCC	TATTGTTTTT	CAAGGTTTCA	CTCCAATTTA	650
10	TTCTTGGTAT	AAATTGGCAT	ATGGATCTTT	TCCTATTACA	GCTGTGGAAG	700
	CCTTGGAGTA	TTCATCCAAT	GCTTACATGG	TTCAAACCGC	TCTTGGAATC	750
	ATGGGCCAGA	CCTATCAACC	AAATATGTTT	GTTGGAACCA	GCAATTTGGA	800
	AACAGCTATG	GGAAAACTTC	GTGCGACCTT	TGGCGAATAT	GGCTTGGGGG	850
	CTGCGACCGG	AATTGACCTA	CCAGATGAAT	CTACTGGATT	TGTTCCCAA	900
15	GAGTATAGCT	TTGCTAATTA	CATCACCAAT	TCCTTTGGGC	AGTTTGATAA	950
	CTATACGCCC	ATGCAGTTGG	CTCAGTATGT	AGCAACTATT	GCAAATAATG	1000
	GTGTTTCGTGT	GGCTCCTCGT	ATTGTTGAAG	GCATTTATGG	TAATAATGAT	1050
	AAGGGAGGAC	TGGGTGACTT	GATTCAGCAA	CTGCAACCGA	CAGAGATGAA	1100
	TAAGGTCAAT	ATATCCGACT	CCGATATGAG	CATCTTGAC	CAAGGTTTTT	1150
20	ATCAGGTTGC	CCATGGTACT	AGTGGATTGA	CAACTGGACG	TGCCTTTTCA	1200
	AATGGTGCCCT	TGGTATCCAT	TAGCGGAAAA	ACAGGTACAG	CCGAAAGCTA	1250
	TGTGGCAGAT	GGTCAGCAAG	CAACCAATAC	CAATGCGGTG	GCCTATGCCC	1300
	CATCTGATAA	TCCCCAAATC	GCTGTCGCAG	TGGTCTTTCC	TCATAATACC	1350
	AATCTAACAA	ATGGTGTAGG	ACCTTCCATT	GCGCGTGACA	TTATCAATCT	1400
25	GTATCAAAAA	TACCATCCAA	TGAACTAGAA	AGGAAATTAT	G	1441

2) INFORMATION FOR SEQ ID NO: 1021

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-03

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1021

45	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
50	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
55	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
60	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGTTGA	ACCAGCAATT	800

	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
5	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
10	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATT	1396

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2) INFORMATION FOR SEQ ID NO: 1022

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1428 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-04

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1022

	AAAGGAGATG	CCTGGCATTG	GTATTTCTAC	TTCTTGGGAT	CGAAAGGTTT	50
	TGGAAACTTC	CCTTTCTTCT	ATAGTAGGGA	GTGTATCCAG	TGAAAAAGCT	100
	GGTCTCCCAG	CGGAAGAAGC	AGAATCCTAT	CTTAAAAAAG	GCTATTCTCT	150
35	AAATGACCGT	GTTGGAACCT	CCTATTTGGA	AAAGCAATAT	GAAGAGACCT	200
	TACAAGGAAA	ACGCTCGGTA	AAAGAAATCC	ATCTGGATAA	ATATGGCAAT	250
	ATGGAAAGCG	TGGACACAAT	TGAGGAAGGT	AGTAAGGGAA	ACAATATCAA	300
	ACTGACCATT	GATTTGGCCT	TCCAAGATAG	CGTGGATGCT	TTGCTGAAAA	350
	GTTATTTCAA	TTCCGAGCTA	GGAAATGGTG	GAGCTAAATA	TTCTGAAGGT	400
40	GTCTATGCAG	TCGCCCTTAA	CCCAAAAACA	GGTGCTGTTT	TATCCATGTC	450
	AGGGATCAAA	CATGACCTGA	AAACGGGAGA	GTTGACTCCT	GATTCCTTGG	500
	GAACGGTAAC	CAATGTCTTT	GTCCCAGGTT	CGGTTGTCAA	GGCTGCGACC	550
	ATCAGCTCAG	GTTGGGAAAA	TGGTGTTTAA	TCAGGAAACC	AAACCTTAAC	600
	AGATCAGCCT	ATTGTTTTCC	AAGGTTTCTG	TCCAATTTAT	TCTTGGTATA	650
45	AATTGGCATA	TGGATCTTTT	CCTATTACAG	CTGTGGAAGC	CTTGGAGTAT	700
	TCATCCAATG	CTTACATGGT	TCAAACCGCT	CTTGGGAATCA	TGGGCCAGAC	750
	CTATCAACCA	AATATGTTTG	TTGGAACCAG	CAATTTGGAA	ACAGCTATGG	800
	GAAAACTTCG	TGCGACCTTT	GGCGAATATG	GCTTGGGGGC	TGCGACCGGA	850
	ATTGACCTAC	CAGATGAATC	TACTGGATTT	GTTCCCAAAG	AGTATAGCTT	900
50	TGCTAATTAC	ATCACCAATT	CCTTTGGGCA	GTTTGATAAC	TATACGCCCA	950
	TGCAGTTGGC	TCAGTATGTA	GCAACTATTG	CAAATAATGG	TGTTCGTGTG	1000
	GCTCCTCGTA	TTGTTGAAGG	CATTTATGGT	AATAATGATA	AGGGAGGACT	1050
	GGGTGACTTG	ATTCAGCAAC	TGCAACCGAC	AGAGATGAAT	AAGGTCAATA	1100
	TATCCGACTC	CGATATGAGC	ATCTTGACCC	AAGGTTTTTA	TCAGGTTGCC	1150
55	CATGGTACTA	GTGGATTGAC	AACTGGACGT	GCCTTTTCAA	ATGGTGCCTT	1200
	GGTATCCATT	AGCGGAAAAA	CAGGTACAGC	CGAAAGCTAT	GTGGCAGATG	1250
	GTCAGCAAGC	AACCAATACC	AATGCGGTGG	CCTATGCCCC	ATCTGATAAT	1300
	CCCCAAATCG	CTGTCGCAGT	GGTCTTTCCT	CATAATACCA	ATCTAACAAA	1350
	TGGTGTAGGA	CCTTCCATTG	CGCGTGACAT	TATCAATCTG	TATCAAAAAT	1400
60	ACCATCCAAT	GAAC TAGAAA	GGAAATTA			1428

2) INFORMATION FOR SEQ ID NO: 1023

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1023

20	TGCCTCTATT	TCAAAGGAGA	TGCCTGGCAT	TAGTATTTCT	ACTTCTTGGG	50
	ATCGAAAGGT	TTTGGAAACT	TCCCTTTCTT	CTATAGTAGG	GAGTGTATCC	100
	AGTGAAAAAG	CTGGTCTCCC	AGCGGAAGAA	GCAGAATCCT	ATCTTAAAAA	150
	AGGCTATTCT	CTAAATGACC	GTGTTGGAAC	CTCCTATTTG	GAAAAGCAAT	200
	ATGAAGAGAC	CTTACAAGGA	AAACGCTCGG	TAAAAGAAAT	CCATCTGGAT	250
25	AAATATGGCA	ATATGGAAAG	CGTGGACACA	ATTGAGGAAG	GTAAGTAAGG	300
	AAACAATATC	AAACTGACCA	TTGATTTGGC	CTTCCAAGAT	AGCGTGGATG	350
	CTTTGCTGAA	AAGTTATTTT	AATTCCGAGC	TAGGAAATGG	TGGAGCTAAA	400
	TATTCTGAAG	GTGTCTATGC	AGTCGCCCTT	AACCCAAAAA	CAGGTGCTGT	450
	TTTATCCATG	TCAGGGATCA	AACATGACCT	GAAAACGGGA	GAGTTGACTC	500
30	CTGATTCCTT	GGGAACGGTA	ACCAATGTCT	TTGTCCCAGG	TTCGGTTGTC	550
	AAGGCTGCGA	CCATCAGCTC	AGGTTGGGAA	AATGGTGTTT	TATCAGGAAA	600
	CCAAACCTTA	ACAGATCAGC	CTATTGTTTT	CCAAGGTTCA	GCTCCAATTT	650
	ATTCTTGGTA	TAAATTGGCA	TATGGATCTT	TTCCTATTAC	AGCTGTGGAA	700
	GCCTTGGAGT	ATTCATCCAA	TGCTTACATG	GTTCAAACCG	CTCTTGAAT	750
35	CATGGGCCAG	ACCTATCAAC	CAAATATGTT	TGTTGGAACC	AGCAATTTGG	800
	AAACAGCTAT	GGGAAAACCT	CGTGCGACCT	TTGGCGAATA	TGGCTTGGGG	850
	GCTGCGACCG	GAATTGACCT	ACCAGATGAA	TCTACTGGAT	TTGTTCCCAA	900
	AGAGTATAGC	TTTGCTAATT	ACATCACCAA	TTCCTTTGGG	CAGTTTGATA	950
	ACTATACGCC	CATGCAGTTG	GCTCAGTATG	TAGCAACTAT	TGCAAATAAT	1000
40	GGTGTTCGTG	TGGCTCCTCG	TATTGTTGAA	GGCATTTATG	GTAATAATGA	1050
	TAAGGGAGGA	CTGGGTGACT	TGATTCAGCA	ACTGCAACCG	ACAGAGATGA	1100
	ATAAGGTCAA	TATATCCGAC	TCCGATATGA	GCATCTTGCA	CCAAGGTTTT	1150
	TATCAGGTTG	CCCATGGTAC	TAGTGGATTG	ACAACCTGGAC	GTGCCTTTTC	1200
	AAATGGTGCC	TTGGTATCCA	TTAGCGGAAA	AACAGGTACA	GCCGAAAGCT	1250
45	ATGTGGCAGA	TGGTCAGCAA	GCAACCAATA	CCAATGCGGT	GGCCTATGCC	1300
	CCATCTGATA	ATCCCCAAAT	CGCTGTCGCA	GTGGTCTTTC	CTCATAATAC	1350
	CAATCTAACA	AATGGTGTAG	GACCTTCCAT	TGCGCGTGAC	ATTATCAATC	1400
	TGTATCAAAA	ATACCATCCA	ATGAAC TAGA	AAGGAAATTA	TG	1442

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2) INFORMATION FOR SEQ ID NO: 1024

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

571

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-06

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1024

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATCGAAAGG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTTGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACGACC	ATTGATTTGG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTGCTGA	AAAGTTATTT	CAATTCCGAG	CTAGGAAATG	GTGGAGCTAA	400
	ATATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCTG	450
	TTTTATCCAT	GTCAGGGATC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCCT	TGGGAACGGT	AACCAATGTC	TTTGTCCCAG	GTTCCGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CAGGTTGGGA	AAATGGTGTT	TTATCAGGAA	600
20	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTTC	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
	AGCCTTGGAG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGAA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAAAC	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
25	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTCCCA	900
	AAGAGTATAG	CTTTGCTAAT	TACATCACCA	ATTCCTTTGG	GCAGTTTGAT	950
	AACTATACAC	CCATGCAGTT	GGCTCAGTAT	GTAGCAACTA	TTGCAAATAA	1000
	TGGTGTTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTGAGC	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGCATCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCCCATGGTA	CTAGTGGATT	GACAACTGGA	CGTGCCTTTT	1200
	CAAATGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACAGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGCA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AATCCCCAAA	TCGCTGTCGC	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AATGAAGTAG	AAAGGAAATT	ATGCT	1445

40 2) INFORMATION FOR SEQ ID NO: 1025

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1025

55

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATCGAAAGA	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTTGGAA	CCTCGTATTT	GGAAAAGCAA	200
60	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250

	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACCTGACC	ATTGATTTGG	CCTTCCAAGA	TAGCGTGGAT	350
	GCTTTGCTGA	AAAGTTATTT	CAATTCCGAG	CTAGGAAATG	GTGGAGCCAA	400
	GTATTCTGAG	GGTGTGTATG	CAGTCGCCCT	TAACCCCAAA	ACAGGTGCTG	450
5	TTTTGTCTAT	GTCAGGACTC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCCT	TGGGAACGGT	AACCAATGTC	TTTGTCCCAG	GTTCCGGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CTGGCTGGGA	AAATGGTGTT	TTATCAGGAA	600
	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTTC	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
10	AGCCTTGGAG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGAA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAAAC	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTCCCA	900
	AAGACTATAG	CTTTGCTAAT	TACATCACCA	ATGCCTTTGG	GCAGTTTGAT	950
15	AACTATACGC	CCATGCAGTT	GGCTCAGTAT	GTAGCAACTA	TTGCAAATGA	1000
	TGGTGTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTACAG	AACTGCAACC	GACAGAGATG	1100
	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTATCTTGC	ACCAAGGATT	1150
	TTACCAAGTA	TCGCATGGAA	CTAGTCCCCT	TACGACAGGA	CGGGCGTTTT	1200
20	CAGATGGCGC	CACTGTTTCT	ATCAGTGGTA	AGACCGGTAC	AGGTGAAAGC	1250
	TATGTAGCTG	GTGGTCAAGA	AGCTAATAAT	ACCAATGCCG	TGGCCTATGC	1300
	TCCAACAGAA	AATCCTCAAA	TTGCAGTTGC	AGTAGTCTTT	CCTCATAATA	1350
	CCAATTTAAC	CAAAAATGTT	GGGCCAGCAA	TTGCTCGCGA	CATTATCAAT	1400
	TTATATAACC	AACACCATCC	AATGAATTAG	AAAGGAAGCC	A	1441
25						

2) INFORMATION FOR SEQ ID NO: 1026

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1443 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - 40 (B) STRAIN: StrR-08

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1026

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
45	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
50	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCCGGT	550
55	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
60	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850

	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
5	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
10	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTA	1443

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2) INFORMATION FOR SEQ ID NO: 1027

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-09

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1027

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
35	AAAAGGCTAT	TCTCTAAATG	ATCGTGTAGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCTTTCCAA	GATAGCGTGG	350
	ATGCTTTACT	GAAAAGTTAT	TTCAATTCCG	AGCTAGAAAA	TGGTGGAGCC	400
40	AAGTATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGGA	TTAAACATGA	CTTGAAAACG	GGAGATTTAA	500
	CACCTGATTC	CTTGGGAACA	GTAACCAATG	TCTTTGTCCC	GGGTTCTGTT	550
	GTCAAGGCGG	CGACCATCAG	CTCTGGTTGG	GAGAATGGAG	TCTTATCAGG	600
	AAATCAGACC	TTGACAGACC	AACCGATTGT	CTTCCAAGGT	TCAGCTCCGA	650
45	TTAATTCTTG	GTACACTCAG	GCTTACGATT	CATTTCCGAT	TACAGCGGTG	700
	GAAGCCTTGG	AGTATTCTTC	TAATGCCTAT	ATGGTCCAAA	CAGCTCTAGG	750
	TCTTATGGGG	CAGACCTACC	AACCCAATAT	GTTTGTCCGC	ACCAGCAATC	800
	TAGAGTCTGC	TATGGGGAAA	TTGCGTTCAA	CCTTTGGTGA	ATATGGCTTG	850
	GGCTCTGCGA	CTGGGATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
50	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	GATGGTGTTC	GTGTGGCTCC	TCGTATTGTG	GAAGGCATTT	ATGGCAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
55	TTTTATCAGG	TTGCTCATGG	GACTAGCGGA	TTGACAACAG	GTCGTGCCTT	1200
	TTCCAATGGT	GCAGCTGTAT	CCATTAGTGG	AAAAACAGGT	ACCGCCGAAA	1250
	GTTATGTAGC	AGGTGGCCAA	GAAGCCAACA	ATACTAATGC	TGTAGCCTAT	1300
	GCACCATCAG	ATAATCCTCA	AATAGCTGTT	GCTGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GATATTATCA	1400
60	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAT	TTA	1443

2) INFORMATION FOR SEQ ID NO: 1028

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1028

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACCTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCTCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	GACTTCTTAC	CTGGAAAAAC	200
	AATACGAGGA	AACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAGTATTCTG	AAGGCGTGTA	TGCAGTCGCC	CTTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGACTTGA	500
30	CGCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGGTCAGTA	550
	GTAAAGGCCG	CTACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	TAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
40	GATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
	TTCAAATGGC	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
45	GCTATGTGGC	AGATGGTTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTT	GCAGTGGTCT	TTCTTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAAC	AGAAAGGAAA	TTATGC	1446

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2) INFORMATION FOR SEQ ID NO: 1029

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1423 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

575

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1029

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTC	TACTTCTTGG	50
	GATAGAAAGG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTTG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAAGCC	TATCTTAAAA	150
	AAGGCTATTTC	TCTAAATGAC	CGTGTAGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGATAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACCTGACC	ATTGATTTGG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTACTGA	AAAGTTATTT	CAATTCTGAG	CTAGAAAATG	GTGGAGCCAA	400
	GTATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCGG	450
	TTTTGTCTAT	GTCAGGGATT	AAACATGACT	TGAAAACGGG	AGAGTTGACG	500
	CCTGATTCCT	TGGGAACGGT	AACCAATGTC	TTTGTTCAG	GTTCCGGTTGT	550
	CAAGGCGGCG	ACCATCAGCT	CAGGTTGGGA	AAATGGAGTC	TTGTCAGGAA	600
20	ACCAGACCTT	GACAGACCAG	TCCATTGTCT	TCCAAGGTTC	AGCTCCCATC	650
	AATTCTTGGT	ATACTCAGGC	TTACGGTTCA	TTCCCTATCA	CAGCGGTCCA	700
	AGCTCTGGAG	TATTCATCCA	ATGCTTATAT	GGTCCAAACA	GCCTTAGGTC	750
	TTATGGGGCA	GACCTATCAA	CCCAATATGT	TTGTCGGCAC	CAGCAATCTA	800
	GAGTCTGCTA	TGGGTAAATT	GCGTTCAACC	TTTGGCGAAT	ATGGCTTGGG	850
25	GGCTGCGACT	GGGATTGATC	TACCAGATGA	ATCTACTGGA	TTTGTTCCCA	900
	AAGACTATAA	CTTTGCCAAT	TTCATTACCA	ATGCCTTTGG	GCAGTTTGAT	950
	AACTATACCC	CAATGCAATT	GGCTCAGTAT	GTAGCAACTA	TTGCAAATGA	1000
	TGGTGTTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTCAGC	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTGTCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCTCATGGGA	CTAGTGGGTT	GACAACTGGC	CGTGCCTTTT	1200
	CAAATGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACGGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGGA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AATCCCCAAA	TCGCTGTTCG	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AAT			1423

40 2) INFORMATION FOR SEQ ID NO: 1030

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1447 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1030

55

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTGTT	AACCTCCTAT	TTGGAAAAGC	200
60	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250

	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
5	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
10	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
15	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
20	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTATGCT	1447
25						

2) INFORMATION FOR SEQ ID NO: 1031

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 40 (B) STRAIN: StrR-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1031

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACCTCTTG	50
45	GGATAGAAAG	GTTTTGGAAA	CTTCTCTTTC	TTCTATAGTA	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
	AAAGGCTATT	CTCTAAATGA	CCGTGTTGGG	ACTTCTTACC	TGGAAAAACA	200
	ATACGAGGAA	ACCTTACAAG	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
50	GGAAACAATA	TCAAACCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCTA	400
	AGTATTCTGA	AGGCGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGACTTGAC	500
	GCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGGTCAGTAG	550
55	TTAAGGCCGC	TACCATCAGC	TCAGGTTGGG	AAAATGGTGT	TTTATCAGGA	600
	AACCAAACCT	TAACAGATCA	GCCTATTGTT	TTCCAAGGTT	CAGCTCCAAT	650
	TTATTCTTGG	TATAAATTGG	CATATGGATC	TTTTCCCTATT	ACAGCTGTGG	700
	AAGCCTTGGA	GTATTCATCT	AATGCTTACA	TGGTTCAAAC	CGCTCTTGGA	750
	ATCATGGGCC	AGACCTATCA	ACCAAATATG	TTTGTTGGAA	CCAGCAATTT	800
60	GGAAACAGCT	ATGGGAAAAC	TTCGTGCGAC	CTTTGGCGAA	TATGGCTTGG	850

	GGGCTGCGAC	CGGAATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
	AAAGAGTATA	GCTTTGCTAA	TTACATTACT	AATGCCTTTG	GGCAGTTTGA	950
	TAACTATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	1050
5	GATAAGGGAG	GACTGGGTGA	CTTGATTGAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	1150
	TTTATCAGGT	TGCCCATGGT	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CCTTGGTATC	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	1250
	CTATGTGGCA	GATGGTCAGC	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	1300
10	CCCCATCTGA	TAATCCCCAA	ATCGCTGTTG	CAGTGGTCTT	TCCTCATAAT	1350
	ACCAATCTAA	CAAATGGTGT	AGGACCTTCC	ATTGCGCGTG	ACATTATCAA	1400
	TCTGTATCAA	AAATACCATC	CAATGAACCTA	GAAAGGAAAT	TATGCT	1446

15

2) INFORMATION FOR SEQ ID NO: 1032

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1032

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	50
	GGATAGAAAG	GTTTTGGAAG	CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
35	AAAGGCTATT	CTCTAAATGA	TCGTGTTGGA	ACCTCCTATT	TGGAAAAGCA	200
	ATATGAAGAG	ACCTTACAAG	GGAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGTGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
	GGAAACAATA	TCAAGCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCCA	400
40	AGTATTCTGA	GGGTGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGAGTTGAC	500
	TCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	550
	TCAAGGCTGC	GACCATCAGC	TCTGGCTGGG	AAAATGGAGT	CTTATCAGGA	600
	AACCAGACCT	TGACAGACCA	GTCCATTGTC	TTTCAAGGTT	CAGCTCCCAT	650
45	CAATTCTTGG	TATACTCAGG	CTTACGGTTC	ATTCCCTATC	ACAGCAGTCC	700
	AAGCTCTGGA	GTATTCATCT	AATGCCTATA	TGGTCCAAAC	AGCTTTAGGT	750
	CTTATGGGGC	AGACCTACCA	ACCTAATATG	TTTGTCGGCA	CCAGCAACCT	800
	AGAGTCTGCT	ATGGGGAAAT	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	850
	GTTCTGCGAC	CGGGATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
50	AAAGACTATA	GCTTTGCTAA	TTACATCACC	AATGCCTTTG	GGCAGTTTGA	950
	TAACTATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGAAATAAT	1050
	GATAAGGGAG	GCCTAGGCGA	CTTGATTGAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCTGATAT	GAGTATTTTG	CACCAAGGTT	1150
55	TTTATCAGGT	TGCTCATGGG	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CAGCGGTATC	CATTAGTGGG	AAAACAGGTA	CTGCCGAAAG	1250
	TTATGTTGAG	GGTGGTCAAG	AAGCTAACAA	TACTAATGCT	GTGGCCTATG	1300
	CACCATCAGA	TAATCCTCAA	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	1350
	ACCAACCTTA	CAAATGGTGT	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	1400
60	CCTCTATAAC	CAACATCATC	CAATGAATTA	GAAAGGAACA	TATGCT	1446

2) INFORMATION FOR SEQ ID NO: 1033

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1033

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTGTTG	AACCTCGTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAGCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCC	400
	AAGTATTCTG	AGGGTGTGTA	TGCAGTCGCC	CTTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
30	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCTGGT	550
	GTAAAGGCCG	CTACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
40	GATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCTCATGG	GACTAGTGGA	TTGACAACTG	GACGTGCTTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGTGG	GAAAACAGGT	ACTGCCGAAA	1250
45	GTTATGTTGC	AGGTGGTCAA	GAAGCCAACA	ATACCAACGC	GGTGGCCTAT	1300
	GCCCCATCAG	ATAATCCTCA	AATCGCTGTT	GCCGTGTGCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TTGGACCTTC	TATTGCACGC	GATATTATCA	1400
	ACCTCTATAA	CCAACACCAT	CCAATGAATT	AGAAAGGAAC	TTATGC	1446

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2) INFORMATION FOR SEQ ID NO: 1034

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-01

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1034

	GGAAACTGCA	GAGGTCAAGG	GGATTGATTT	TACAACCAGT	CCCAATCGTA	50
	GTTATCCAAA	CGGACAATTT	GCTTCTAGTT	TTATCGGACT	AGCTCAGCTC	100
10	CATGAAAATG	AAGATGGCAG	CAAGAGCTTA	CTGGGAACCT	CTGGAATGGA	150
	GAGTTCCTTG	AACAGTATTC	TTGCAGGGAC	AGACGGTATT	ATTACCTATG	200
	AAAAAGACCG	TGTAGGAAAT	ATCGTACCAG	GTACAGAACT	GGTATCGCAA	250
	CAAACGTGG	ATGGCAAGGA	TGTTTATACA	ACATTGTCTA	GTCCGCTACA	300
	ATCTTTCATG	GAAACTCAGA	TGGATGCCTT	TCTAGAAAAA	GTAAAAGGTA	350
15	AGTATATGAC	CGCGACCTTG	GTCAGTGCAA	AGACCGGTGA	AATCCTCGCT	400
	ACCACCCAAC	GACCTACCTT	TAATGCAGAT	ACTAAAGAAG	GAATCACTGA	450
	GGACTTTGTT	TGGCGTGATA	TTCTTTATCA	AAGTAACTAT	GAACCAGGAT	500
	CAGCCATGAA	GGTTATGACG	TTAGCTTCTT	CTATTGATAA	TAATACCTTC	550
	CCAAGTGGAG	AATACTTCAA	TAGCAGTGAA	TTCAAAATAG	CGGATGCGAC	600
20	GACTCGAGAT	TGGGATGTTA	ATGATGGTTT	GACTACTGGT	GGGATGATGA	650
	CTTTCTTACA	AGGTTTCGCT	CACTCCAGTA	ATGTTGGAAT	GAGTCTACTT	700
	GAACAAAAAA	TGGGAGATGC	TACTTGGTTG	GATTATCTAA	AACGCTTTAA	750
	ATTTGGGGTT	CCAACCTCGCT	TTGGCTTGAC	AGATGAATAC	GCTGGTCAAC	800
	TTCCAGCTGA	TAATATTGTT	AGTATTGCTC	AAAGCTCATT	TGGGCAAGGA	850
25	ATTTCACTGA	CACAAACACA	AATGCTTCGT	GCCTTTACAG	CTATTGCTAA	900
	TGATGGAGTT	ATGCTGGAGC	CAAAATTTAT	AAGTGCTATT	TATGATACTA	950
	ACAATCAGTC	TGTACGTAAG	TCACAAAAAG	AAATAGTAGG	AAATCCTGTT	1000
	TCCAAAGAGG	CAGCAAGCAC	AACTCGAAAT	CACATGATCT	TAGTTGGGAC	1050
	GGACCTCTA	TATGGAACCTA	TGTATAATCA	CTACACAGGA	AAGCCAATTA	1100
30	TAACAGTTCC	TGGACAAAAT	GTAGCAGTTA	AATCCGGTAC	GGCTCAAATC	1150
	GCTGATGAGA	AAAATGGAGG	ATACTTGGTT	GGTTCTACCA	ATTATATTTT	1200
	CTCAGTTGTG	ACTATGAATC	CTGCTGAAAA	TCCTGATTTT	ATCTTGTATG	1250
	TAACGGTTCA	ACAGCCTGAG	CATTATTCAG	GTATCCAGTT	GGGAGAATTT	1300
	GCCACCCCAA	TCTTGGAGCG	GGCTTCAGCT	ATGAAAGAAT	CTCTCAATCT	1350
35	TCAATCTCCA	GCCAAAAATT	TAGATAAAGT	TACGACAGAA	TCTTCTTATG	1400
	CAATGCCTAG	CATCAAGGAT	ATTTCACCTG	GTGAGTTGGC	GGAAGCCTTA	1450
	CGCCGAAATA	TTGTGCAACC	AATCGTTGTA	GGTACTGGAA	CAAAGATTAA	1500
	AGAGACTTCT	GTAGAAGAAG	GGACCAATCT	TGCACCAAAC	CAACAAGTTC	1550
	TCCTTTTATC	GGATAAGGTA	GAAGAAATTC	CAGACATGTA	TGGCTGGAAA	1600
40	AAAGAGACTG	CCGAGACCTT	TGCTAAATGG	TTGGATATTG	AACTGGAATT	1650
	TGAAGGTTCA	GGTTCCGTTG				1670

45 2) INFORMATION FOR SEQ ID NO: 1035

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1683 bases

(B) TYPE: Nucleic acid

50 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1035

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	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	CAACCAGTCC	50
	CAATCGTAGT	TACCCAAATG	GACAATTTGC	TTCTAGTTTT	ATCGGTCTAG	100
	CTCAGCTCCA	TGAAAATGAA	GATGGAAGCA	AGAGTTTGCT	GGGAACCTCT	150
	GGAATGGAGA	GTTCCTTGAA	CAGTATTCTT	GCAGGGACAG	ACGGCATTAT	200
5	TACCTATGAA	AAGGATCGTC	TGGGCAATAT	TGTACCCGGA	ACAGAACAAG	250
	TTTCCCAACA	AACGGTGGAT	GGCAAGGATG	TTTACACAAC	CATTTCCAGC	300
	CCCCTCCAGT	CCTTCATGGA	AACTCAGATG	GATGCCTTTC	TAGAAAAAGT	350
	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	ACCGGTGAAA	400
	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	TAAAGAAGGA	450
10	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	GTAACATATGA	500
	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	ATTGATAATA	550
	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	CAAAATAGCG	600
	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	CTACTGGTGG	650
	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	GTTGGAATGA	700
15	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTGGTTGGA	TTATCTAAAA	750
	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	ATGAATACGC	800
	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	AGCTCATTTG	850
	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	CTTTACAGCT	900
	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	GTGCTATTTA	950
20	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	ATAGTAGGAA	1000
	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	CATGATCTTA	1050
	GTTGGGACGG	ACCCTCTATA	TGGAACATATG	TATAATCACT	ACACAGGAAA	1100
	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	TCCGGTACGG	1150
	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGGTTGG	TTCTACCAAT	1200
25	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	CTGATTTTAT	1250
	CTTGTATGTA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	ATCCAGTTGG	1300
	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	GAAAGAATCT	1350
	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	CGACAGAATC	1400
	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTCACCTGGT	GAGTTGGCGG	1450
30	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	TACTGGAACA	1500
	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	CACCAAACCA	1550
	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTCCA	GACATGTATG	1600
	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	GGATATTGAA	1650
	CTGGAATTTG	AAGGTTTCAGG	TTCCGTTGTT	CAG		1683
35						

2) INFORMATION FOR SEQ ID NO: 1036

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1682 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 50 (B) STRAIN: StrR-03

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1036

	TCAAAAAAGA	ATTGGAAACT	GCAGAGGTCA	AGGGGATTGA	TTTTACAACC	50
55	AGTCCCAATC	GTAGTTACCC	AAATGGACAA	TTTGCTTCTA	GTTTTATCGG	100
	TCTAGCTCAG	CTCCATGAAA	ATGAAGATGG	AAGCAAGAGT	TTGCTGGGAA	150
	CCTCTGGAAT	GGAGAGTTCC	TTGAACAGTA	TTCTTGACAGG	GACAGACGGC	200
	ATTATTACCT	ATGAAAAGGA	TCGTCTGGGC	AATATTGTAC	CCGGAACAGA	250
	ACAAGTTTCC	CAACAAACGG	TGGATGGCAA	GGATGTTTAC	ACAACCATTT	300
60	CCAGCCCCCT	CCAGTCCTTC	ATGGAAACTC	AGATGGATGC	CTTTCTAGAA	350

	AAAGTAAAAG	GTAAGTATAT	GACCGCGACC	TTGGTCAGTG	CAAAGACCGG	400
	TGAAATCCTC	GCTACCACCC	AACGACCTAC	CTTTAATGCA	GATACTAAAG	450
	AAGGAATCAC	TGAGGACTTT	GTTTGGCGTG	ATATTCTTTA	TCAAAGTAAC	500
	TATGAACCAAG	GATCAGCCAT	GAAGGTTATG	ACGTTAGCTT	CTTCTATTGA	550
5	TAATAATACC	TTCCCAAGTG	GAGAATACTT	CAATAGCAGT	GAATTCAAAA	600
	TAGCGGATGC	GACGACTCGA	GATTGGGATG	TTAATGATGG	TTTGACTACT	650
	GGTGGGATGA	TGACTTTCTT	ACAAGGTTTC	GCTCACTCCA	GTAATGTTGG	700
	AATGAGTCTA	CTTGAACAAA	AAATGGGAGA	TGCTACTTGG	TTGGATTATC	750
	TAAAACGCTT	TAAATTTGGG	GTTCCAACCTC	GCTTTGGCTT	GACAGATGAA	800
10	TACGCTGGTC	AACTTCCAGC	TGATAATATT	GTTAGTATTG	CTCAAAGCTC	850
	ATTTGGGCAA	GGAATTTTCAG	TGACACAAAC	ACAAATGCTT	CGTGCCTTTA	900
	CAGCTATTGC	TAATGATGGA	GTTATGCTGG	AGCCAAAATT	TATAAGTGCT	950
	ATTTATGATA	CTAACAATCA	GTCTGTACGT	AAGTCACAAA	AAGAAATAGT	1000
	AGGAAATCCT	GTTTCCAAAG	AGGCAGCAAG	CACAACTCGA	AATCACATGA	1050
15	TCTTAGTTGG	GACGGACCCCT	CTATATGGAA	CTATGTATAA	TCACTACACA	1100
	GGAAAGCCAA	TTATAACAGT	TCCTGGACAA	AATGTAGCAG	TTAAATCCGG	1150
	TACGGCTCAA	ATCGCTGATG	AGAAAAATGG	AGGATACTTG	GTTGGTTCTA	1200
	CCAATTATAT	TTTCTCAGTT	GTGACTATGA	ATCCTGCTGA	AAATCCTGAT	1250
	TTTATCTTGT	ATGTAACGGT	TCAACAGCCT	GAGCATTATT	CAGGTATCCA	1300
20	GTTGGGAGAA	TTTGCCACCC	CAATCTTGGA	GCGGGCTTCA	GCTATGAAAG	1350
	AATCTCTCAA	TCTTCAATCT	CCAGCCAAA	ATTTAGATAA	AGTTACGACA	1400
	GAATCTTCTT	ATGCAATGCC	TAGCATCAAG	GATATTTTAC	CTGGTGAGTT	1450
	GGCGGAAGCC	TTACGCCGAA	ATATTGTGCA	ACCAATCGTT	GTAGGTACTG	1500
	GAACAAAGAT	TAAAGAGACT	TCTGTAGAAG	AAGGGACCAA	TCTTGACCA	1550
25	AACCAACAAG	TTCTCCTTTT	ATCGGATAAG	GTAGAAGAAA	TTCCAGACAT	1600
	GTATGGCTGG	AAAAAAGAGA	CTGCCGAGAC	CTTTGCTAAA	TGGTTGGATA	1650
	TTGAACTGGA	ATTTGAAGGT	TCAGGTTCCG	TT		1682

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2) INFORMATION FOR SEQ ID NO: 1037

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1681 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-04

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1037

	CAAAAAAGAA	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAATCG	TAGTTATCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TACTGGGAAC	150
50	CTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGTA	200
	TTATTACCTA	TGAAAAAGAC	CGTGTAGGAA	ATATCGTACC	AGGTACAGAA	250
	CTGGTATCGC	AACAAACTGT	GGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
55	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	650
60	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700

	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
5	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
10	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
	CAATTATATT	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
15	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTTACC	TGGTGAGTTG	1450
	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
20	TGAACTGGAA	TTTGAAGGTT	CAGGTTCCGT	T		1681

2) INFORMATION FOR SEQ ID NO: 1038

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1038

40	AAAAAAGAAT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTATCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	ACTGGGAACC	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGTAT	200
	TATTACCTAT	GAAAAAGACC	GTGTAGGAAA	TATCGTACCA	GGTACAGAAC	250
45	TGGTATCGCA	ACAAACTGTG	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
	AGTCCGCTAC	AATCTTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
50	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
55	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTTCAGTG	ACACAAACAC	AAATGCTTCG	TGCCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
60	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050

	TTAGTTGGGA	CGGACCCTCT	ATATGGAACT	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
5	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACACCT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
10	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAATT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAACTGGAAT	TTGAAGGTTC	AGGTTCCGTT	GTTCA		1685

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2) INFORMATION FOR SEQ ID NO: 1039

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1679 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-06

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1039

	AAAAGAATTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTATCCAAAC	GGACAATTTG	CTTCTAGTTT	TATCGGACTA	100
35	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTAC	TGGGAACCTC	150
	TGGAATGGAG	AGTTCCTTGA	ACAGTATTCT	TGCAGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAACTG	250
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
40	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
45	GGATGCGACG	ACTCGAGATT	GGGATGTAA	TGATGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTTG	ATTATCTAAA	750
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	850
50	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAACT	CACAAAAAGA	AATAGTAGGA	1000
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCCTCTAT	ATGGAAGTAT	GTATAATCAC	TACACAGGAA	1100
55	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGTTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
	TCTTGTATGT	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
60	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400

	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550
	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
5	GGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1650
	ACTGGAATTT	GAAGG TTCAG	GTTCCGTTG			1679

10 2) INFORMATION FOR SEQ ID NO: 1040

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1040

25	TAAAAAGGAT	CTAAAAGACG	CTAGTGTTGA	AGGAATTGAC	TTCACAACTA	50
	GCCCTAATAG	AAGCTATCCA	AATGGACAAT	TCGCTTCTAG	TTTTATTGGT	100
	TTGGCCCAAC	TCCATGAAAA	TGAGGATGGT	AGCAAGAGTT	TGCTGGGAAC	150
	TTCTGGGATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	AAAGACGGTA	200
30	TTATTACCTA	TGAAAAAGAT	CGTCTGGGTA	ATATTGTCCC	TGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
35	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCAAGTG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGAAGGT	TTGACTACTG	650
	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700
40	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
45	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
50	CAATTATATT	TTCTCAGCTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTTACC	TGGTGAGTTG	1450
55	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGACCAAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
60	TGAACTGGAA	TTTGAAGGTT	CAGGTTCCGT	CGTTC		1685

2) INFORMATION FOR SEQ ID NO: 1041

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 15 (B) STRAIN: StrR-08

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1041

	GTCTATCAAA	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	50
20	CAACCAGTCC	CAATCGTAGT	TATCCAAACG	GACAATTTGC	TTCTAGTTTT	100
	ATCGGACTAG	CTCAGCTCCA	TGAAAATGAA	GATGGCAGCA	AGAGCTTACT	150
	GGGAACCTCT	GGAATGGAGA	GTTCCCTTGAA	CAGTATTCTT	GCAGGGACAG	200
	ACGGTATTAT	TACCTATGAA	AAAGACCGTG	TAGGAAATAT	CGTACCAGGT	250
	ACAGAACTGG	TATCGCAACA	AACTGTGGAT	GGCAAGGATG	TTTATACAAC	300
25	ATTGTCTAGT	CCGCTACAAT	CTTTCATGGA	AACTCAGATG	GATGCCTTTC	350
	TAGAAAAAGT	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	400
	ACCGGTGAAA	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	450
	TAAAGAAGGA	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	500
	GTAACATATGA	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	550
30	ATTGATAATA	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	600
	CAAAATAGCG	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	650
	CTACTGGTGG	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	700
	GTTGGAATGA	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTGGTTGGA	750
	TTATCTAAAA	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	800
35	ATGAATACGC	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	850
	AGCTCATTTG	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	900
	CTTTACAGCT	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	950
	GTGCTATTTA	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	1000
	ATAGTAGGAA	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	1050
40	CATGATCTTA	GTTGGGACGG	ACCCTCTATA	TGGAACATATG	TATAATCACT	1100
	ACACAGGAAA	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	1150
	TCCGGTACGG	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGGTTGG	1200
	TTCTACCAAT	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	1250
	CTGATTTTAT	CTTGTATGTA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	1300
45	ATCCAGTTGG	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	1350
	GAAAGAATCT	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	1400
	CGACAGAATC	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTCACCTGGT	1450
	GAGTTGGCGG	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	1500
	TACTGGAACA	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	1550
50	CACCAAACCA	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTCCA	1600
	GACATGTATG	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	1650
	GGATATTGAA	CTGGAATTTG	AAGGTTTCAGG	TTCCGTTGTT	CAGAAG	1696

55

2) INFORMATION FOR SEQ ID NO: 1042

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-09

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1042

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	GCTGGGAACC	150
15	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGCAT	200
	TATTACCTAT	GAAAAGGATC	GTCTGGGAAA	TATTGTCCCC	GGAACGGAAC	250
	AAGTTTCCCA	ACAAACTGTÀ	GATGGCAAGG	ATGTTTATAC	GACTATTTCC	300
	AGCACCTTC	AGTCCTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
20	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
25	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACCTCGC	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTCAAGT	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
30	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
	TTAGTTGGGA	CGGACCCTCT	ATATGGAAct	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
35	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGAGC	GGGCTTCAGC	TATGAAAGAC	1350
	TCTCTCAATC	TTCAAACAAC	AGCTAAAGCT	TTGGAGCAAG	TAAGTCAACA	1400
40	AAGTCCTTAT	CCTATGCCTA	GTGTCAAGGA	TATTTACCT	GGTGATTTAG	1450
	CAGAAGAATT	GCGTCGCAAT	CTTGTAACAAC	CCATCGTTGT	GGGAACAGGA	1500
	ACGAAGATTA	AAAACAGTTC	TGCTGAAGAA	GGGAAGAATC	TTGCCCCGAA	1550
	TCAGCAAGTC	CTTATCTTAT	CTGATAAAGT	AGAGGAAGTT	CCAGATATGT	1600
	ATGGTTGGAC	AAAGGAGACT	GCTGAGACCC	TTGCTAAGTG	GCTCAATATA	1650
45	GAACTTGAAT	TTCAAGGTTC	GGGTTCTACT	GTGCAGAAG		1689

2) INFORMATION FOR SEQ ID NO: 1043

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1690 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1043

5	CAAAAAAGAG	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCTAATCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGT	100
	CTAGCTCAAC	TCCATGAAAA	TGAAGATGGA	AGCAAGAGTT	TGCTGGGAAC	150
	TTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	AAAGACGGTA	200
	TTATTACTTA	TGAAAAGGAT	CGTCTGGGTA	ATATTGTCCC	TGGAACAGAA	250
10	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTC	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
15	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	650
	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700
	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
20	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
25	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
	CAATTATATT	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
30	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTTACC	TGGTGAGTTG	1450
	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
35	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
	TGAACTGGAA	TTTGAAGGTT	CAGGTTCCGT	TGTTCAGAAG		1690

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2) INFORMATION FOR SEQ ID NO: 1044

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1668 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1044

	AGTTGGAAAC	TGCAGAGGTC	AAGGGGATTG	ATTTTACAAC	CAGTCCTAAT	50
	CGTAGTTACC	CAAACGGACA	ATTGCTTCT	AGTTTTATCG	GACTAGCTCA	100
60	GCTCCATGAA	AATGAAGATG	GCAGCAAGAG	CTTGCTGGGA	ACCTCTGGGA	150

	TGGAGAGTTC	TTTAAATAGA	ATTCTTGCAG	GGACAGACGG	CATTATTACC	200
	TATGAAAAGG	ATCGTCTGGG	AAATATTGTC	CCCGGAACGG	AACAAGTTTC	250
	CCAACAAACG	GTAGATGGCA	AGGATGTTTA	TACGACTATT	TCCAGCACCC	300
	TTCAGTCCTT	CATGGAGACC	CAGATGAATG	CCTTTCAAGA	AAAAGTAAAA	350
5	GGCAAGTATA	TGACGGCTAC	CTTGGTCAGT	GCTAAAACAG	GGGAAATTCT	400
	TGCAACAACG	CAACGGCCGA	CCTTCGATGC	TGATACTAAG	GAAGGACTTA	450
	CCAAGGACTT	TGTTTGGCGT	GATATCCTCT	ATCAAAGTAA	CTATGAGCCA	500
	GGGTCAACCA	TGAAGGTCAT	GACGCTTGCT	GCTGCTATTG	ATAATAACAC	550
	TTTCCCAGGA	GGAGAAGTTT	TCAATAGTAG	TGAATTAAAA	ATAGCGGATG	600
10	CGACAATTTCG	AGATTGGGAT	GTTAATGATG	GTTTGACGAC	TGGTGGGATG	650
	ATGACTTTCT	TACAAGGTTT	CGCTCACTCC	AGTAATGTTG	GAATGAGTCT	700
	ACTTGAACAA	AAAATGGGAG	ATGCTACTTG	GTTGGATTAT	CTAAACCGCT	750
	TTAAGTTTGG	GGTGCCGACG	CGTTTTGGTC	TGACTGATGA	GTATTCAGGT	800
	CAATTGCCTG	CAGATAATAT	TGTTAATATT	GCCATGAGTG	CATTTGGTCA	850
15	GGGGATTTC	GTGACCCAGA	CGCAAATGAT	TCGTGCCTTT	ACAGCTATTG	900
	CTAATGATGG	TGTTATGCTG	GAGCCTAAAT	TTATTAGTGC	CATTTATGAT	950
	CCAAATGATC	AAACTGCTCG	GAAATCTCAA	AAAGAAATTG	TGGGAAATCC	1000
	TGTTTCTAAA	GATGCAGCTA	GTCTAACTCG	GACTAACATG	ATTTTGGTAG	1050
	GGACGGATCC	GGTTTATGGA	ACCATGTATA	ACCACAGCAC	AGGTAAGCCA	1100
20	ACTGTAAGT	TTCCTGGGCA	AAATGTAGCC	CTCAAGTCTG	GTACGGCTCA	1150
	GATTGCTGAC	GAGAAAAATG	GTGGTTATCT	AGTCGGGTTA	ACCAACTATA	1200
	TTTTCTCGGC	TGTATCGATG	AATCCGGCTG	AAAATCCTGA	TTTTATCTTG	1250
	TATGTAACGG	TACAGCAACC	TGAACATTAT	TCAGGTATCC	AGTTGGGAGA	1300
	ATTTGCCACC	CCAATCTTGG	AGCGGGCTTC	AGCTATGAAA	GAATCTCTCA	1350
25	ATCTTCAATC	TCCAGCCAAG	AATTTAGATA	AAGTTACGAC	AGAATCTTCT	1400
	TATGCAATGC	CTAGCATCAA	GGATATTTCA	CCTGGTGAGT	TGGCGGAAGC	1450
	CTTACGCCGA	AATATTGTGC	AACCAATCGT	TGTAGGTACT	GGAACAAAGA	1500
	TTAAAGAGAC	TTCTGTAGAA	GAAGGGACCA	ATCTTGCACC	AAACCAACAA	1550
	GTTCTCCTTT	TATCGGATAA	GGTAGAAGAA	ATTCCAGACA	TGTATGGCTG	1600
30	GAAAAAAGAG	ACTGCTGAAA	CCTTTGCTAA	ATGGTTGGAT	ATTGAGCTGG	1650
	AATTTGAAGG	GTCAGGTT				1668

35 2) INFORMATION FOR SEQ ID NO: 1045

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1045

50	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	GTCCCAATCG	50
	TAGTTACCCA	AATGGACAAT	TTGCTTCTAG	TTTTATCGGT	CTAGCTCAGC	100
	TCCATGAAAA	TGAAGATGGA	AGCAAGAGTT	TGCTGGGAAC	CTCTGGAATG	150
	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	TTATTACCTA	200
55	TGAAAAGGAT	CGTCTGGGCA	ATATTGTACC	CGGAACAGAA	CAAGTTTCCC	250
	AACAAACGGT	GGATGGCAAG	GATGTTTACA	CAACCATTTC	CAGCCCCCTC	300
	CAGTCCTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	AAGTAAAAGG	350
	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	GAAATCCTCG	400
	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	AGGAATCACT	450
60	GAGGACTTTG	TTTGCGGTGA	TATTCTTTAT	CAAAGTAACT	ATGAACCAGG	500

	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	AATAATACCT	550
	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	AGCGGATGCG	600
	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	GTGGGATGAT	650
	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	ATGAGTCTAC	700
5	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	AAAACGCTTT	750
	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	ACGCTGGTCA	800
	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	TTTGGGCAAG	850
	GAATTTCACT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	AGCTATTGCT	900
	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	TTTATGATAC	950
10	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	GGAAATCCTG	1000
	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	CTTAGTTGGG	1050
	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	GAAAGCCAAT	1100
	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	GCGGCTCAAA	1150
	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	CAATTATATT	1200
15	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	TTATCTTGTA	1250
	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	TTGGGAGAAT	1300
	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	ATCTCTCAAT	1350
	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	AATCTTCTTA	1400
	TGCAATGCCT	AGCATCAAGG	ATATTTTACC	TGGTGAGTTG	GCGGAAGCCT	1450
20	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	AACAAAGATT	1500
	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	ACCAACAAGT	1550
	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	TATGGCTGGA	1600
	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GTTTGGATAT	TGAACTGGAA	1650
	TTTGAAGGTT	CAGGTTCCGT	TGTTCAGAAG			1680
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2) INFORMATION FOR SEQ ID NO: 1046

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1689 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - 40 (B) STRAIN: StrR-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1046

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
45	TCCTAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGTC	100
	TAGCTCAACT	CCATGAAAAT	GAAGATGGAA	GCAAGAGTTT	GCTGGGAACT	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	AAGACGGTAT	200
	TATTACTTAT	GAAAAGGATC	GTCTGGGTAA	TATTGTCCCT	GGAACAGAAC	250
	AAGTTTCCCA	ACAAACGGTA	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
50	AGTCCGCTCC	AATCTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
55	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACCTCGC	TTTGGCTTGA	CAGATGAATA	800
60	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850

	TTGGGCAAGG	AATTTTCAGTG	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
5	TTAGTTGGGA	CGGACCCTCT	ATATGGAACT	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
10	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACCTT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
15	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAATT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAAGTGAAT	TTGAAGGTTC	AGGTTCCGTT	GTTCAGAAG		1689

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2) INFORMATION FOR SEQ ID NO: 1047

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1690 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-14
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047

	CAAAAAAGAA	TTGGAAGCTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAACCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TGCTGGGAAC	150
40	TTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	200
	TTATTACCTA	TGAAAAGGAT	CGTCTGGGTA	ATATTGTACC	CGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTACA	CAACCATTTT	300
	CAGCCCCCTC	CAGTCCTTTA	TGGAAACCCA	GATGGATGCT	TTTCAAGAGA	350
	AGGTAAAAGG	AAAGTACACG	ACAGCGACTT	TGGTCAGTGC	TAAACAGGG	400
45	GAAATTCTGG	CAACAACGCA	ACGACCGACC	TTTGATGCAG	ATACAAAAGA	450
	AGGCATTACA	GAGGACTTTG	TTTGGCGTGA	TATCCTTTAC	CAAAGTAACT	500
	ATGAGCCAGG	TTCCCTTATG	AAAGTGATGA	TGTTGGCTGC	TGCTATTGAT	550
	AATAATACCT	TTCCAGGGGG	AGAAGTCTTC	AATAGTAGTG	AGTTAAAAAT	600
	TGCAGATGTC	ACGATTTCGAG	ATTGGGACGT	CAATGAAGGA	TTGACTGGTG	650
50	GCAGAATGAT	GACCTTTTCT	CAAGGGTTCG	CTCACTCAAG	TAACGTTGGG	700
	ATGACGCTTC	TTGAGCAAAA	GATGGGAGAT	GCTACATGGC	TTGATTATCT	750
	AAATCGCTTT	AAATTTGGTG	TTCCGACTCG	TTTTGGCTTG	ACGGATGAAT	800
	ATGCAGGCCA	ACTTCCAGCT	GACAATATCG	TAAATATTGC	TCAGAGTTCA	850
	TTTGGACAAG	GGATTTTCAGC	GACCCAGACG	CAAATGATTC	GTGCCTTCAC	900
55	GGCTATTGCC	AACGATGGAG	TCATGTTAGA	ACCTAAATTT	ATCAGTGCCA	950
	TTTATGATCC	AAATGATCAA	ACTGCTCGGA	AATCACAAAA	AGAAGTTGTG	1000
	GGAAATCCTG	TGTCTAAAGA	TGCAGCGAGC	TTGACGCGAA	CGCATATGGT	1050
	TTTAGTCGGT	ACCGATCCAG	TATATGGAAC	TATGTATAAT	CATAAGACAG	1100
	GGAAACCAAC	TGTAAGTGT	CCTGGGCAAA	ATGTAGCCCT	CAAGTCTGGT	1150
60	ACGGCTCAGA	TTGCCGATGA	GAAAAATGGA	GGTACTTAG	TTGGTACGAC	1200

	CAATTACATT	TTTTCGGCTG	TATCGATGAA	CCCTGCTGAA	AATCCTGATT	1250
	TTATTCTCTA	TGTGACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATTCAG	1300
	TTGGGGGAAT	TTGCCAATCC	TATCTTGGAA	AGGGCAGTGG	CTATGAAAGA	1350
	TTCCCTTAAC	CTCCAATCTA	CCGCTAAAAC	GTTAAATCAG	GTAACCAATC	1400
5	AAAGCGCTTA	TGCCATGCCT	AGCATCAAGG	ACATTTCCACC	TGGCGATTTG	1450
	GCGGAAGCCT	TACGTCGCAA	TATTGTGCAA	CCAATCGTTG	TAGGAACAGG	1500
	AACAAAAATT	AAAGAATCAT	CTGTAGAAGA	AGGGACGGAT	CTTGACACCTA	1550
	ACCAGCAAGT	TCTTCTCTTA	TCTGATAAAG	CAGAGGAAGT	TCCAGATATG	1600
	TATGGTTGGA	CAAAAGAGAC	TGCTGAGACC	TTTGCTAAGT	GGCTCAATAT	1650
10	AGAACTTGAA	TTTGAAGGTT	CGGGCTCTAC	TGTGCAGAAG		1690

2) INFORMATION FOR SEQ ID NO: 1048

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1682 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048

30	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTACCCAAAC	GGACAATTTG	CTTCTAGCTT	TATTGGCTTA	100
	GCCCAACTTC	ATGAAAATGA	GGATGGTAGT	AAGAGTTTGT	TAGGGACTTC	150
	TGGTTTGGAG	AGTTCTTTAA	ATACCATTCT	TGCTGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAAGCTG	250
35	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
40	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
	GGATGCGACG	ACTCGAGATT	GGGATGTTAA	TGAAGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	750
45	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	850
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1000
50	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCCTCTAT	ATGGAAGTAT	GTATAATCAC	TACACAGGAA	1100
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
55	TCTTGTATGT	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
60	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550

AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
GGCTGGAAAA	AAGAGACTGC	TGAAACCTTT	GCTAAATGGT	TGGATATTGA	1650
GTTGGAATTT	GAAGGTTCAG	GTTCCGTCGT	TC		1682

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2) INFORMATION FOR SEQ ID NO: 1049

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1241 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R690

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049

GCAGCGTTGC	GTGATACCGT	TGAAAAAACC	ATTAAAAACT	GTTTGGATTT	50
TGAAAGGAGA	CAGGAGCATG	AATAGAATAA	AAGTTGCAAT	ACTGTTTGGG	100
25 GGTGCTCAG	AGGAGCATGA	CGTATCGGTA	AAATCTGCAA	TAGAGATAGC	150
CGCTAACATT	AATAAAGAAA	AATACGAGCC	GTTATACATT	GGAATTACGA	200
AATCTGGTGT	ATGGAAAATG	TGCGAAAAAC	CTTGCGCGGA	ATGGGAAAAC	250
GACAATTGCT	ATTCAGCTGT	ACTCTCGCCG	GATAAAAAAA	TGCACGGATT	300
ACTTGTTAAA	AAGAACCATG	AATATGAAAT	CAACCATGTT	GATGTAGCAT	350
30 TTTGAGCTTT	GCATGGCAAG	TCAGGTGAAG	ATGGATCCAT	ACAAGGTCTG	400
TTTGAATTGT	CCGGTATCCC	TTTTGTAGGC	TGCGATATTC	AAAGCTCAGC	450
AATTTGTATG	GACAAATCGT	TGACATACAT	CGTTGCGAAA	AATGCTGGGA	500
TAGCTACTCC	CGCCTTTTGG	GTTATTAATA	AAGATGATAG	GCCGGTGGCA	550
GCTACGTTTA	CCTATCCTGT	TTTTGTTAAG	CCGGCGCGTT	CAGGCTCATC	600
35 CTTGCGGTGTG	AAAAAAGTCA	ATAGCGCGGA	CGAATTGGAC	TACGCAATTG	650
AATCGGCAAG	ACAATATGAC	AGCAAAATCT	TAATTGAGCA	GGCTGTTTCG	700
GGCTGTGAGG	TCGGTTGTGC	GGTATTGGGA	AACAGTGCCG	CGTTAGCTGT	750
TGGCGAGGTG	GACCAAATCA	GGCTGCAGTA	CGGAATCTTT	CGTATTCATC	800
AGGAAGTCGA	GCCGGAAAAA	GGCTCTGAAA	ACGCAGTTAT	AACCGTTCCC	850
40 GCAGACCTTT	CAGCAGAGGA	GCGAGGACGG	ATACAGGAAA	CGGCAAAAAA	900
AATATATAAA	GCGCTCGGCT	GTAGAGGTCT	AGCCCGTGTG	GATATGTTTT	950
TACAAGATAA	CGGCCGCATT	GTAAGTGAACG	AAGTCAATAC	TCTGCCCCGGT	1000
TTCACGTCAT	ACAGTCGTTA	TCCCCGTATG	ATGGCCGCTG	CAGGTATTGC	1050
ACTTCCCGAA	CTGATTGACC	GCTTGATCGT	ATTAGCGTTA	AAGGGGTGAT	1100
45 AAGCATGGAA	ATAGGATTTA	CTTTTTTTAGA	TGAAATAGTA	CACGGTGTTC	1150
GTTGGGACGC	TAAATATGCC	ACTTGGGATA	ATTTACCGG	AAAACCGGTT	1200
GACGGTTATG	AAGTAAATCG	CATTGTAGGG	ACATACGAAT	T	1241

50

2) INFORMATION FOR SEQ ID NO: 1050

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1249 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
10	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
15	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
20	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCC	CAGACCTTTC	AGCAGAGGAG	900
25	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
30	TTTTTTAGAT	GAAATAGTAC	ACGGTGTTTC	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCG	1249

35 2) INFORMATION FOR SEQ ID NO: 1051

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051

50	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAAACCA	TTAAAAACTG	50
	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	100
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	150
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	200
55	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	GCGAAAAACC	TTGCGCGGAA	250
	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCGG	ATAAAAAAAT	300
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	350
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	400
	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	450
60	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	500

	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	550
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	600
	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	650
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	700
5	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	GTATTGGGAA	ACAGTGCCGC	750
	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	800
	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	GCTCTGAAAA	CGCAGTTATA	850
	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	900
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCGTGTGG	950
10	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1000
	CTGCCCCGGT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1050
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1100
	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	TTTTTTTAGAT	GAAATAGTAC	1150
	ACGGTGTTTCG	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1200
15	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAATT	1250
	GGCTTGAATC	GCTTTTTTGAA	GG			1272

20 2) INFORMATION FOR SEQ ID NO: 1052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052

35	TCCCCCGGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGAATTTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
40	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
45	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
50	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
55	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCCGGT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTTAGAT	GAAATAGTAC	ACGGTGTTTCG	TTGGGACGCT	AAATATGCCA	1200
60	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTA		1237